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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and
uses thereof.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such
 5 polynucleotides, along with uses for these polynucleotides and proteins, for example in
 therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as
 10 lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past
 decade. The now routine hybridization cloning and expression cloning techniques clone novel
 polynucleotides "directly" in the sense that they rely on information directly related to the
 discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of
 hybridization cloning; activity of the protein in the case of expression cloning). More recent
 15 "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences
 based on the presence of a now well-recognized secretory leader sequence motif, as well as
 various PCR-based or low stringency hybridization-based cloning techniques, have advanced the
 state of the art by making available large numbers of DNA/amino acid sequences for proteins
 that are known to have biological activity, for example, by virtue of their secreted nature in the
 20 case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based
 techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for
 example, diagnostics, forensics, gene mapping; identification of mutations responsible for
 genetic disorders or other traits, to assess biodiversity, and to produce many other types of data
 25 and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel
 isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules,
 30 cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic
 variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more
 epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression
 vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such
 35 polynucleotides and cells genetically engineered to express such polynucleotides.

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The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-6180. The polypeptides sequences are designated SEQ ID NO: 6181-12360. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-6180 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-6180. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-6180 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-6180. The sequence information can be a segment of any one of SEQ ID NO: 1-6180 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-6180.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

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full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-6180 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-6180 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-6180; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-6180; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-6180. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-6180; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NO: 6181-12360); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-6180; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

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The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

5 The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the
10 protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA
15 or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as
20 expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide
25 of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition
30 which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein
35 expression or biological activity.

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The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides

5 a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the

10 invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal

15 antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate

20 (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a

25 compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound that binds to a polypeptide of the invention is

30 identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that

35 modulate the overall activity of the target gene products. Compounds and other substances can

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effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and
5 polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic
15 and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the
20 natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of
25 polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of
30 complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady
35 and continuous source of germ cells for the production of gametes. The term "primordial germ

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cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells
 5 not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked
 10 sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or
 15 "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T
 20 (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising
 25 regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and
 30 most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30
 35 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

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be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-6180.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-6180. The sequence information can be a segment of any one of SEQ ID NO: 1-6180 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-6180. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1+4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

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The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding
5 sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of
10 differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino
15 acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient
20 length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full
25 length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been
30 produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

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The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur
5 in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing
10 the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon
15 substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain
20 affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic
25 nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or
30 "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or
35 non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

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can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

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in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et al. (1998) Annu. Rev. Immunol. 16:27-55).

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

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In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

- 5 As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about
- 10 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a
- 15 listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid
- 20 sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide
- 25 sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99%
- 30 sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J.

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(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

5 The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

10 As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated
15 with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

20

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-6180; a polynucleotide encoding any one of the peptide
25 sequences of SEQ ID NO: 6181-12360; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 6181-12360. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-6180; (b) nucleotide sequences encoding any one of
30 the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 6181-12360. Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in
35 receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

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domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

5 The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

10 The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that
15 corresponds to any of the polynucleotides of SEQ ID NO: 1-6180 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-6180 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-6180 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

20 The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

25 The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at
30 least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-6180, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most
35 preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that

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are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-6180, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-6180 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-6180 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J. Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

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acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

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of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-6180, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-6180 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-6180 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

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known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example.

Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia).

5 Eukaryotic: pWLneo, pSV2cat, pOG44, PX11, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many
10 suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed
15 (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine
20 kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct
25 transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the
30 periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination
35 signals in operable reading phase with a functional promoter. The vector will comprise one or

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more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-6180, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

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NO: 6181-12360 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-6180 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-6180), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxycarboxymethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methyl ester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

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antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5 The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of
10 an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified
15 such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the
20 control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The
25 antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

30 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit
35 translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

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designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-6180). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

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combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-1124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

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recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

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cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

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sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultschi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 6181-12360 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-6180 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-6180 or

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A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., *Scopes, Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

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retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 6181-12360.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

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methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

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The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

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another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*.

The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

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example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked
5 in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal
10 activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example,
15 Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or
20 artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease
25 states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be
30 inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

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the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

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added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the

5 property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial

10 xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

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4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or

20 inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be

25 prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT

30 Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even

35 replacing the homologous promoter to provide for increased protein expression. The homologous

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promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

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polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides

(including recombinant DNA molecules, cloned genes and degenerate variants thereof) or

polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or

indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic

disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making

oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as

an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

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The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

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confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTL.L2, TF-1, Mo7c, CMK,

5 HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in
10 Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation,
15 Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells
20 include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse
25 and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin
30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in
35 Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

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sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci., U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

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- Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

- 20 A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of
- 25 artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

- A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of
- 30 bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

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Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular

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endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or
5 regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

10 Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

15 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

20 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including
25 severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be
30 treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention
35 include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus,

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rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic

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composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnoli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

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- Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. a. Coligan eds. Vol 1 5 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. 10 M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by 15 dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of 20 Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 25 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

- Assays for proteins that influence early steps of T-cell commitment and development 30 include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

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Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 5 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

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4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

- 25 Therapeutic compositions of the invention can be used in the following:
Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

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4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention

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may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

5 Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic
10 cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps
15 associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central
20 nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be
25 administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, *e.g.* reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

30 The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination
35 with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide,

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Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide,

5 Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguanzone, Pentostatin,

10 Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically

15 effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21),

20 tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al.,

25 Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor,

30 receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins,

35 integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen

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recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such

transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding

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molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

5 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used
10 to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention.
15 Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the
20 polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

25 The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating
30 the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

4.10.16 LEUKEMIAS

4.10.17 NERVOUS SYSTEM DISORDERS

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disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or

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differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- 5 (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or

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elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain
5 reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen
10 in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such
15 polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a
20 polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally
25 involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a
30 single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the
35 present invention can be used to detect polymorphisms. The array can comprise modified

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nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*, by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holosnitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of

administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

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The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (*e.g.*, at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic

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factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

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4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

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Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

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The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

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4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be

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manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen.

When a therapeutically effective amount of protein or other active ingredient of the present

- 5 invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or
- 10 other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol.
- 15 When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or

- 20 other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the
- 25 present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions,
- 30 preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

- For oral administration, the compounds can be formulated readily by combining the
- 35 active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers

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enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding
5 suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents
10 may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be
15 added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as
20 lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of
25 tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*,
dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or
30 other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for
35 injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

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known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent.

5 Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

10 The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically
15 acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

20 The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following
25 presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as
30 well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as
35 micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable

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lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated
5 herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active
10 ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the
15 various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition
20 topically, systemically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other
25 active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or
30 cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the
35 compositions will define the appropriate formulation. Potential matrices for the compositions

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may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential

5 matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and

10 biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

15 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

20 poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the

25 protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and

30 insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue

35 regeneration will be determined by the attending physician considering various factors which

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modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the

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population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the

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invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 6181), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of a related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte

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Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the

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target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

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5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,

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California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin

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polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

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antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983, Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

5 In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon
10 challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (*Bio/Technology* 10, 779-783 (1992)); Lonberg et al. (*Nature* 368 856-859 (1994)); Morrison (*Nature* 368, 812-13 (1994)); Fishwild et al. (*Nature Biotechnology* 14, 845-51 (1996)); Neuberger (*Nature Biotechnology* 14, 826 (1996)); and
15 Lonberg and Huszar (*Intern. Rev. Immunol.* 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The
20 endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate
25 transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a
30 polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

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An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotype to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)2} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)2} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the

binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunacker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to

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stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular

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defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest
5 binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies
10 have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond.
15 Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimide and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as
20 to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992)
25 and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

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5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a
35 radioconjugate).

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Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon

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a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

5 A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer
10 readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded
15 thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-6180 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-6180 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly
20 available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments
25 and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present
30 invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and
35 software means for supporting and implementing a search means. As used herein, "data storage

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means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see

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Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard,

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T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the

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invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-6180, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the

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invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

5 The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kasieczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems.

Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-6180. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-6180 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or
5 predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for
10 example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be
15 achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin
20 interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies
25 (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. Covalink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. Covalink Modules may be
30 purchased from Nunc Laboratories. DNA molecules may be bound to Covalink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of Covalink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed

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(Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

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One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of

this enzyme (*CviJI***), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus

5 M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5

10 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed)

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled

15 quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an

20 array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same

25 gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

30 Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic

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strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

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The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-6180 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-6180) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 1-6180. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-6180 were obtained by a BLASTX version 2.0a1 19MP-WashU search against Genpept release 121 and Geneseq release 200101 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-6180. The nearest neighbor results for SEQ ID NO: 1-6180 are shown in Table 2.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 4 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

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Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 5 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain

5 within the sequence.

Tables 1-5 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-6180. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homolog with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3

10 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO: in USSN 09/519,705.

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TABLE 1

5

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	2 4 17 75 137 426 501 817 939 1070 1111 1119 1167 1429 1538 1597 1670 1765 1780 1842 1862 1906 1920 2029 2122 2421 2650 2683 2697-2698 2731 2746 2879 2900 2926 3065 3119 3134 3136 3184 3199 3277 3312 3316 3325 3358 3368 3380 3388 3402 3405 3409 3448 3614 3691 3705 3712 3744 3746 3844 3931 3936 3940 3943 3960 4134 4149 4152 4159 4205 4209 4244 4308 4366 4377-4379 4497 4533 4537 4539 4548 4608-4609 4612 4656 4681 4688 4703 4784 4809 4830 4862 5011 5025 5032 5045 5069 5225 5230 5246 5254-5255 5266 5269 5275 5280 5282 5288 5292 5295 5305 5326 5328 5356- 5357 5364 5379 5398 5401-5403 5408-5409 5422 5429 5433 5435 5443 5458 5484-5486 5490 5499-5500 5512- 5513 5519 5525 5527 5530 5532-5533 5538-5539 5542 5548 5553 5555-5556 5560 5563 5567 5573 5580-5581 5588 5591 5594 5596 5598 5602 5611 5620 5624 5638 5645 5651 5680 5710 5717 5720 5726 5729 5734 5738 5745 5761 5774 5810 5848 5866 5884 5961-5962 5966- 5967 5974 6038 6111 6142
adult brain	GIBCO	ABD003	2 4 9 17 75 127 176 264 293 365 426 501 540 636 650 682 713 772 775 790 798 800-801 817 929 934 939 1010 1113 1129 1138 1141 1144 1347 1404 1421 1527 1574 1579 1604 1609 1627 1631 1640 1642 1644-1645 1673 1676 1770 1780-1781 1825 1829 1900 1955 2007 2030 2050 2089 2421 2437 2464 2477 2498 2544 2558 2583 2599 2650 2679 2683 2692 2696 2705-2706 2712 2722 2726 2733 2755 2804 2860 2904 2913 2926 2951 2979 3023 3036 3050 3061-3062 3065 3092 3134 3136 3140 3144 3148 3161 3163 3189 3197 3199 3203 3209 3251 3272 3287 3307 3324 3332 3334 3357-3358 3361 3365 3368 3388 3390 3392 3402-3403 3409 3412 3416-3417 3440 3448 3483 3592 3595 3609 3614-3616 3618 3680 3691 3702 3704 3714 3723 3726-3727 3744 3746-3747 3763 3822 3844 3868 3904 3919 3940 3943 3945 3960 3962 3964 3968 3971 3995 3997 4002 4036 4066 4121 4142 4149 4152 4159 4166 4173 4180 4182 4184-4185 4192 4195 4197-4198 4200 4206 4209 4217 4220 4224 4229- 4230 4236 4245 4247 4298 4366 4377-4378 4394 4406 4409 4440 4486 4488 4499-4500 4503-4504 4533 4537- 4539 4545-4546 4548 4553-4554 4575 4591 4601 4609 4612 4656 4671 4673 4678 4689 4784 4788 4830-4833 4881 4883-4884 4902 4935 4956 4964 4983 5013 5032 5038 5042 5062 5066 5135 5159 5165 5168 5172 5183 5194 5224-5225 5229 5231 5234-5235 5240-5241 5245- 5246 5251 5254-5255 5257 5260 5266 5272 5275 5281- 5282 5290 5305 5307 5312 5319 5326 5328 5334 5348 5364 5367 5370 5379 5394 5396 5398-5399 5402-5403 5405 5407-5409 5411 5413 5415 5422 5426 5429 5431 5436 5438 5443 5445 5453-5454 5480 5482-5486 5489- 5491 5493-5499 5501 5506 5512 5515 5517 5519 5524- 5526 5530 5532-5535 5538-5539 5541 5547-5549 5553- 5555 5557 5561 5567-5568 5570-5573 5580-5583 5585 5587-5589 5591 5594 5596 5598 5609 5612 5619-5620

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			5622 5624 5633 5636 5638 5645-5646 5657 5665 5672 5677 5680 5682 5687 5707 5710 5713 5716-5717 5719 5722-5723 5725 5729 5734 5736-5738 5741 5745-5746 5752 5756 5761-5763 5765 5767 5769-5770 5772-5774 5777-5778 5783 5848 5865-5866 5872 5880 5885 5895 5943 5945 5961 5965 5967 5970-5971 5974 5990 6002 6033 6038-6039 6051 6058 6062 6106 6111 6146 6157 6168 6176-6177
adult brain	Clontech	ABR001	4 163 532 618 713 780-781 937 1065 1128 1333 1347 1393 1395 1470 1641 1698 1861 1923 1970 2032 2124 2421 2486 2551 2600 2631 2651 2698 2739 2782 2823 2835 2849 3036 3063 3080 3117 3184 3186 3199 3312 3365 3380 3390 3392 3409 3440 3448 3634 3686 3756 3771 3904 3943 3998 4027 4172 4188 4192 4266 4366 4397 4514 4543 4553 4632 4673 4876 4976 5013 5173 5179 5231 5266 5319 5326 5328 5367 5371 5407 5415 5452 5465 5484 5486-5487 5494 5511 5515 5519 5538-5539 5556 5561 5587 5597 5610 5612 5667 5693 5698 5725 5737 5808 5847-5848 5939 6033 6042 6065
adult brain	Clontech	ABR006	9 338 622 631 690 713-714 760 785 814 858-861 955 1020 1037 1061 1124 1261-1262 1525 1702 1786-1789 1825 1835 1847 1877 1976 2043 2089 2092 2414 2421 2423 2437 2439 2601 2716 2721 2725 2728 2736 2739 2759 2856-2857 2900 2904 2999 3050 3073 3129 3163 3258 3307 3316 3327 3359 3373 3385 3401 3519 3614 3705 3726 3729 3837 3905 3920 3946 3966 4161 41874197 4214-4215 4304 4314 4409 4445 4490 4495 4533 4545 4548 4832 4860 4862 4873 4940 5056 5062 5141 5159 5172 5174 5220 5223 5236 5239 5241 5249 5288 5326 5328 5334 5399 5406-5407 5422 5429 5433 5443 5447 5454 5483-5484 5486 5489-5490 5498-5499 5506-5507 5534 5539 5542 5547-5548 5568 5581 5583 5588 5592- 5593 5619 5636 5639 5648 5660 5667 5669 5710 5716 5718 5726 5732 5744 5773 5775 5816 5835 5939 5972 6002 6042 6064 6093 6100 6109
adult brain	Clontech	ABR008	9 20 41 54-55 58-61 63-65 69 127 158 164 370 402 456 497 512 583 619-620 622-638 647 651 664-665 667-671 673-735 737-747 749 752-763 765-767 771 785 795 798 812 827-830 858 861 907 910-911 915 934 939 1020-1023 1025 1030 1032-1039 1041-1050 1052-1054 1056-1067 1069-1070 1072-1107 1110-1112 1119 1124 1129 1131 1176 1178-1179 1256 1262 1269 1333 1338 1393 1395 1443 1523-1532 1534-1536 1545 1549-1557 1559-1571 1573-1622 1624 1628 1637 1643 1645 1648 1659 1661 1667 1670 1676 1701-1705 1783 1786 1823 1829 1842 1847 1858 1872 1877 1892 1900 1922 1925 1946 1959 1967 1987 1997-1998 2006 2019 2024 2030 2033 2038 2074 2089 2098 2108 2110 2114 2402-2409 2411-2416 2418-2426 2436 2441-2442 2447-2465 2467-2468 2470- 2481 2483-2494 2496-2520 2522-2525 2527-2556 2558- 2594 2596-2613 2615-2628 2630-2643 2645-2656 2658- 2659 2661-2666 2668-2675 2683 2694-2695 2697-2698 2706 2708 2710 2712 2715 2722 2728-2729 2746-2767- 2772 2836 2839 2856 2865 2879 2904 2926 2979 2999 3021 3028 3116-3119 3122 3126-3132 3134-3150 3153- 3157 3164 3170 3177 3186 3199 3214-3217 3256 3283 3321 3328 3340 3357-3358 3364 3366-3372 3374-3383 3385-3389 3391-3393 3395-3396 3398 3409 3414-3415 3422 3446 3494 3509 3538 3565 3606 3621 3638 3671 3679-3688 3690-3704 3709 3715-3716 3744 3747 3753 3758-3759 3833 3868 3878 3887 3893 3914 3942-3943

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PCT/US01/04941

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			3959 3965 3967 3987-3989 3991-3992 4018 4035 4037 4040-4041 4050 4057-4058 4114 4118 4124-4128 4130- 4145 4147-4189 4192 4206 4209 4212 4217 4224-4225 4228 4237 4249 4258 4265-4267 4281 4308 4335 4378 4401-4403 4407 4409 4435 4439 4476-4482 4485-4486 4488 4490-4495 4497 4500-4514 4516 4518-4526 4529 4533 4539 4544-4545 4548 4550-4551 4553-4554 4558- 4560 4569-4570 4592 4605-4606 4612 4629 4647-4651 4656-4668 4671-4673 4684 4687 4693 4700-4701 4769 4790 4822-4829 4832 4836-4850 4852-4862 4867 4871 4873 4876 4880 4892 4894-4899 4944 4962 4977 4981 4985 4987 4992 5008 5016-5018 5022 5043 5045 5055 5062 5065-5066 5081 5131-5139 5141-5144 5146 5148- 5155 5163 5165-5168 5170 5172-5176 5178-5190 5192 5194-5213 5221-5225 5229-5230 5239 5242-5243 5245 5247-5251 5253 5261-5264 5266 5273 5281-5282 5285 5296 5310 5319 5328 5331 5334-5335 5354 5364 5367 5370-5371 5374 5377 5385 5387 5390 5398-5399 5402 5405-5406 5408-5409 5413 5415 5421-5422 5430-5434 5438 5443-5444 5448 5450 5454 5458 5461-5462 5465 5480-5503 5506-5507 5510-5553 5555-5564 5566-5569 5573 5581-5585 5588-5589 5591 5596 5610-5611 5613 5615 5619-5620 5622 5628-5631 5633 5636-5637 5642 5645 5649 5651 5660 5663 5669 5671 5673-5674 5678 5682 5687-5688 5691 5696 5698 5710-5717 5722-5729 5732-5748 5750 5754 5761-5762 5766 5770 5772-5774 5776 5778 5783 5787-5790 5802 5827 5835 5888 5910 5934-5935 5938-5957 5961 5964 5966 5970 5972 5974- 5975 5990 5993 6001 6008 6036 6038 6042-6043 6049 6051 6068-6069 6093 6096 6103 6106 6109 6116 6123 6141-6143 6146-6147 6149-6159 6161-6167 6169 6177
adult brain	Clontech	ABR011	694 798 1116 1597 1628 3277 3981 4202 4533 4545 4809 5168 5170 5328 5422 5486 5494 5609 5636 5710
adult brain	BioChain	ABR012	1628 1959 2104 2421 3179 3203 3844 4178 4206 4983 5230 5265 5328 5407 5481 5486 5532 5605 5636 5710 6111
adult brain	Invitrogen	ABR013	340 668 1566 1628 1668 2421 3199 3203 3392 3448 3951 4188 4500 4539 5056 5069 5224 5230 5239 5328 5402 5407 5511 5530 5539 5607 5659 5710 5724 5726 5972 6002
adult brain	Invitrogen	ABT004	4 34 75 164 365 460 468 501 637 685 713 727 782 798-799 803 805 931 959 1020 1116 1119 1125-1126 1133 1262 1574 1579 1628 1631 1640 1654 1659 1661 1668 1935 2019 2402 2421 2423 2457 2477 2642 2650-2651 2684- 2685 2694 2699 2717 2733 2737 2804 2879 2967 3036 3068 3116-3117 3122 3136 3146-3147 3163 3186 3189 3197 3287 3357 3375 3380 3392 3401 3404 3409 3452 3711 3716 3726 3758 3825 3955 3959 4045 4050 4057 4137 4174 4183 4192 4201-4202 4237 4258 4281 4377 4385-4386 4391 4422 4450 4486 4501 4504-4505 4513 4520 4545 4548 4608 4687 4790 4828 4832 4838 4888 4944 4977 5037 5050 5064 5138 5141 5179 5225 5229- 5230 5239 5241-5242 5247 5249 5251-5253 5260 5262- 5263 5266 5269 5290 5328 5367 5398 5402 5408 5415 5421 5430 5436 5443-5444 5452 5454 5480-5481 5483- 5484 5490 5492 5495-5498 5510 5513 5515 5529 5532 5534 5537-5540 5547-5550 5554 5556-5557 5561 5568 5573 5581 5583 5585 5591 5607 5612 5620 5636 5645 5665 5669 5671 5680 5686 5710 5717 5732 5736 5753 5762 5766 5770 5773 5775-5776 5782-5783 5939 5961

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
cultured preadipocytes	Stratagene	ADP001	5966 5970 5972 5974 5976 5990 6011 6026 6043 6068 6089 6168 176 311 316-317 340 497 734 785 803 811 813 894 1061 1113 1325 1347 1388 1531 1538 1575 1628 1661 1666- 1669 1676 1858 1878 1959 2074 2104 2110 2353 2405 2413 2437 2502 2566 2651 2672 2679 2683 2697 2743 2747 2762 2865 2948 2979 3122 3161 3195 3199 3251 3324 3358 3368 3375 3400 3417 3423 3448 3551 3585 3593 3613 3638 3704 3709 3733 3744 3762 3881 3893- 3894 3972 3994 4045 4152 4157 4161 4166 4198 4202 4206 4216 4233 4238 4240 4242 4308 4406 4419 4488 4533 4537-4538 4540 4553 4570 4656 4830-4831 4868 4873 4876 4884 4938 4969-4971 4983 5038 5064 5159 5173 5224 5230-5231 5235 5246 5250 5254-5255 5259- 5261 5280 5305 5312 5319 5323 5326 5328 5364-5365 5370 5374 5394-5395 5402 5405 5421 5429 5436-5438 5446 5449 5451-5452 5480 5485 5491 5493 5495 5530 5532 5541 5573 5575 5583 5585 5591 5594 5596 5603 5607 5611-5612 5616-5617 5620 5636-5637 5645 5684 5691 5713 5717 5720 5723 5753 5769 5845 5964 6032 6042-6043 6052 6111 6172 6178
adrenal gland	Clontech	ADR002	9 24 43 228 312 374 536 618 650-651 775 793-794 798 814 923 955 1136 1230 1385 1388 1426 1460 1543 1588 1604 1628 1636 1645 1659 1668 1780-1781 1826 1887 1935 1959 2011 2040 2061 2080-2081 2104 2122 2429 2464 2477 2529 2599 2668 2681 2683 2693 2712 2782 2800 2804 2829 2835 2849 2861 2907 2979 3011 3116 3119 3132 3134 3136 3171 3179 3199 3251 3259 3275 3283 3307 3316 3319 3340 3390 3402 3451-3452 3499 3586 3595 3609 3616 3643 3702 3705 3708-3709 3723 3729 3744 3759 3844 3927 3968 3971 4017 4039 4041 4102 4147-4148 4165 4200 4206 4209 4215 4217 4281 4293 4335 4366 4385 4391 4398 4403 4476 4514 4533 4548 4551 4554 4610 4612 4649 4654 4672-4673 4676 4678 4691 4725 4832 4844 4871-4873 4876 4881 4932 5009 5011 5021 5050 5057 5064 5078 5081 5135 5159 5230 5233 5246 5250 5254 5257 5260 5266 5272 5277 5285 5287 5310 5326 5328 5334 5337 5364-5365 5370 5394 5396-5397 5402 5407-5408 5413 5417 5422 5429 5432 5436 5438-5439 5443 5446 5454 5480 5483-5484 5493 5495 5497-5499 5502 5504 5510 5513 5515 5517 5532 5537 5542 5555 5572-5574 5580 5582 5585 5589 5610-5611 5620 5624 5638 5641 5650 5660 5664 5672 5681 5688 5691 5713 5715 5717 5741 5747 5762-5763 5769 5773 5775 5777 5823 5836 5857 5895 5965 5977 6008 6053 6069 6103 6157
adult heart	GIBCO	AHR001	2 9 12 17 20 66 75 137 176 264 406 410 426 433 460 532 540 650 771 775-776 782 792 798 801 817 922 944 957 1030 1046 1101 1111 1113 1128-1129 1139 1182 1211 1248 1278 1288 1388 1429 1468 1604 1627-1628 1631 1633-1634 1636 1645 1659 1662 1668 1676 1698 1706 1731 1755 1770 1780-1781 1809 1900 1916 1925 1930 1954-1955 1964 1970 1998 2011 2019 2025 2029 2038 2040 2052-2053 2074 2104 2110 2114 2122 2405 2413 2437 2529 2532 2599 2612 2675 2679 2681 2683 2692 2694 2697 2726 2730 2746 2762 2774-2775 2778 2781 2800 2804 2831 2848-2849 2866 2879 2900 2904 2913 2924 2926 2967 2979 2981 2999 3008 3023 3049-3050 3057 3062 3065 3072 3084 3119 3134 3136 3138 3140 3144 3146 3150 3154 3162 3166 3179 3184 3186 3188 3197 3199 3218 3230 3248 3251 3277 3328 3332 3334

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			3358 3361 3368 3372 3388 3390 3403 3412 3416-3417 3421 3423 3447-3448 3461 3538 3593 3614 3618 3634 3638 3698 3705 3710 3712 3714 3722-3723 3736 3744 3746 3756 3763 3792 3822-3823 3833 3844-3845 3894 3899 3919 3927 3940 3947 3955 3959-3960 3968 3981 3991 4018 4037 4039-4040 4043 4047-4048 4061 4117 4128 4142 4157 4165-4166 4173 4182 4189 4194-4195 4205-4206 4209 4212 4230 4242 4244 4251 4281 4350 4367 4386 4406 4413 4415 4435 4439 4447 4450 4486 4488 4497 4500-4501 4503 4506 4533 4538 4545 4548 4553-4554 4575-4576 4591 4596 4609 4612 4626 4648 4656 4658 4676 4678-4679 4684 4688 4703 4727 4784 4809 4827 4830-4832 4862-4864 4867 4873 4876 4881 4884 4888 4895 4900-4901 4935 4938 4956 4964 4983 4985 4997 5013 5032 5037-5038 5042 5047 5055 5062 5064 5066 5069 5135 5159 5165 5167-5168 5170 5176 5179 5213-5215 5218 5221 5224 5229-5232 5234-5235 5246 5250 5254-5255 5257 5260-5262 5264 5266 5270 5272 5279-5281 5288 5290 5296 5305 5310 5313 5323 5326 5328 5330 5334-5335 5356 5362 5364-5365 5370- 5371 5374 5377 5383 5392 5395-5397 5399 5402 5405 5407 5411 5413 5415 5417 5419 5421-5422 5426 5429- 5432 5436-5438 5443-5445 5447 5449-5450 5453-5454 5462 5481 5483 5485-5486 5489 5492-5499 5501 5504 5512-5513 5515-5517 5520 5527-5530-5532 5534 5537 5541 5543-5545 5550-5551 5553-5555 5560 5563 5567- 5568 5570-5575 5578 5580-5583 5585 5587-5589 5591 5594 5596 5598 5601 5603 5605 5607 5609-5611 5614 5617 5620 5624 5633 5636 5638 5643 5645 5656-5657 5660 5665 5674 5680-5682 5685 5687 5689 5691-5692 5713 5715-5717 5719-5720 5723-5724 5727 5738 5748 5752 5754-5756 5761-5762 5765-5767 5769-5770 5772- 5774 5777 5823 5854 5870 5884 5899 5934 5938 5942- 5943 5961-5962 5974 5981 5990 6008 6010 6033 6038 6040 6047 6051-6053 6057 6068 6079-6080 6086-6087 6093 6109 6111 6142 6144 6146 6148 6165-6166 6168- 6169 6172
adult kidney	GIBCO	AKD001	9 17 69 164 176 340 417 426 444 462 497 501 521 683 685 713 734 740 742 775 783 798 800 805 817 897 914 922 934 936 943 958-959 1010 1030 1111 1114 1116 1126 1128 1138 1183-1184 1188 1347 1388 1438 1525 1538 1543 1604 1628 1631-1632 1634 1636 1644-1645 1659 1668 1676 1752 1767 1770 1779-1781 1792 1829 1887 1900 1916 1925 1946 1959 1980 1985 1987 2019 2038 2040-2041 2043 2078 2089 2118-2119 2122 2402 2413 2437 2440 2445 2464 2513 2523 2558 2602 2638 2642 2651 2657 2672 2678 2681 2683 2690 2693-2694 2697- 2698 2704 2706 2726 2729-2731 2742 2745-2746 2762 2772 2777 2782 2797 2804 2849 2864 2878-2879 2889 2907 2913 2926 2979 2981 2998-2999 3004 3014 3023 3034 3036 3061-3062 3065 3079 3084 3116-3117 3119 3122 3130 3132 3134 3136 3140 3146 3150 3154 3161- 3162 3169 3171-3172 3181 3186-3187 3189 3191 3196 3199 3251 3255 3259 3277 3283 3287 3291 3304 3307 3311-3312 3317 3324-3325 3333-3334 3340 3357-3358 3361 3363 3365-3366 3368 3375 3388 3390 3400 3402 3404-3405 3409 3412 3414 3416-3417 3419 3421 3440 3448 3451 3467 3563 3593 3595 3611 3613-3615 3634 3638 3689 3691 3705 3710-3711 3714 3726 3729 3733 3744 3746 3756 3759 3761 3763 3788 3823 3833 3844 3861 3878 3887 3899 3904-3905 3907 3919-3921 3925

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PCT/US01/04941

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			<p>3928 3933-3934 3936 3940 3943-3946 3951 3959-3960</p> <p>3968 3972 3974 3976 3979 3981 3987 3992 4011 4013</p> <p>4017-4018 4036-4037 4039 4041 4056 4059 4061 4117</p> <p>4134 4139 4147 4149 4152 4165-4166 4173 4184 4189-</p> <p>4190 4192-4195 4197-4198 4202 4206-4207 4209 4211-</p> <p>4212 4215 4217-4218 4227-4228 4230-4233 4237 4241</p> <p>4243-4244 4248 4258 4263 4303-4304 4308 4318 4377-</p> <p>4378 4394 4403 4406-4407 4409-4410 4418 4422 4435</p> <p>4440 4449-4450 4482 4486 4488 4497 4500 4508 4533-</p> <p>4534 4536-4539 4545 4548 4553 4558 4575 4606 4609</p> <p>4623 4627 4630 4656 4673 4684 4757 4770 4784 4788</p> <p>4790 4809 4830-4832 4835 4863-4864 4868 4871 4882</p> <p>4884 4935 4938 4964 4977 4983 4991 4995 5020 5025</p> <p>5030 5037-5038 5041 5062 5064 5074 5135 5159 5165-</p> <p>5166 5168 5173-5175 5183 5194 5206 5213 5223-5226</p> <p>5229-5232 5238-5239 5242 5245-5246 5254-5255 5257</p> <p>5260-5263 5265-5266 5275 5277 5280 5288 5295 5305</p> <p>5310-5312 5317 5319 5323 5326 5328 5334-5335 5345</p> <p>5348 5354 5356 5359 5364-5365 5370-5371 5374 5390</p> <p>5392 5394-5397 5399-5400 5402-5403 5405 5407-5413</p> <p>5415 5417 5421-5422 5426 5429-5432 5434 5436-5439</p> <p>5443-5444 5446-5447 5450 5453-5454 5458 5480-5481</p> <p>5483-5485 5489 5492-5493 5496-5501 5504 5512-5513</p> <p>5515 5517 5520 5523 5525-5528 5530 5532 5534-5536</p> <p>5540-5542 5545 5547-5548 5551 5553-5557 5560-5561</p> <p>5563 5567-5573 5575 5578 5580-5582 5585 5587-5589</p> <p>5592-5594 5596-5599 5601-5603 5608-5612 5615-5618</p> <p>5620 5622 5624 5630 5636-5638 5642-5643 5645-5646</p> <p>5649 5651 5657 5659 5665 5667 5669 5671-5672 5674-</p> <p>5675 5677 5680-5682 5685 5687-5688 5691 5694 5696</p> <p>5698 5715-5717 5719-5721 5723-5724 5726 5729 5734</p> <p>5737-5738 5741 5744-5745 5748-5749 5753-5754 5756</p> <p>5761-5762 5764-5765 5767-5770 5772-5774 5776-5777</p> <p>5783 5836 5845 5848 5861-5862 5866 5869 5884 5895</p> <p>5942-5943 5960-5962 5964-5965 5974-5976 5979 5981</p> <p>5990 6002 6008 6012 6026 6038-6041 6047 6051-6053</p> <p>6057 6065 6069 6073 6085 6087 6095-6096 6100 6103-</p> <p>6104 6109 6111 6142 6146 6165-6166 6168 6172 6177</p>
adult kidney	Invitrogen	AKT002	<p>69 97 99 120 158 176 306 365 456 497 521 713 798 843</p> <p>909 940 955 1111 1144 1347 1388 1451 1574 1604 1635</p> <p>1645 1648 1667 1770 1780-1781 1792 1925 2043 2429</p> <p>2437 2558 2681 2683 2689 2745 2781-2782 2796-2798</p> <p>2849 2879 2900 2932 3014 3023 3062 3079-3080 3161</p> <p>3168 3190 3199 3283 3307 3319 3334 3339 3357 3359</p> <p>3368 3373 3397 3404 3420 3422-3423 3448 3563 3579</p> <p>3595 3638 3704 3712 3726 3743-3744 3762 3792 3868</p> <p>3887 3904 3919 3928 3943 3952 3992 4013 4018 4043</p> <p>4050 4062 4139 4159 4165-4166 4186 4195 4217 4227</p> <p>4231 4237 4308 4366 4418 4436 4445 4449-4450 4534</p> <p>4537-4538 4627 4670 4681 4683 4780 4832 4836 4873</p> <p>4881 4884 4964 5013 5030 5038 5047 5134 5141 5179</p> <p>5218 5224 5229-5231 5234 5246 5254 5258 5262 5266</p> <p>5280-5282 5300 5310 5312 5319 5323 5328 5356 5364</p> <p>5379 5383 5393 5402 5405 5409 5411 5413 5417 5430-</p> <p>5431 5436 5438 5450 5480 5484-5485 5489-5490 5497-</p> <p>5499 5512 5523 5530 5532 5534 5538 5541-5542 5551</p> <p>5555-5557 5560 5566-5567 5570-5571 5573 5580 5585</p> <p>5588 5592 5594 5596 5599-5601 5607 5611 5620 5624</p> <p>5636-5639 5643 5657 5659 5665 5672 5680 5682 5698</p> <p>5710 5719 5724 5745 5749 5753 5769 5772 5799 5836</p> <p>5895 5899 5965 6051-6052 6059 6065 6073 6098 6157</p>

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PCT/US01/04941

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
adult lung	GIBCO	ALG001	6168-6169 6175
			17 67 176 388 426 532 685 691 742 772 775 922 1111 1138 1187 1404 1648 1668 1676 1829 1900 1906 1959 2025 2032 2405 2437 2683 2697 2782 2791 2793 2849 2985 3008 3073 3116 3134 3136 3144 3179 3184 3197 3199 3307 3312 3319 3324 3339 3357-3358 3375 3388 3390 3402 3424 3440 3448 3469 3614 3691 3698 3705- 3706 3710 3726 3729 3744 3746 3759 3762-3763 3792 3823 3844 3878 3919 3960 3972 3976 3981 3989 4017 4036 4048 4118 4152 4157 4165 4191 4198 4233 4335 4407 4418 4422 4439 4486 4533 4536-4537 4545 4548 4553 4560 4575 4605 4608 4656 4671 4673 4679 4790 4827 4830 4864 4868 4873 4884 4935 4938 4983 5013 5032 5159 5213 5218 5224 5229-5231 5246 5266 5280- 5281 5305 5323 5328 5354 5364 5370 5377 5383 5399 5402-5403 5410 5415 5422 5429-5430 5436 5483-5484 5492-5493 5497-5499 5512 5515 5523 5530 5532-5533 5541 5551 5560 5568-5570 5573 5578 5580 5587 5594 5596 5602-5603 5606 5612 5614 5619 5631 5636 5638 5645 5657 5665 5672 5680-5681 5685 5719-5720 5738 5742-5743 5749 5754-5755 5760-5761 5767 5769 5771 5776 5974 5979 5990 6001 6010 6014 6047 6051 6073 6079 6106 6111 6146 6165-6166 6168
lymph node	Clontech	ALN001	68 176 775 1030 1113 1347 1388 1404 1574 1628 1668 1676 1780 1959 1964 2104 2429 2437 2583 2630 2683 2772 2782 2904 2970 2979 2999 3014 3136 3141 3161 3186 3199 3277 3324 3327 3334 3358 3364 3368 3400 3402 3409 3563 3638 3705 3723 3744 3762 3788 3844 3878 3919 4040 4120 4165-4166 4198 4206-4207 4217 4263 4281 4304 4406 4413 4436 4440 4533 4536 4609 4656 4780 4809 4830 4873 4884-4885 4983 5013 5037- 5038 5062 5159 5194 5213 5230 5246 5254 5270 5326 5328 5356 5359 5364 5370 5392-5393 5401 5403 5407- 5408 5415 5422 5427 5434 5438 5483 5493 5504 5512- 5513 5527 5530 5550 5577 5580 5594 5596 5607 5610 5620 5678 5680 5717 5721 5749 5764-5765 5773 5960 5974 5979 6053 6068 6110-6111 6151
young liver	GIBCO	ALV001	17 169 383 501 780-781 806 811 944 1095 1106 1111 1123 1359 1388 1431 1625 1628 1632 1634 1655 1659 1668 1673 1765 1767 1770 1780 1782 1858 1921 1947 2020 2041 2066 2084 2106 2110 2473 2602 2675 2678 2681 2683 2688 2690-2691 2694 2776 2782 2852 2860 2879 2913 2926 2981 2998 3050 3072 3132 3134 3136 3144- 3146 3171 3179 3186 3191 3196 3199 3287 3324 3333 3388 3440 3448 3593 3705-3706 3712 3744 3746 3756 3758 3845 3868 3921 3940 3960 3974 4039 4045 4061 4152 4159 4172-4173 4193 4216 4233 4244 4376 4403 4410 4450 4488 4497 4533 4535 4548 4553 4601 4612 4632 4658 4689 4797 4881-4882 4884 4956 4977 4983 5028 5036 5038 5047 5062 5069 5071 5190 5204 5213 5230-5231 5233 5236 5246 5251 5254 5256 5258 5260- 5261 5263 5305 5317 5326 5331 5358 5364 5372 5383 5394 5402 5405 5413 5422 5447 5450 5480 5483 5490 5493 5499 5506 5515 5517 5519 5523 5534 5537 5544 5549 5555 5563 5568 5571 5573 5575 5580 5587-5588 5590 5592 5594 5596 5602-5603 5609 5611 5618 5624 5649 5665 5682 5716 5729 5733 5738 5745 5748 5755 5757 5761 5767 5769 5772-5773 5836 5857 5869 5884 5974 5999 6012 6026 6049 6051 6064 6069 6096 6100 6106 6109 6165 6172

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
adult liver	Invitrogen	ALV002	169 311 318-323 365 501 636 685 716 780 806 929 936 958 1029 1112 1128 1138 1185-1186 1326-1329 1331- 1332 1359 1379 1393 1402 1535-1536 1543 1631 1640 1659 1667 1707 1765 1782 1796 1856-1860 1923 1941 1947 1973 1979 2018-2020 2030 2043 2058 2077 2080 2106 2464 2489 2523 2530 2537 2651 2672 2683 2688 2690 2694 2772 2777 2788 2823 2879 2889 2949-2952 2967 2998 3015 3021 3044 3063 3119 3136 3140 3146 3150 3161 3177 3199 3209 3298 3307 3316 3375 3388 3404 3448-3450 3483 3552 3588 3608 3615 3681 3698 3706 3730 3744 3758-3760 3882-3887 3934 3944 3955 3968 3992 4036 4039-4040 4042 4134 4165 4207 4241 4268 4361 4376-4377 4385-4386 4410 4435 4500 4534 4537 4552-4553 4570 4593-4594 4608 4688-4689 4743 4754-4755 4757 4830 4832-4833 4871 4902 4972 4974- 4975 5064 5066 5224 5230-5231 5233 5239 5246 5253- 5254 5290 5295 5302 5317 5319 5331 5364-5366 5371 5395 5402-5403 5405 5407 5412 5417 5426 5433 5438- 5439 5446-5447 5454 5458 5483 5485 5502 5506 5515 5519 5525 5527 5549 5555-5556 5561 5568 5570 5581 5585 5588 5591-5594 5596 5607 5615 5636 5649 5664- 5665 5677 5680 5696 5710 5715-5716 5724 5741 5757 5761 5763 5767 5772 5776 5846-5847 5885 5942 5976 5994-5995 6043 6049 6069 6079 6096 6107 6116 6172 6175
adult liver	Clontech	ALV003	1359 1668 2683 3245 3621 4676 4809 5027-5028 5038 5218 5230 5246 5317 5402 5499 5519 5577 6111
adult ovary	Invitrogen	AOV001	9 222 69-70 75 86 150 158 164 176 280 293 318 365 371 373 378 414 420-421 426 456-457 469 496 501 526 540 634 638 647 653 693 700 713 729 747 760 772 774-776 781-782 784-785 787 796 798-799 801 805-806 811 870 875 922 932 936 939 944 1010 1030 1043 1063 1111 1113- 1114 1116 1123 1128-1129 1134 1174 1211 1347 1387- 1388 1395 1404 1428 1449 1451 1525 1527 1538 1574 1579 1582 1604 1615 1627-1628 1631 1634-1638 1640 1659 1662 1667-1670 1676 1708 1731 1770 1780-1781 1792 1805 1809 1837 1858 1872 1887 1891 1898 1900 1905 1910 1913 1925 1935 1945 1952 1964 1966 1982 1984 1987 1997-1999 2007-2008 2011 2019 2040 2043 2049 2058 2074 2078 2080 2089 2096 2098 2103 2110 2402 2421 2429 2437 2486 2496 2499 2502 2530 2550 2558 2583 2620 2638 2642 2651 2658 2679 2681 2683 2685 2689 2692-2695 2697-2698 2705 2725 2731 2745- 2747 2762-2763 2772 2778-2779 2782-2783 2791 2793- 2794 2804 2836 2849 2879 2900 2907 2917 2926 2942- 2943 2966 2979 2981 2990 2996 3008 3019 3021 3028 3036 3045 3050 3062 3065 3068 3072 3079 3092-3093 3116-3117 3119 3130 3134 3136 3144-3146 3150 3156 3160-3161 3164 3166-3167 3169 3171-3172 3174-3175 3177 3179 3184 3191 3193 3195-3196 3199 3209 3220- 3222 3248 3251 3256 3277 3307 3316 3319 3324-3325 3328 3334 3345 3357 3358 3360 3363 3365 3368 3375 3377 3396-3397 3401-3402 3406-3407 3410 3412 3415- 3417 3421 3440 3448 3451-3452 3478 3483 3509 3537- 3538 3559 3563 3572 3577 3585 3593 3598 3607-3608 3614-3616 3618 3678 3680 3691 3704-3705 3708-3709 3711-3712 3714 3721-3723 3733 3744 3746-3747 3761- 3762 3767 3788 3822 3837 3844 3868 3878 3887-3888 3890 3899 3904-3905 3907 3919 3926 3934 3936 3938 3940 3942-3945 3949 3955-3956 3960 3962 3966-3967 3979 3981 3987 3990 3995 4013 4017-4018 4036 4040-

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PCT/US01/04941

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			4041 4048 4061 4117 4121 4128 4136-4137 4142 4146- 4149 4155 4157 4159 4165-4166 4172 4182-4184 4189 4192 4198 4202 4205-4207 4212-4213 4216-4217 4224 4229-4231 4233 4244-4245 4247 4249 4258-4259 4268- 4269 4298 4304 4335 4350 4363 4366 4377 4383 4386 4395-4396 4398 4406 4418-4419 4422 4435-4436 4440 4445 4449-4450 4486 4495 4497 4500 4503 4506 4508 4533 4536-4539 4545 4548 4551 4553 4591 4606 4608- 4609 4624 4632 4673 4677-4679 4684 4688 4705 4727 4747 4757 4769 4784 4788 4790 4809 4830-4832 4853 4864 4867-4868 4871 4873 4881 4883-4885 4900 4932 4938 4944 4956 4964 4977 4983 4985 5001-5002 5011 5013 5017 5020 5025 5030 5035-5038 5041 5064-5066 5078 5141 5159 5165-5167 5173-5174 5194 5206 5211 5213 5218 5221 5223-5225 5229-5231 5234-5237 5245- 5246 5249-5251 5253-5254 5258 5260 5262-5264 5266 5269 5272-5273 5275-5277 5280-5282 5288 5295-5296 5302 5305-5307 5310-5311 5313-5314 5319 5323-5324 5326 5328 5330-5331 5334 5345 5354 5356 5359 5364 5367 5370-5372 5374 5377 5379 5383 5385 5389 5392- 5396 5398-5399 5402 5405 5407-5408 5410 5415 5417 5421-5422 5426 5428-5429 5431 5433 5436-5439 5443- 5446 5448-5454 5458 5461 5463 5480-5481 5483 5485 5489 5492-5494 5496-5501 5504 5506-5507 5510 5512- 5513 5517 5520 5527-5528 5530 5532 5534-5536 5540 5542-5543 5548-5551 5553-5557 5560-5561 5563 5566- 5568 5570-5575 5580-5581 5583 5585-5586 5589 5592 5594-5598 5601-5603 5605 5607 5609-5612 5614 5616- 5617 5620 5622 5624 5630 5636-5639 5641-5643 5645- 5646 5649 5651 5656-5657 5665 5669 5671-5674 5677- 5682 5684-5687 5691-5692 5694 5696 5710 5712-5713 5716 5720-5721 5723-5725 5729 5734 5737-5738 5741 5745-5746 5752-5753 5757 5762-5770 5772-5778 5783 5792 5794 5804 5808 5810-5811 5823-5824 5834 5847 5857 5861 5865 5870 5872 5880 5884-5885 5890 5895- 5896 5899 5938 5942-5943 5948 5955 5958-5960 5962 5965 5967 5970 5974-5975 5981-5982 5990 5996 6000- 6001 6011-6012 6033 6038-6039 6047 6050-6053 6058 6065-6066 6069 6073 6079 6085 6091 6093 6098 6104 6106 6111 6116 6142 6152 6163 6165-6166 6168-6169 6172-6173 6175 6181
adult placenta	Clontech	APL001	29 445 1627 1970 1998 2025 2104 2402 3136 3154 3179 3327 3365 3396 3412 3448 3603 3922 4166 4203 4212 4533 4553-4554 4935 4964 5238 5328 5370 5402 5407 5421-5422 5430 5434 5436 5439 5443 5446 5463 5532- 5533 5541 5555 5633 5638 5649 5684 5761 5857-5858 5974 6026 6051 6083 6169
placenta	Invitrogen	APL002	417 456 497 501 782 798 934 1116 1640 1858 1916 2007 2018-2019 2030 2658 2707 2782 3014 3017 3117 3122 3130 3146 3189 3270 3325 3407 3422 3448 3538 3698 3718 3968 3977 4200 4203 4209 4445 4500 4504 4508 4537 4548 4560 4684 4757 4770 4809 4831 4835 4876 5037-5038 5063 5171 5218 5225 5231 5257 5277 5288 5290 5295-5296 5364 5398-5399 5405 5421 5429-5430 5432-5434 5443 5481 5491 5497 5506 5527-5528 5553- 5554 5563 5568 5575 5581-5583 5598 5600 5609 5612 5620 5633 5637 5669 5684 5691 5693 5724 5734 5746 5749 5759 5763 5773 5981 6011 6069 6079 6157
adult spleen	GIBCO	ASP001	9 17 75 176 311 774-775 794 811 834 951 1111 1248 1388 1451 1633 1636-1637 1659 1668 1673 1676 1731 1780- 1781 1842 1959 1979 2029 2050 2053 2402 2427 2429

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2437 2473 2502 2530 2631 2651 2658 2679 2681 2683 2685 2704 2728 2782 2913 2926 2979 3014 3050 3084 3117 3136 3146 3171 3186 3191 3199 3248 3287 3307 3324-3325 3358 3368 3400 3402 3448 3452 3494 3577 3595 3615 3618 3691 3704-3705 3739 3743-3744 3746 3762-3763 3899 3919 3931 3945 3960 3976 3981 4004 4012-4013 4036 4039-4040 4115 4117-4118 4152 4165- 4166 4172 4184 4192 4198 4205-4206 4209 4212 4217 4248 4304 4350 4394 4397 4418 4440 4447 4450 4486 4500 4533 4536-4538 4540 4545 4553-4554 4591 4671 4673-4674 4676 4757 4790 4830-4832 4835 4864 4873 4884 4888 4935 4938 4956 4977 4981 4983 5003 5022 5025 5037-5038 5042 5048 5062 5066 5173 5213 5218 5223-5225 5230-5231 5246 5254 5260-5261 5266 5295- 5296 5305 5313 5328 5334 5348 5357 5364 5370-5372 5374 5383 5385 5394 5398-5399 5402 5413 5417 5421 5426 5429 5431 5433 5436 5443-5444 5450 5454 5489 5492-5495 5497-5499 5515 5517 5525 5527 5530 5532 5544 5554 5557 5568 5570-5571 5573-5574 5578-5583 5585 5587 5589 5592 5594 5596 5602 5605 5608-5609 5619-5620 5624 5633 5637-5638 5645 5649 5656-5657 5660 5674 5680-5681 5685 5687 5691 5693-5694 5719- 5721 5724 5729 5738 5746 5753-5754 5762-5764 5768- 5769 5772 5939 5943 5965-5966 5974 5990 6042 6051 6053 6059 6085 6107 6109 6111 6142 6146 6168
testis	GIBCO	ATS001	9 17 20 176 370 457 540 773 934 939 1111 1128 1347 1404 1428-1429 1460 1538 1551 1633 1645 1655 1659 1662 1668 1676 1709 1780-1781 2437 2486 2558 2583 2675 2681 2683 2689 2694 2718 2731 2745 2864 2879 2913 2967 2979 3023 3044 3132 3136 3164 3196 3199 3248 3277 3308 3312 3319 3325 3334 3358 3375 3402 3422 3448 3451 3579 3609 3617 3691 3705 3709 3712 3746 3758 3762-3763 3788 3878 3899 3960 3972 4018 4025 4134 4165-4166 4185 4206-4207 4218 4233 4237 4440 4450 4488 4500 4506 4524 4533 4545 4548 4553 4575 4606 4609 4656 4672 4809 4830 4832 4868 4881 4884 5030 5032 5038 5068 5159 5166 5173 5218 5224 5230-5231 5246 5251 5254-5255 5260 5266 5280-5281 5312 5326 5328 5331 5346 5359 5364 5370-5371 5377 5383 5394-5395 5403 5407-5408 5415 5428 5434 5443 5454 5483 5486 5489 5493 5496 5499-5501 5506 5510 5512 5517 5520 5527 5530 5532 5542 5554 5556 5563 5567 5570-5571 5573-5575 5580-5582 5587 5594 5596 5602-5603 5611-5612 5620 5637 5641 5645 5657 5665 5669 5680 5687 5689 5692 5716 5720-5721 5736 5738 5756 5762-5763 5767 5772 5774 5796 5857 5885 5965 5974 5976 5979 5990 5996 6033 6039 6042 6051-6052 6062 6085 6111 6146 6166 6168 6172
Genomic DNA from BAC 63118	Research Genetics (CITB BAC Library)	BAC001	444 598 1003 1015 2136 2153 2156-2157 2162 2168 2171 2195 2211 2235 2247 2256 2259 2307 2319-2320 2335 2353 2356 2370 2378 2382 2384 2389 3356 3692 4091 4095 4111 4534 4812 5087 5099 5107 5468 5471-5472
Genomic DNA from BAC 39316	Research Genetics (CITB BAC Library)	BAC002	598 986 1000 1003 1008 1015 2153 2185 2188 2272 2291 2297 2302 2312 2327 2339 2384 3356 4106 4111 4635 4812 5099 5468 5471-5472 6127
Genomic DNA from	Research Genetics	BAC003	986 1015 2147 2153 2185 2199 2202-2203 2205 2232- 2233 2259 2261 2297 2316 2319 2335-2338 2360 2366

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PCT/US01/04941

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
bone marrow	Clontech	BMD002	6087 6103 6106-6108 6111 6146 6163 6165 6168 6175
			293 297-298 301-305 520 639-643 645 647 693 727 760 785 798 885-888 913 1026-1027 1037 1111 1128 1314- 1316 1318-1320 1322 1388 1442 1451 1537-1538 1540- 1541 1550-1551 1636 1668 1676 1766 1770 1780 1792 1805 1829 1843 1845-1849 1894 1898 1989 2011 2095 2102 2110 2380 2405 2422 2427-2435 2440 2484 2539 2571 2679 2683 2692 2720 2782 2879 2904-2905 2943- 2946 2982 3072 3081 3121 3136 3146 3171 3295-3296 3358-3362 3368 3402 3420 3448 3544-3547 3565 3649 3672 3675-3677 3682 3722 3726 3743-3744 3747 3833 3844 3871 3873-3874 3876-3877 3931 3969 4037 4040 4064 4115-4119 4142 4165 4173 4187 4198 4205-4206 4212 4350 4355-4357 4377 4418 4482-4483 4488 4536 4538 4545 4551 4592 4652 4672 4674 4676 4750 4790 4809 4830-4831 4864 4868 4873 4938 4960-4966 4969 4973 4983 5013 5038 5045 5062 5155-5159 5174 5211 5224-5225 5230 5235 5246 5254 5270 5277 5281 5319 5321 5364 5374 5390 5398 5402 5407-5408 5413 5422 5430 5433 5443 5454 5481 5485 5487 5489 5498 5501 5505 5513 5524 5530 5532 5534 5537 5554 5568 5571 5573 5576-5582 5596 5602 5617 5620 5636 5646 5649 5657 5659 5661-5662 5671 5680 5685 5687 5691 5693 5712 5719-5721 5727 5732 5738 5749 5774 5776 5843 5936 5981 6026 6035-6036 6042 6051 6144 6159 6168
bone marrow	Clontech	BMD004	1780 2032 2782 3976 4118 4205 4308 4440 4545 4674 4676 4873 4888 4985 5218 5246 5484 5577 5579 5585 5647 5713 6103
bone marrow	Clontech	BMD007	798 2782 3194 3448 3726 3743 3997 4115 4118 4440 4553 4674 4676 4828 4850 4900 4936-4937 4983 5042 5218 5257 5390 5530 5579 5647 5748
adult colon	Invitrogen	CLN001	636 910 1111 1604 1668 1913 1989 2019 2071 2428 2681 2683 2690 2698 2729 2951 3015 3079 3136 3147 3199 3277 3283 3357-3358 3373 3407 3477 3538 3744 3907 3942 3979 3998 4152 4165 4206 4215 4237 4241 4308 4335 4409 4548 4553 5038 5066 5132 5224 5236 5277 5295 5328 5346 5364 5390 5407 5409 5421 5439 5480 5513 5533 5536 5549 5563 5567 5596 5620 5633 5649 5657 5674-5675 5679 5682 5724-5725 5755 5763 5765 5776 5961 5972 6069 6079 6111 6168 6175
Mixture of 16 tissues - mRNAs*	Various Vendors*	CTL016	780 1111 1438 1449 1661 2106 3144 3199 3567 3710 3744 4376 4964 5224 5246 5296 5317 5429 5445-5446 5499 5535 5557 5606 5710 5965
Mixture of 16 tissues - mRNAs*	Various Vendors*	CTL021	775 1061 1111 1676 1780 1917 2421 2683 2782 2999 3358 3379 3452 3550 3888 3912 4118 4166 4210 4215 4609 4674 4676 4730 4983 5218 5230-5231 5246 5255 5315 5317 5328 5364 5446 5499 5502 5556 5645 5759 5776
adult cervix	BioChain	CVX001	34 73 75 134 176 280 307 318 365 439 469 532 540 798- 799 801 813 870 901 922 940 955 1057 1064 1113 1187 1302 1347 1388 1393 1395 1400 1435 1615 1628 1630 1633-1634 1636 1645 1656 1659 1666 1668 1676 1781 1898 1906 1957 1985 1999 2004 2007 2032 2061 2112 2122 2567 2609 2658 2678 2683 2692 2712 2730 2744 2760 2762 2780 2784 2791 2830 2835 2849 2862 2900 2904 2923 2925-2926 2944 2951 2963 2979 2985 2995 3008 3014 3017 3029 3034 3065 3072 3116 3118 3130 3144-3145 3166 3171-3172 3177 3179 3181 3184 3188 3190 3251 3271 3307 3319 3324 3327 3359 3375 3402 3404 3409-3410 3416 3422 3448 3452 3454 3559 3577 3614 3616 3618 3674 3682 3705 3721 3723 3726-3727

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			3736 3744 3746-3747 3756 3765 3767 3788 3792 3844 3878 3893 3904-3905 3907 3919 3932 3934 3938 3944- 3945 3951 3962 3981 3990 3998 4011 4018 4040 4042 4059 4139 4165-4166 4170 4174 4197-4199 4203 4206- 4207 4218 4233 4237 4244-4245 4264 4335 4350 4367 4378 4396 4400 4418 4422 4449-4450 4500 4533 4548 4553 4606 4609 4638 4656-4657 4670 4681 4713 4726 4759 4764 4788 4797 4809 4830 4874 4881 4884 4904- 4905 4938 4947 4982-4983 4991 5001 5008 5011 5017 5025 5037-5038 5062 5066 5069 5136 5165 5173 5188 5213 5231 5236 5246 5254 5260 5266 5269 5277 5280- 5281 5284-5285 5307 5311 5326 5328 5345-5346 5348 5356 5362 5364-5365 5372 5375 5377 5383 5385 5387 5389 5393-5394 5399 5402-5403 5405 5407 5411 5415 5417 5419 5421-5422 5429-5430 5432 5434 5437 5444 5446 5448-5449 5456 5481 5483 5493 5497-5500 5504 5513 5520 5525 5528 5532-5533 5535-5536 5538 5542 5547 5550 5553-5555 5557 5559-5561 5566-5568 5570- 5574 5580-5583 5585 5587 5594 5600 5603 5605 5607 5609-5610 5614 5620 5632 5638 5641 5643 5646 5660 5671 5677 5680-5681 5684-5686 5694 5716-5719 5721 5729 5733 5738 5741 5745 5749 5752 5756 5758-5759 5761-5763 5765 5767 5774 5776 5778 5818 5844 5884 5895 5938 5942-5943 5960-5962 5965-5966 5972 5974 5979 5998-5999 6001-6002 6033 6038-6039 6041 6047 6056 6058 6062 6068-6069 6073 6080 6083 6091 6093 6098 6101 6103 6111 6146 6168 6175
diaphragm	BioChain	DIA002	1628 1770 2683 3307 3416 4117 4244 4440 5225 5230 5489 5511-5512 5524 5544 5553 5596 5719
endothelial cells	Strategene	EDT001	9 20 69 75 176 365 426 444 460 501 627 685 709 734 760 774 776 792 798 801 806 811-812 814 834 910 936 939- 940 955 1010 1113-1114 1116 1123 1136-1139 1347 1364 1387-1388 1435 1519 1538 1543 1598 1604 1625 1628 1635 1638 1650 1659 1662 1667-1670 1676 1690 1754 1770 1780-1781 1783 1825 1829 1858 1898 1900 1906 1938 1943 1966 1970 1989 2007 2018 2030 2040 2058 2078-2079 2110 2405 2429 2437 2464 2502 2530 2558 2592 2658 2683 2690 2692-2694 2700 2704 2706 2712 2731 2744-2747 2762 2793-2794 2849 2879 2900 2913 2962 2979 2981 3023 3028 3036 3050 3072 3076 3084 3116-3117 3122 3136 3140 3144 3146 3161 3167 3171- 3172 3176-3177 3180 3186 3196-3199 3251 3277 3287 3307 3316-3317 3319 3324-3325 3332-3334 3357-3358 3365 3368 3375 3388 3390 3400 3402 3404 3411-3412 3414 3416-3417 3419-3424 3440 3448 3488 3538 3550 3563 3579 3592-3593 3613 3615 3638 3691 3698 3704- 3705 3710 3714 3723 3729 3744 3746 3756 3771 3822- 3823 3844-3845 3847 3868 3878 3887 3890-3891 3893- 3894 3907 3913 3925 3936 3942 3946 3964 3968 3979 3987 3989 3997 4008 4011-4013 4018 4040 4043 4047 4049 4061 4134-4135 4139 4147-4148 4158 4165-4166 4172-4173 4183-4184 4189-4190 4198 4200 4205 4207 4209 4220 4230 4233 4236-4237 4240-4248 4263 4308 4329 4335 4396 4406 4409 4418 4435 4439-4441 4450 4497 4500 4503 4508 4533 4537-4538 4545 4548-4549 4553 4560 4591 4609 4612 4632 4673 4681 4684 4695 4703 4705 4757 4780 4784 4788 4790 4809 4828 4830- 4832 4835-4836 4850 4873 4881-4882 4884-4885 4888 4896 4938 4956 4962 4969 4983 4995 5013 5025 5037- 5038 5064 5066 5069 5135 5141 5143 5159 5173 5211 5213 5228-5231 5234-5236 5246 5251 5254 5257-5259

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	554 556 559 561 564-568 570-573 583 587 589 598 604 610-611 615-616 964-970 972-976 978-980 983 986 988 991 996 1003 1010 1015 1476 1480 1484-1485 1487-1488 1490-1492 1494-1499 1501 1511 1513 1516-1517 1520- 1521 1825 2129 2132-2133 2135-2138 2142 2144-2146 2149-2153 2156-2157 2159 2161-2164 2167-2172 2174- 2181 2183-2208 2210-2211 2213-2215 2217-2227 2229- 2246 2250 2261 2270 2274 2276 2278 2281 2284 2286- 2287 2297 2303 2307 2316 2320 2322 2327 2334 2340 2352 2360 2367 2376 2378 2382 2384 2399 3097-3098 3100-3101 3104 3110-3111 3115 3349-3350 3352-3353 3356 3655-3662 3666 4068 4071-4074 4076-4081 4083- 4085 4089-4093 4097-4098 4102 4107-4111 4452-4453 4456 4460 4462-4463 4465 4467-4471 4631 4633-4638 4811 4817-4818 4821 5086-5093 5095-5097 5099-5100 5107-5108 5120 5125-5126 5128 5464-5469 5471-5473 5478 5700-5703 5705-5707 5709 5903 5905-5906 5908- 5916 5918 5921-5923 5925 5927 5929-5930 6113-6121 6123-6129 6132 6134-6137
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM003	550 575-576 578 580 582-583 585 588-592 598 604 610- 611 613-616 965 969 979 983 989-991 993-996 998-1011 1015 1500-1503 1505-1511 1513 1516-1517 1520-1521 1825 2133 2149 2153 2232 2247-2250 2252 2255-2259 2261-2265 2268-2272 2274-2279 2281-2283 2285-2307 2309-2314 2316-2317 2319-2325 2327-2329 2331-2332 2334-2346 2352 2370 2378 2384 2388 2399 3106-3109 3111-3112 3114-3115 3351-3353 3664 4068 4072 4075 4081 4089 4094-4099 4101-4102 4104 4107-4109 4111 4452-4453 4456 4463 4465 4467-4471 4634 4638 4640 4812-4815 4817-4819 4821 5099 5104-5105 5107-5108 5112 5115 5120-5125 5455 5468-5473 5478 5703-5707 5709 5903 5907 5913-5923 5925 5929-5931 5933 6115- 6116 6118 6122 6125 6129 6132 6134-6137 6140
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM004	578 583 585 587 589 593 596-600 602-605 609-611 613- 616 963-965 979 983 989 993 996 1003 1010 1012 1014- 1016 1476 1501 1507 1511 1513-1517 1519-1521 1825 2129 2133 2149 2153 2185 2204 2232 2272 2276-2277 2286 2311 2331 2339 2347-2350 2352-2353 2355-2360 2362-2364 2366-2376 2378 2380-2392 2394-2397 2399 3096 3100 3106 3111-3115 3350-3351 3353-3354 3356 3662-3663 3665-3667 3669-3670 4072 4075 4085 4100 4103-4112 4452-4453 4456 4463 4465-4469 4472 4474-

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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esophagus	BioChain	ESO002	1538 2666 3317 4983 5246 5580 5594 5609
fetal brain	Clontech	FBR001	733 1668 2040 2423 2706 3144 3368 3969 3995 4206 4500 4504 4530 5225 5254 5405 5407-5408 5422 5484 5537 5539 5567 5589 5607 5610 5617 6002 6068 6111
fetal brain	Clontech	FBR004	34 69 805 1542 2602 2682 2725 3163 3178 4185 4192 4504 4866 4873 5055 5079 5166 5180 5246 5254 5282 5388 5429 5482 5502 5568 5749 5816
fetal brain	Clontech	FBR006	9 20 61 409 456 627 629 647 649-661 663 696 713-714 733-734 744 767 770-771 794 798 805 827 858 1028-1031 1070 1090 1104 1107-1108 1116 1119 1123 1132 1141 1249 1313 1338 1394 1400 1536 1542 1544-1549 1575 1597 1608 1622-1625 1634 1642 1645 1659 1786 1829 1847 1878 1927 1946 2010 2019 2038 2074 2089 2098 2402 2409 2421 2429 2436-2439 2441-2447 2452 2461 2464 2467 2477-2478 2496 2508 2525 2537 2546 2560 2575 2579 2585 2593 2599 2602 2607-2608 2630-2631 2646 2675-2679 2689 2692 2706 2730 2746 2796 2836 2904 2913 2967 2979 3028 3075 3119 3122-3125 3135- 3136 3144 3146-3148 3158-3160 3186 3199 3259 3316 3324 3358 3363-3365 3368 3373 3375 3379 3387 3392 3396 3399 3409 3414 3417 3422 3448 3538 3592 3606 3616 3678 3686 3693 3726 3747 3823-3824 3868 3904 3928 3988 3991 4039 4061 4120-4124 4132 4143 4148- 4149 4152 4161 4163 4183-4184 4187 4202 4206 4209 4225 4236-4237 4241 4249 4397 4402 4422 4476 4482 4484-4489 4497 4510 4514 4539 4545 4548 4553 4558 4569 4592 4624 4629 4648-4649 4654-4658 4672 4676 4790 4826 4832-4836 4850 4859 4867 4873 4880 4892 4902 4985 5001 5021 5041 5047 5055 5062 5133 5136 5146-5147 5154-5155 5160-5180 5182 5186 5192 5194 5211 5213 5217 5222-5223 5225 5229-5230 5247 5251 5254 5263 5266 5290 5296 5312 5319 5331 5364 5370 5374 5377 5380 5398 5401-5402 5407-5409 5413 5415 5420 5422 5430 5432-5434 5436-5438 5443 5450 5461 5480 5482 5484-5485 5489-5491 5493 5495-5499 5501 5506-5513 5517 5525 5527 5530 5532-5535 5537 5541 5546 5550 5553-5555 5557 5560 5569-5570 5573 5581- 5583 5585 5588 5591-5592 5598 5603 5605 5607 5609 5615 5620 5622 5637 5642 5651 5656 5659 5671 5678 5680 5683 5687-5688 5696 5713 5716 5722-5723 5726- 5727 5732 5734-5735 5747 5749 5751 5761 5766 5769 5772-5773 5776 5790 5810 5835 5937 5943 5958 5961 5967 5972 5974 5990 6035-6036 6042 6051 6062 6067 6087 6093 6106 6141-6142 6145-6146 6169 6172
fetal brain	Clontech	FBRs03	365 1596 1780 2400 2437 2477 3136 3259 3424 3943 4185 4233 4683 5246 5275 5491 5525 5724 5749 5773
fetal brain	Invitrogen	FBT002	4 75 176 501 526 532 653 740 790 806 1116 1125 1129 1131 1138 1364 1536 1597 1628 1640 1645 1653 1668- 1670 1676 1781 1783 1792 1829 1858 1913 2040 2043 2423 2438 2502 2558 2650 2658 2682-2683 2701 2725 2733 2783 2879 3072 3117 3136 3146 3163-3164 3171 3184 3186 3189 3227 3311 3314 3325 3357-3358 3360 3365 3369 3372 3379 3400 3414 3440 3448 3452 3593 3615 3691 3722 3788 3940 3942 3968 3992 3998 4043 4136 4142 4166 4183 4185 4197 4202 4209 4217 4221

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal heart	Invitrogen	FHR001	3194 3400 4040 4115 4676 5230 5254 5489 5501 5974
fetal kidney	Clontech	FKD001	2 75 176 647 897 922 929 1388 1404 1634 1765 1780-1781 1959 2104 2429 2437 2671 2683 2907 3145 3189 3245 3259 3327 3358-3359 3402 3448 3478 3563 3638 3701 3721 3788 3844 3878 4145 4166 4198 4206 4310 4435 4500 4528 4538 4570 4651 4672 4727 4784 4830 4884 4974 4983 5027 5032 5037-5038 5159 5213 5230 5236 5246 5254 5265 5277 5290 5313 5319 5328 5348 5359 5362 5364 5367 5377 5415 5422 5429 5446 5449 5462 5481 5484 5498 5506 5512-5513 5520 5527 5530 5533 5542 5551 5567-5568 5571 5573 5582 5585 5587 5594- 5595 5600 5609-5610 5620 5674 5680 5682 5692 5752 5756 5766-5767 5771 5773-5775 5811 5943 5955 5962 5967 5972 5974 6026 6033 6042 6069 6073 6106 6111 6168
fetal kidney	Clontech	FKD002	1780 2683 2705 2710 3245 3762 3847 4193 4212 4440 4938 4983 5038 5167 5246 5422 5530 5620 5719
fetal kidney	Invitrogen	FKD007	75 1388 1543 3358 3448 4115 4166 4676 4938 4983 5038 5231 5260 5383 5484 5645 5756
fetal lung	Clontech	FLG001	501 1061 1092 1095 1538 1645 1676 1792 2018 2529 2683 2697 3036 3045 3079 3136 3172 3334 3756 3878 3969 4118 4146 4221 4281 4674 4730 4827 4884 4935 5038 5041 5064 5138 5254-5255 5260 5315 5370-5371 5438 5454 5458 5465 5480 5493 5495 5500 5521 5532 5537 5556-5557 5573 5610 5645 5647 5657 5729 5743 5752 5760 5762 5771 5783 6051 6073 6172 6176
fetal lung	Invitrogen	FLG003	67-68 526 719 738 775 806 1111 1131 1628 1668 1959 2218 2551 2683 2692 2698 2751 2793 2835 2940 2999 3021 3161 3199 3245 3251 3314 3358 3404 3409 3469 3708 3756 3919 3943 3979 3998 4017 4039-4040 4118 4152 4166 4227 4237 4440 4499 4676 4876 4882 5027 5164 5211 5218 5224 5231 5235 5238 5253-5254 5291 5295 5323 5335 5383 5385 5393 5396 5402 5417 5421 5429-5430 5432-5433 5437-5438 5443 5446 5454 5480 5483 5494-5495 5499 5540 5542 5550 5553 5567 5575 5578 5587 5594 5596 5603 5607 5624 5636-5637 5643 5646 5651 5669 5674 5698 5713 5720 5738 5743 5757 5760-5762 5771-5772 5938 5948 5990 6051 6103 6116 6169
fetal lung	Clontech	FLG004	333 2913 3762 5231 5328 5422 5741 5771
fetal liver-spleen	Columbia University	FLS001	3 68-69 75 97 127 158 160 162-167 169-180 182-192 236 260 343 359 369 371 380 385 404 416-417 426 444 457- 458 460-461 463 475 484 497-498 501-504 511-512 521 525 527 529 541 544 654 685 698 713 733 738 760 775 780-782 793-794 796 798-800 805 811-812 814 830 834 838 851-856 867 897 912 916 922 926 929 931 934 936 940 943-944 954-955 957 958 1029 1043 1053-1054 1065 1067 1112-1113 1116 1127-1129 1131 1138 1182 1186-

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal liver-spleen	Columbia University	FLS002	9 20 69 75 89 127 160 162 164 174 190 193-197 200-201 203-207 209 211-218 221-222 224 227-230 232-233 235- 239 241 243-245 247 250 252-261 263-266 281 293 318 340-353 355-360 362-367 369-374 376-381 383-394 399- 407 409-418 420-422 424-426 430-433 435-438 440-441 444-449 451-452 455-473 475-484 486-487 489-490 492- 493 495-515 517 519-527 529-548 585 685 709 716 742 746 771-772 780-781 785 798 803 811-812 834 856 862 864-871 874-875 886 897 902 904-912 914-916 918-920 922-937 939-947 949-950 952-962 1043 1056 1062 1113 1116 1120 1122-1123 1126-1128 1131 1230 1249 1255 1259 1263-1266 1269-1270 1273-1278 1280-1297 1299 1345-1357 1359-1362 1364 1366-1372 1375-1376 1378- 1383 1385 1387-1389 1391-1406 1408 1410-1431 1433- 1453 1455-1464 1466-1472 1521 1543 1551 1561 1582 1604 1613 1615 1623 1627 1632 1635 1642 1644-1645 1648-1649 1662 1665 1676 1693 1698 1765 1770 1780 1782 1790-1794 1796-1798 1803-1806 1809-1810 1814 1816-1818 1820-1821 1825 1847 1856 1858 1865 1872 1879-1883 1885-1888 1890-1892 1894 1896 1898 1900 1903-1911 1913-1916 1918-1928 1930-1935 1937 1939- 1941 1944-1946 1948-1950 1952-1965 1967-1977 1979- 1985 1987-1988 1990-1991 1993 1996-2002 2004-2007 2009-2015 2017-2020 2022 2024-2026 2029-2034 2037- 2043 2045-2054 2056-2059 2061-2085 2087-2100 2102- 2123 2422 2452 2461 2464 2499 2502 2506 2528 2530 2537 2539 2551 2571 2579 2672 2675 2678-2679 2686 2689 2692 2698 2721 2725 2731 2740 2742 2744-2746

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2754 2762 2771-2772 2776 2783 2793 2800 2823 2825 2845 2849 2861-2879 2881-2897 2900-2905 2907-2919 2967-2968 2970-2975 2977-2983 2985-2991 2993-2999 3001-3008 3010-3024 3026-3030 3032-3036 3038-3040 3042-3093 3116-3117 3121-3122 3128-3129 3136 3140- 3142 3145-3146 3150 3154 3169 3177 3179 3181 3186 3190-3191 3195-3196 3209-3210 3221-3222 3224 3247 3251 3253 3256 3259-3273 3275-3280 3282-3285 3287 3290 3304-3309 3311-3319 3321-3323 3325-3335 3337- 3344 3358 3361 3365 3368 3375 3380 3388 3390 3392 3397 3404-3407 3409 3412-3413 3416 3419-3420 3422 3436 3440 3459 3487 3495 3499-3503 3505-3523 3525 3527-3531 3538 3562 3572-3583 3585-3611 3613-3623 3626-3629 3631-3632 3634-3638 3640-3652 3681 3692 3698 3704 3706 3708 3710 3714 3717-3718 3722 3726 3729 3742 3746 3756 3758 3761-3762 3775 3780 3792 3831 3834 3838-3843 3845-3851 3853-3863 3868 3878 3896-3897 3902-3928 3930-3937 3939-3947 3949-3951 3953 3955-3957 3959-4019 4021-4031 4033-4050 4053- 4063 4134 4138-4139 4142 4147-4149 4159 4183 4192 4194-4195 4200 4203 4206 4208-4211 4216-4217 4229 4236 4241-4242 4245 4247 4253 4301 4308 4311 4315- 4320 4322-4323 4325-4343 4345-4346 4350 4363 4374- 4405 4407-4416 4418-4427 4429-4451 4476 4482 4485- 4486 4488 4500 4503 4506-4508 4514 4516 4536-4539 4545-4546 4551 4553 4568 4570 4580-4590 4601-4614 4616-4619 4621-4631 4656 4660-4661 4671 4674 4681 4688-4689 4705 4726 4731-4732 4735-4741 4743-4747 4764-4766 4769-4770 4773-4774 4776-4792 4794-4804 4806-4809 4818 4821 4828 4830-4831 4835-4836 4868 4872 4876 4881 4890 4938 4941-4948 4956 4964 4969 4981 4983 4985 4988-4994 4996 4998 5000-5003 5005- 5006 5008-5009 5011-5018 5021-5050 5052-5060 5062- 5067 5069-5073 5075-5078 5081-5082 5141 5154-5155 5159 5166 5168 5170 5181 5183 5212 5215 5219 5226 5230 5232-5234 5237 5250-5251 5254 5256 5266 5270 5272 5277 5280-5282 5287 5290 5294 5302 5305-5306 5310-5311 5313-5314 5316-5317 5320-5322 5324 5326 5328 5330-5339 5341-5349 5351-5354 5356 5365 5370- 5381 5383-5394 5396-5431 5433 5435 5438-5454 5456- 5463 5465 5480-5481 5483-5485 5491-5494 5497-5500 5506 5508 5510 5512 5514 5517 5519 5523 5525 5527- 5528 5530 5533-5534 5537-5538 5540 5542 5548 5550- 5551 5554-5557 5563 5566 5568 5570-5571 5573 5577 5580-5583 5585-5595 5601-5602 5605-5611 5614-5615 5620 5622 5633 5637-5638 5642 5649-5655 5660 5662 5665-5682 5684-5688 5691-5699 5712-5713 5715-5717 5719-5721 5723-5726 5732 5734 5738 5742 5744-5745 5747 5749 5754 5756 5761 5763-5766 5772-5777 5783 5789 5799 5802-5803 5811 5813 5817-5837 5844 5847 5855-5863 5865-5887 5889-5902 5916 5943 5945 5948- 5949 5962 5966-5967 5972 5974 5979 5981 5987 5999- 6000 6002 6008 6011 6013-6015 6017-6029 6043 6047 6049-6050 6052-6057 6059-6069 6071-6074 6076-6077 6079-6081 6083-6109 6111-6112 6146 6163 6165 6168 6172 6175 6177-6178 6181
fetal liver-spleen	Columbia University	FLS003	1359 1632 1668 1782 1921 1986 2106 2683 2688 4118 4209 4376 4545 4576 4676 4730 4983 5027 5218 5254 5261 5316 5446 5519 5594 5620 5765 6049 6100
fetal liver	Invitrogen	FLV001	34 61 69 164 169 500-501 512 637 783 798 910 934 958 1111 1131 1138 1359 1362 1364 1402 1427 1442 1536

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal liver	Clontech	FLV002	861 940 2104 3844 4445 5490 5499 5547 5553 5669
fetal liver	Clontech	FLV004	1359 1451 1632 1767 1986 2539 2904 3245 3847 4115 4118 4193 4376 4403 4538 4674 4727 4983 5028 5071 5224-5225 5230 5246 5261 5316-5317 5364 5422 5429 5447 5499 5513 5519 5553 5588 5592 5620 5715 5719 5970 5987 6064 6168
fetal muscle	Invitrogen	FMS001	10 20 60 69 340 469 473 501 532 742 798 801 1095 1336 1371 1388 1421 1449 1628 1668 1676 1780 1796 1805 1862 2019 2022 2043 2429 2460 2679 2698 2716 2745- 2746 2772 2774 2835 3117 3136 3144-3145 3177 3186 3191 3199 3250 3259 3277 3287 3312 3316 3404 3721 3744 3831 3925 3979 3998 4115 4117 4166 4197 4200 4202 4215 4242 4500 4533 4575 4610 4674 4678 4688 4884 4956 4977 5025 5181 5231 5246 5249 5254 5260 5311 5314 5328 5334 5364-5365 5367 5371 5405 5413 5421 5433 5436 5443 5446 5448 5454 5465 5481 5483 5485 5489 5491 5493-5494 5499 5502 5531 5544 5548 5550 5553 5568 5571-5572 5580-5581 5596 5607 5620 5636 5641 5645 5651 5665 5672 5691 5737 5741 5765 5970 5974 6093 6111 6163 6175
fetal muscle	Invitrogen	FMS002	2 798 1388 1668 2697 3199 3540 4538 5166 5230 5246 5260 5364 5422 5446 5495 5499 5580 5594 5645
fetal skin	Invitrogen	FSK001	5 17 20 22 34 75 109 120 122-123 134 164 176 439 456 458 501 638 641 649-650 685 713 760 775 785 794 798 800-801 838 901 922 958 1112-1113 1139 1211 1218 1265 1388 1451 1536 1575 1628 1637 1640-1641 1659 1668 1676 1725 1731 1780-1781 1792 1858 1872 1887 1899 1913 1925 1939 1959 1970 2007 2010-2011 2019 2022 2404 2437 2440 2460 2528-2529 2558 2591 2599 2642 2650 2657-2658 2678 2683 2696 2699 2705 2720 2735 2757 2772 2795 2800 2802 2804-2805 2808-2809 2813 2815-2816 2835 2860 2900 2913 2926 2951 2979 2998 3004 3036 3050 3117 3119 3122 3129-3130 3136 3146 3161 3166 3184 3191 3194 3197 3199 3227 3229-3230 3232 3245 3251 3311 3321 3324 3334 3358-3359 3364- 3366 3368 3373 3397 3402 3404 3409-3410 3416-3417 3424 3452 3471-3473 3476-3478 3563 3574 3593 3606- 3607 3691 3708-3709 3743-3744 3823 3828 3831 3868

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal skin	Invitrogen	FSK002	1650 1668 1690 1753 2537 2679 3714 4042 4503 5167 5194 5224-5225 5236 5319 5377 5397 5402 5421 5430 5433 5437 5480 5494 5519 5541 5570 5573 5578 5583 5585 5603 5619 5636 5649 5722 5972 6146 6168
fetal spleen	BioChain	FSP001	711 1648 2437 3245 3736 3744 4450 4969 4983 5038 5230 5246 5408 5504 5580 5592 5620 5716 5719
umbilical cord	BioChain	FUC001	2 75-76 127 134-135 137-138 141-145 148-156 158-161 164 176 307 358 378 445 636 685 740 742 771 781 785 811 848-850 910-911 922 1054 1057 1083 1137-1138 1211 1226 1229-1230 1232 1234-1237 1265 1278 1302 1388 1395 1575 1604 1625 1627 1668 1676 1753 1755-1756 1758-1763 1781 1805 1842 1878 1923 1959 1970 1987 2007 2030 2074 2104 2437 2638 2650 2675 2683 2692 2694 2725 2730 2762 2777 2781-2784 2819-2827 2829- 2838 2852 2857 2865 2879 2913 2923 2979 2999 3008 3034 3117-3118 3129 3136 3167 3184 3196-3197 3199 3223 3236-3237 3239-3242 3245 3248 3251 3277 3307 3316 3325 3327 3333 3358 3361 3365 3368 3402 3409 3413-3414 3416 3421 3448 3451 3459 3478 3483-3488 3494 3509 3572 3593 3607 3616 3635 3638 3691 3704 3709 3729 3743-3744 3756 3762 3775 3815 3820-3821 3824-3828 3844 3868 3877-3878 3902 3904 3922 3936 3943-3945 3947 3955 3979 3998 4006 4048 4115 4118 4134 4145 4149 4166 4173 4185 4189 4197-4198 4202 4207 4216 4228 4231 4233 4244 4247 4259 4271 4292- 4300 4310 4366 4386 4406 4418 4435 4445 4449 4488 4500-4501 4503 4533-4534 4537 4545 4571-4572 4576 4671 4676 4688 4691 4721 4728 4730 4788 4808 4830- 4831 4864 4868 4884 4890 4931-4933 4935-4937 4944 4956 4983-4984 5001 5003 5013 5027 5042 5056 5138 5166 5218 5224-5225 5230-5231 5238-5239 5246 5254 5260-5261 5265 5272 5280-5281 5287-5288 5291 5304- 5308 5310 5323 5328 5334-5335 5346 5356 5364-5365 5370 5374 5383 5385 5393 5395 5399 5402-5403 5405 5408 5410-5411 5413 5415 5417 5422 5429-5431 5433-

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			5434 5438-5439 5444 5446 5450 5452 5454 5458 5462 5480 5483 5485 5489-5490 5493 5498-5499 5501 5512- 5513 5515-5516 5524-5525 5532 5535 5542 5549 5551 5554 5557 5560 5567 5570-5571 5573-5574 5580 5582- 5583 5585 5587 5591 5594 5603 5605 5609-5610 5615- 5617 5620 5624 5636-5637 5641-5643 5645-5647 5671 5680 5684 5691 5696 5719-5721 5725 5727 5729 5738 5741 5746 5752-5753 5756 5759 5761-5763 5769 5772 5776 5792 5807-5809 5811 5815 5834 5845 5866 5870 5885 5895 5938 5974 5982 5990 5998 6002 6007-6012 6033 6039 6042 6047 6065 6073 6085 6087 6095 6106 6111 6146 6157 6166 6172
fetal brain	GIBCO	HFB001	2 4 12 17 20 34 75 127 176 365 374 426 456-457 468 532 627 631 713 727 760 772 781 798-799 801 803 805 834 897 922 934 944 955 1043 1070 1106 1111 1116 1119 1129 1131-1132 1144 1278 1347 1404 1460 1597 1628 1631 1634 1645 1650 1659 1667-1668 1676 1682 1731 1761 1770 1780-1781 1829 1887 1906 1913 1958-1959 1985 2004 2019 2029 2032 2110 2112 2405 2421 2429 2437 2464 2483 2499 2537 2558 2583 2650 2658 2679 2683 2695 2704 2706 2725-2726 2728 2730-2731 2733 2746 2784 2804 2821 2849 2900 2913 2926 2951 2979 2981 2985 3023 3045 3050 3062 3065 3070 3072 3079 3119 3134 3136 3144 3146 3150 3161 3163-3164 3166- 3167 3181 3186 3189 3197 3199 3265 3307 3316 3319 3324 3334 3357-3359 3366 3372 3375 3392 3402 3405 3409 3411 3413-3415 3419 3422-3423 3448 3451 3563 3592 3615 3634 3691 3693 3704-3705 3712 3714 3726 3729 3746 3759 3822 3844 3847 3853 3868 3878 3899 3904 3914 3928 3942-3943 3946 3951 3960 3962 3966 3972 3997-3998 4013 4018 4040-4042 4061 4118 4134 4137 4152 4165 4172-4173 4184-4185 4192 4202 4206 4217-4218 4220 4224 4229 4231 4236 4243-4245 4247 4249 4251 4366-4367 4378 4396 4406 4440 4445 4447 4486 4488 4497 4500 4503-4504 4533 4537-4538 4540 4545 4548-4549 4553 4560 4608 4612 4624 4648 4656 4658 4673 4679 4683 4688 4757 4788 4790 4809 4828 4830 4832 4835 4862 4864 4868 4873 4876 4878 4884 4938 4956 4983 5013 5025 5037-5038 5048 5062 5064 5132 5138 5143 5159 5165 5171 5175 5178 5180 5183 5187 5221 5223-5225 5229-5231 5235-5236 5238-5239 5242 5246-5247 5251 5254-5255 5259-5260 5262 5266 5277 5281-5282 5285 5292 5296 5301 5305-5306 5311 5326 5328 5345 5354 5356 5358 5364 5370-5372 5374 5377 5379 5385 5392 5394-5399 5402-5403 5405 5408 5413 5415 5417 5421 5426 5428-5430 5433-5434 5436- 5438 5443 5445 5452-5453 5458 5482-5486 5489-5496 5498-5499 5501 5504 5506-5507 5510 5512-5513 5516- 5518 5525 5527-5530 5532 5535 5537 5539 5541 5543- 5544 5547-5551 5553-5555 5557 5559-5560 5563 5566- 5568 5570-5573 5575 5580-5583 5585 5587-5589 5591 5594 5596 5603 5605 5608-5612 5614 5617 5619-5620 5622 5624 5637-5638 5645-5646 5651 5665 5669 5671- 5672 5674 5677 5680 5682 5689 5698 5710 5717 5721 5723-5726 5729 5734 5738 5741 5745-5746 5749 5752- 5755 5762-5763 5765 5769-5770 5773-5774 5777 5783 5811 5835 5884 5939 5942-5943 5945 5959-5962 5965 5967-5969 5972 5974 5990 6002 6032 6035 6038 6043 6051 6057 6059 6069 6079 6087 6097 6104 6106 6111 6146 6165 6168-6169 6175-6176 6181
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
infant brain	Columbia University	IB2002	5224 5254 5370 5402 5405 5524 5537 5568-5569 5580 5596 5649 5691 5974
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infant brain	Columbia University	IB2003	5 17 69 164 318 324 365 456 532 713 787 793-794 799-810 834 897 1063 1129-1134 1187 1333 1335 1473-1474 1536 1642 1645 1649 1651 1659-1663 1668 1670 1787 1796 1858 1862 1894 1925 2032 2045 2124-2127 2421 2423 2464 2515 2599 2634 2675 2679 2683 2697 2699 2707 2710 2717 2723-2733 2735 2750 2784 2804 2879 2900 2953 3136 3146-3147 3163 3172 3174-3175 3183-3190 3195 3199 3299-3300 3327 3345 3365 3407 3409-

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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infant brain	Columbia University	IBM002	566 787 805 811 1141 1658 1664 1668 1671 2534 2697 2703 2706 2728 2734-2736 2985 3146 3163 3184 3191 3319 3416 3448 3585 3928 4178 4191 4234 4363 4456 4537 4562 4606 4687 4862 4873 5050 5146 5167 5176 5190 5246 5282 5334 5372 5398 5496 5588 5667 5675 5753 5773 5776 5778 5959 5975 6136
infant brain	Columbia University	IBS001	3 69 798 805 812 834 868 1119 1131 1135 1645 1665 1770 1780 2043 2423 2683 2699 2711 2729 2737-2742 2793 3192-3194 3415 3722 3726 3968 4154 4235-4237 4249 4363 4545 4552-4554 4668 4680 4687 4689-4690 4710 4830 4841 4878 4880 4977 5037 5213 5241 5257-5258 5288 5328 5398 5454 5532 5541 5547 5553 5559 5583 5585-5586 5612 5741 5753 5763 5766 5773 5779 5781 6059
lung, fibroblast	Stratagene	LFB001	317 326-329 541 800 811 868 1325 1336 1424 1519 1538 1545 1668 1676 1864-1866 1900 1920 2110 2218 2668 2681 2746 2849 2955-2962 2979 3050 3065 3134 3144-3145 3161 3171 3277 3295 3301-3302 3307 3324 3358 3361 3368 3372 3402 3409 3411 3416 3421 3448 3555-3558 3560-3563 3579 3595 3613 3634 3638 3714 3756 3761 3788 3888-3891 3893-3894 3896 3904 3945 3962 3979 3987 4011 4036 4128 4138 4146-4147 4165-4166 4185 4198 4233 4242 4244 4365-4366 4378 4406 4418 4497 4500 4533 4553 4575 4596-4598 4609 4758-4759 4780 4788 4790 4815 4830 4884 4956 4965 4978 5232 5266 5277 5281 5306 5311 5326 5328 5330 5335 5370-5371 5377 5402 5413 5417 5422 5424 5429-5431 5436 5453 5499 5501 5504 5526 5530 5532 5536 5542-5543 5551 5559 5568 5570-5573 5575 5580-5581 5583 5585 5587 5594 5603 5605 5609-5610 5613 5624 5637 5675 5685 5715 5723 5727 5761 5765-5766 5775 5788 5799 5849-5850 5858 5974 5990 5999 6002 6043 6045 6087 6101 6111 6158 6176
lung tumor	Invitrogen	LGT002	20 34 67 69 79 81 86 88 164 333 340 456 500-501 505 526 532 685 707 713 738 760 770 773 781-785 798 812 814 834 836-838 904 927 936 955 1111 1113-1114 1123 1139 1195-1196 1347 1444 1536 1538 1604 1628 1630 1637 1639-1640 1645 1650 1656 1659 1667-1668 1676 1704 1731 1770 1781 1796 1829 1843 1858 1913 1923 1925 1935 1956 1985 1987 2007 2029-2030 2040 2052 2066 2110 2122-2123 2218 2405 2537 2558 2658 2676 2678-2679 2681 2683 2685 2689 2692-2693 2695-2697 2699-2700 2704-2705 2720 2725 2728 2730-2731 2746 2782

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PCT/US01/04941

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2785-2789 2791 2793 2849 2862 2879 2900 2913 2926 2951 2979 2981 3006 3014-3015 3023 3036 3044 3072 3117 3119 3134 3136 3140 3144 3146 3154 3161 3164 3167-3168 3184 3197 3224 3256 3271 3277 3307 3319 3333 3339 3357 3360 3366 3368 3388 3411 3415-3416 3419-3420 3440 3448 3451-3452 3461-3463 3467 3478 3538 3577 3579 3583 3586 3595 3608 3621 3638 3680 3692 3694 3710 3721 3723 3726 3729 3744 3747 3761- 3762 3779-3782 3786 3868 3893 3905 3919 3921 3934 3940 3943 3946 3966 3969 3971-3973 3987 4012 4017 4023 4027 4036 4039 4042-4043 4048 4056 4061 4139 4149 4152 4159 4163 4165-4166 4174 4190 4198 4206- 4207 4209-4210 4213 4216-4217 4231-4232 4234 4245 4273 4304 4308 4328-4329 4338 4377 4384 4386 4397- 4398 4406-4407 4419 4422 4435 4437 4439-4440 4486 4488 4497 4508 4515 4533 4536-4538 4545-4546 4548 4553 4563-4564 4575 4606 4612 4627 4670 4681 4688 4713 4783 4788 4790 4803 4809 4830 4832 4835 4873 4882 4884 4902 4916 4938 4956 4973 4977 4983 5002 5016 5038 5041 5061 5064 5066 5159 5165-5166 5174 5204 5213 5223-5225 5230-5231 5235-5236 5238 5243 5246 5254 5257 5259 5262-5263 5266 5269-5270 5277 5280-5282 5290-5292 5295-5296 5302 5305-5306 5310- 5312 5319 5328 5330 5334-5335 5356 5359 5362 5364 5367 5370-5371 5374 5379 5385 5389 5392-5399 5402 5407-5409 5415 5417 5421 5426 5428-5430 5432-5433 5436-5439 5443 5447 5450 5452 5454 5458 5480-5481 5484-5486 5489-5490 5492-5501 5512 5515 5517 5523 5525 5527-5528 5530 5533-5537 5550 5553 5555 5560 5563 5566-5568 5570-5571 5575 5577-5578 5580-5583 5585 5591-5592 5594 5599-5600 5603 5605 5609-5613 5620 5632-5633 5636 5645 5649 5651 5659 5665 5669 5671-5672 5675 5680 5682 5684-5686 5688 5691 5693 5715 5717 5719-5721 5724 5732 5741 5743 5746-5747 5756 5760 5762 5764-5769 5771 5773 5775-5776 5794 5796 5827 5835 5853 5857 5862-5863 5884-5885 5902 5942 5948 5956 5960-5962 5965-5968 5990 5994 5999- 6002 6012 6014 6033 6039 6043 6047 6050-6051 6053 6057 6069 6073 6079 6081 6087-6088 6093 6096 6103- 6104 6109 6111 6146 6148 6163 6165-6166 6168 6172 6176
Lymphocytes	ATCC	LPC001	9 22 76 152 267-272 275-276 279-281 283-290 292-293 307 469 627 641 729 785 803 811 877-879 881-883 897 922 1037 1085 1111 1116 1123 1128 1300-1301 1303- 1309 1311-1312 1393 1451 1525 1537 1569 1604 1634 1637 1668 1676 1780-1781 1823-1839 1841-1842 1846 1858 2025 2042 2421 2437 2672 2675 2681 2683 2713 2777 2782 2835 2879 2913 2920-2929 2931-2937 2939 2963 3050 3065 3116-3117 3136 3147-3148 3171 3199 3248 3259 3286-3288 3290-3294 3314 3334 3390 3397 3401-3402 3410 3440 3485 3494 3533-3541 3559 3700 3704 3733 3744 3747 3828 3864-3870 3878 3940 3962 4018 4040 4061 4137 4143 4149 4151 4165-4166 4195 4202 4216 4241 4347-4352 4378 4397 4425 4439 4450 4500 4541 4545 4553 4571 4591 4655 4676 4748-4749 4815 4872 4876 4888 4949-4950 4953-4959 5001 5016 5037-5038 5066 5081 5159 5179 5213 5218 5223-5226 5232 5235 5246 5254 5270 5280-5281 5296 5311 5319 5328 5349 5355-5359 5364 5370 5374 5398 5407 5413 5415 5421 5433 5438-5439 5443 5448 5480 5483 5494- 5495 5499 5512-5513 5518 5524-5525 5530 5548 5554

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PCT/US01/04941

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			5556-5557 5563 5566-5568 5571 5573 5575-5577 5580-5581 5585 5594 5596 5603 5606 5609 5611-5612 5624 5630 5646 5657-5660 5671 5673 5685 5687 5691 5713 5718-5719 5738-5739 5746 5753 5762 5764 5774 5838-5839 5870 5872 5942 5968 5970 5972 5990 6025 6030-6033 6038 6050-6051 6057 6085 6093 6109 6156 6159 6177-6178
leukocyte	GIBCO	LUC001	8-10 12-27 69 75 97 158 176 418 438 457 501 534 622 627 647 682 704 710 760 772-774 782 785 790 801 803 811 813 816-817 838 922 929 934 940 943 1010 1030 1054 1056 1077 1106 1111 1113 1116 1128 1138-1139 1145-1148 1152-1159 1278 1336 1347 1387-1388 1404 1429 1438 1449 1451 1460 1524 1537-1538 1575 1604 1627-1628 1634-1635 1643 1648 1657 1662 1668-1669 1675-1678 1681-1682 1731 1762 1766 1770 1780-1781 1783 1796 1829 1842 1858 1872 1887 1898 1900 1906 1916 1923 1945 1959 1964 1966 1971-1972 1979 1981 1985 1988 1998-2000 2019-2020 2025 2029 2032 2049 2068 2074 2089 2108 2110 2119 2402 2405 2409 2415 2421 2429 2437 2464 2496 2515 2519 2537 2558 2571 2612 2638 2658 2668 2672 2675 2678-2679 2681 2683 2689 2693-2694 2697-2698 2700 2704-2707 2712 2725 2728 2731 2751-2754 2762 2772 2782 2786 2793-2794 2821 2836 2849 2879 2900 2904 2907 2913 2926 2966 2979 2981 2985 2996 2998 3028 3034 3036 3050 3065 3076 3079 3088 3116 3130 3136 3140-3141 3144 3146 3150 3156 3161-3162 3164 3171-3172 3177 3181 3186 3189-3191 3194 3199-3202 3230 3248 3259 3265 3287 3307 3324-3326 3334 3340 3345 3358-3359 3368 3378 3388 3397 3402 3407 3414 3417 3420-3421 3426-3427 3429-3432 3434 3436 3440 3448 3483 3537 3559 3563 3593 3595 3598 3608 3613-3614 3616 3634 3676 3686 3692 3698 3704-3705 3708 3714 3730 3732 3734 3736-3741 3743-3747 3753 3756 3762-3763 3765 3788 3792 3838 3844 3847 3868 3878 3899 3919 3921 3928 3940 3945 3947 3951 3955 3960 3968-3969 3974 3976 3981 3989 4012-4013 4017 4027 4033 4035-4036 4039-4040 4043-4044 4048 4060-4062 4066 4118 4121 4128 4140 4148-4149 4152 4159 4161 4165-4166 4172-4173 4190 4192 4194-4195 4198 4200 4202 4205-4206 4209-4210 4212 4217-4218 4230 4233 4236 4244 4247-4248 4252-4255 4304 4308 4349-4350 4378 4386 4397-4398 4406 4419 4422 4435 4440 4449-4450 4485-4486 4495 4500 4507 4533 4536 4538 4543 4545 4548 4553 4558 4575 4591 4608-4609 4612 4649 4656 4668-4669 4671-4673 4676 4679 4684 4689 4692-4695 4726-4727 4737 4764 4784 4788 4797 4809 4830-4831 4835 4853 4856 4862 4864 4871 4873 4881-4888 4937-4938 4944 4956 4964 4977 4983 5002 5013 5016 5027 5032-5033 5037-5038 5041-5042 5045 5047-5048 5062 5064 5066 5074 5081 5135 5159 5165 5168 5173-5174 5178-5179 5183 5190 5196 5213 5218-5219 5221 5223-5225 5229-5231 5234-5236 5245-5246 5250 5252 5254 5257 5260-5263 5265-5266 5269-5277 5280-5282 5285 5292 5295-5296 5305 5307 5310-5312 5319 5323 5326 5328 5335 5345-5346 5348 5356 5359 5364 5367 5370-5372 5377 5385 5389 5392-5394 5397-5399 5401-5403 5405 5407-5409 5413 5415 5421-5422 5426 5429-5434 5436-5439 5443 5450 5452 5457-5458 5462-5463 5480-5481 5483 5485 5492-5495 5497-5501 5504 5512-5513 5515 5519-5520 5525 5527-5528 5530-5534 5537 5540-5545 5547-5548 5550-5551

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			5553-5557 5560 5563 5567-5568 5570-5571 5573 5575-5582 5585 5587 5589 5591 5594 5596 5599 5601-5603 5608-5612 5614 5616 5619-5620 5623-5624 5630 5633 5636-5637 5645-5647 5649 5651 5657 5660 5665 5669 5671-5672 5675 5680-5683 5685 5687 5689 5691-5693 5713 5715 5719-5721 5723-5724 5727 5729 5732 5738 5741 5746-5748 5756 5762 5764-5767 5769-5770 5772-5774 5776 5783-5785 5824 5884 5939 5942-5943 5946 5955 5960-5963 5965-5966 5974 5977-5979 5981 5990 5994 5999-6000 6002 6008 6012 6033 6035 6038 6047 6053 6057 6069 6093-6095 6098 6109 6111 6146 6152 6165 6168 6178
leukocyte	Clontech	LUC003	75 439 457 922 1049 1111 1144 1388 1872 1959 2022 2110 2649 2679 2683 2689 2745 2762 2791 2913 2926 3036 3146 3199 3209 3334 3368 3563 3707 3736 3743-3744 3756 3762-3763 3878 4040 4152 4165-4166 4281 4308 4403 4422 4500 4506 4533 4545 4553 4558 4673 4737 4747 4888 4938 4956 5049 5062 5133 5180 5215 5218 5224-5225 5230 5238 5246 5262 5305 5311 5323 5328 5364 5383 5390 5399-5400 5402 5407 5410 5415 5422 5432 5438 5450 5452 5481 5493 5498 5510 5515 5525 5530 5541 5567 5576 5580 5596 5607 5609 5620 5624 5633 5638 5657 5680 5687 5693 5712-5713 5719 5722 5734 5746-5747 5764 5773 5956 5974 6103 6111 6146 6152 6168
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	89 134 176 279 311 365 456 627 774 929 1099 1113 1138 1302 1400 1536 1676 1690 1858 1980 1997 2040 2045 2079 2502 2602 2678 2683 2693 2726 2835 2900 2913 2926 3061 3065 3072 3084 3136 3166-3167 3179 3186 3199 3210 3225 3236 3251 3283 3316 3324 3327 3415 3424 3448 3485 3494 3550 3649 3689 3722 3736 3762 3788 3828 3868 3887-3888 3905 3951 3981 4018 4057 4061 4165 4207 4209 4216 4244 4263 4280 4304 4335 4377 4435 4439 4449 4476 4485 4506 4533 4538 4612 4769 4780 4827 4830 4854 4864 4876 4884 4969 4983 5025 5029 5064 5151 5159 5229 5234 5254-5255 5260 5265 5269 5272 5281 5285 5290-5291 5294 5305 5324 5356 5364 5371 5377 5389 5392-5393 5403 5409 5411 5417 5422 5426 5433 5449 5454 5457 5462 5484 5493 5497-5499 5504 5521 5541 5548 5567 5572-5573 5589 5594 5603 5609 5612 5618 5632 5638 5645 5665 5680 5691 5698 5712 5717 5720 5731 5738 5741 5747 5756 5765 5767 5790 5840 5847 5884 5899 5943 5965 5990 6008 6047 6068 6111 6143 6157 6176 6178
mammary gland	Invitrogen	MMG001	9 67 69 75 90 92 94 127 164 176 311 365 456-457 497 501 526 532 637 705 713 738 743 760 775 782 785 798-800 813 865 904 911 934 936 942 958 1030 1067 1095-1096 1111-1113 1115-1116 1123 1125 1128 1131 1133 1138 1200 1253 1387-1388 1393 1428 1468 1538 1579 1604 1609 1628 1630 1636-1637 1640 1643 1645 1655-1656 1659 1661 1668 1670 1673 1676 1731 1783 1792 1828 1858 1910 1913 1946 1979 1987 2019-2020 2040 2043 2046 2050 2089 2102 2402 2465 2537 2558 2612 2638 2651 2657-2658 2675 2681 2683 2685 2692 2694 2697-2699 2704 2706 2709 2715 2717 2720 2729 2742 2747 2762 2777 2782 2784-2785 2791 2793-2795 2804 2879 2913 2942 2981 2998-2999 3004 3015 3017 3023 3036 3050 3062 3072 3080 3088 3094 3116-3118 3122 3130 3136 3140 3144 3146 3150 3156 3161 3164 3166-3167 3171 3176 3179 3184 3187 3189 3197 3199 3226-3227 3251 3287 3307 3314 3321 3328 3332 3339 3345 3357-

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			3358 3360 3362 3365 3368 3372-3373 3375 3378 3380 3388 3409-3410 3415 3448 3467 3469-3470 3477 3483 3538 3593 3608 3616 3692 3698 3704 3714 3718 3736 3744 3747 3756 3758 3763 3788-3789 3845 3878 3885 3905 3927-3928 3934 3940 3942-3944 3955 3967-3970 3972 3974 3989 3992 4013 4036 4039-4040 4042-4044 4050 4117 4134 4149 4152 4166 4170 4174 4183 4192 4198 4202 4206-4207 4209 4215 4233 4237 4239 4241 4245 4273 4281-4282 4308 4335 4386 4398 4409 4419 4422 4440 4445 4449-4450 4488 4500 4503 4507-4508 4514 4533 4536-4538 4545 4548 4553 4558-4559 4570 4591 4605-4606 4608-4609 4632 4656 4660 4670 4673 4684 4687 4689 4714 4727 4749 4757 4770 4784 4790 4797 4824 4830 4832 4835 4848 4862-4863 4868 4871 4876 4884 4919 4927 4935 4938 4956 4973 4977 5022 5037-5038 5064 5066 5069 5074 5079 5141 5144 5146 5159 5171 5211 5213 5223-5226 5229-5231 5237 5239 5243 5245 5249 5253-5257 5260-5263 5265-5266 5269 5277 5281 5288 5290 5292 5295-5297 5299 5304 5310 5312 5319 5323 5328 5362 5364-5365 5367 5370-5371 5379 5389-5390 5395-5397 5399 5402 5405 5407-5408 5413 5417 5421 5428-5430 5432-5433 5436-5438 5443- 5444 5447-5448 5450 5454 5458 5480-5481 5483-5485 5489 5492-5497 5499 5506 5510 5512-5513 5515 5521 5524 5527-5528 5530 5532-5534 5537-5538 5540 5544 5547-5550 5553-5557 5559 5561 5563 5566-5568 5575- 5576 5580-5583 5586-5587 5592 5594 5596 5600 5603 5606-5607 5612 5615 5619-5620 5630-5631 5635-5636 5643 5645 5649 5656-5657 5665 5669 5671 5674 5677- 5678 5680 5688 5693-5694 5710 5712-5713 5716-5717 5720 5724-5725 5732-5734 5741-5742 5744 5746-5747 5749 5753-5755 5759 5761 5763 5765-5766 5769 5772- 5773 5776-5777 5783 5788 5811 5816 5827 5858 5880 5899 5942 5952 5961-5963 5965 5969-5972 5974-5975 5978 5990 6000-6001 6012 6042-6043 6051 6053 6059 6061 6063 6065 6069 6072-6073 6079 6085 6087 6095 6098 6104 6106 6111-6112 6116 6143 6148 6168 6172- 6174 6177 6181
induced neuron cells	Stratagene	NTD001	20 137 306-309 311-313 890-893 942 1128 1323-1324 1406 1460 1519 1529 1634 1667 1670 1676 1731 1780 1851 1853 1855 1858 1906 2045 2110 2725 2731 2900 2913 2947 3068 3084 3116 3176-3177 3199 3260 3297 3316 3324 3358 3368 3397 3448 3538 3548-3550 3579 3747 3756 3758 3878-3880 3891 3894 3899 3971-3972 4018 4152 4166 4197 4212 4229 4308 4358-4359 4435 4485 4500 4533 4609 4683 4788 4830 4873 4956 4967 5159 5236 5246 5290-5291 5295 5305 5335 5361 5370 5374 5402 5408 5415 5426 5438 5484-5485 5491 5498- 5499 5504 5512 5525 5530 5535 5541 5544 5567 5581 5583 5594 5609 5630 5659 5665 5675 5677 5725 5729 5734 5749 5752 5756 5778 5844 5895 5965 6037-6040 6085 6109
retinoid acid induced neuronal cells	Stratagene	NTR001	1650 2679 2683 2695 2697 2879 3199 3265 3420 4249 4440 4983 5038 5159 5230 5246 5254 5260 5399 5432 5436-5437 5499 5550 5563 5594 5607 5624 5716 5962 6069
neuronal cells	Stratagene	NTU001	176 313-314 650 713 733 798 1096 1116 1129 1249 1406 1630 1668 1676 1829 1851 1855 1925 2111 2299 2440 2631 2675 2683 2706 2725 2879 3117 3144 3176 3199 3297 3364 3375 3419 3448 3451 3593 3879 3917 3971 4045 4048 4050 4166 4435 4485 4524 4538 4540 4670

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PCT/US01/04941

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
salivary gland	Clontech	SAL03	1668 2742 2772 3136 4206 4495 4832 5064 5228 5254 5447 5525 5563 5698
skin fibroblast	ATCC	SFB001	1668 3368 3448 3615 4184 4233 5038 5254 5328 5422 5581
skin fibroblast	ATCC	SFB002	1668 1676 3368 4233 5254 5422
skin fibroblast	ATCC	SFB003	811 1628 3136 4233 4964 5038 5254 5511 5525 5603 6153
small intestine	Clontech	SIN001	9 257 318 411 526 678 774 801 811 834 912 967 1112 1345 1392 1404 1439 1455 1536 1613 1631 1634 1645 1659 1668 1677 1694 1752 1781 1804 1820 2122 2683 2692 2698 2744 2777 2913 2999 3078 3081 3083 3173 3184 3191 3199 3218 3364 3402 3538 3710 3744 3747 3761 3767 3855 3919 4035 4040 4258 4439 4500 4503 4506 4532 4670 4788 4830 4938 5141 5166 5216 5260 5282 5295 5297 5328 5348 5364 5385 5394 5396 5420 5422 5454 5499 5501 5513 5540 5551 5554 5561 5563 5620 5713 5725 5732 5744 5754 5761 5769 5773 5858 5884 5892 5895 5974 5999 6001-6002 6008 6051 6098 6146 6157
skeletal muscle	Clontech	SKM001	478 798 943 1347 1770 1805 1862 1959 2039 2537 2679 2685 2732 2835 2879 2923 3022 3036 3199 3447 3726 3828 3893 3899 4200 4538 4545 4548 4609 4676 4678 4935 5027 5230 5328 5356 5402 5407-5408 5413 5422 5436 5448 5450 5471 5485 5489 5499 5513 5560 5567 5570 5601 5612 5636 5645 5683 5716 5739 5977 6057 6111 6178
skeletal muscle	Clontech	SKM002	1628 5225
skeletal muscle	Clontech	SKM03	4233 5525
skeletal muscle	Clontech	SKM04	1781 2879 3368
spinal cord	Clontech	SPC001	307 364 457 541 775 785 805-806 811 827 931 939 1551 1597 1661 1668 1676 1780-1781 2039 2110 2421 2528 2553 2562 2651 2657 2678 2683-2684 2692 2782 2823 2835 2839 2883 2900 2923 3065 3079 3136 3144 3172 3186 3196 3312 3364 3402 3448 3451 3509 3592 3613-3614 3635 3651 3691 3744 3747 3757 3822 3844 3899 3907 3919 3931 3943 3997 4018 4035-4036 4120 4159 4166 4195 4203 4209 4237 4271 4335 4350 4378 4394 4402 4409 4449 4485 4533 4538 4540 4545 4549 4591 4609 4649 4673 4676 4713 4721 4737 4757 4830-4832 4873 4884 4935 4938 5002 5006 5032 5038 5042-5043 5048 5064 5134 5218 5225 5229-5230 5238 5246 5254 5260 5266 5277 5281 5290 5313-5314 5328 5335 5371 5385 5399 5407 5411 5421-5422 5435 5438 5443 5445 5450 5453-5454 5462 5482 5486 5495-5496 5501 5506 5508 5510 5513 5515-5516 5519 5526 5530 5532 5537-5539 5542 5548 5567 5571 5573 5578 5580-5582 5587 5592 5594 5601 5603 5606 5609-5610 5636 5655 5659 5672 5678 5680 5691 5710 5713 5721-5722 5732 5748 5759 5766 5772-5773 5775 5811 5872 5881 5961 5970 5987 5990 6012 6038 6052 6062 6109 6144 6146 6165
adult spleen	Clontech	SPLc01	69 206 760 910 1111-1112 1138 1388 1631 1650 1780-1781 1922 1987 2499 2519 2679 2712 2782 2883 2900 3186 3190 3423 3448 3718 3723 3744 3762 3919 4165 4304 4350 4500 4601 4675 4769 4864 4883 5037 5062 5224 5239 5245-5246 5270 5364 5367 5370 5398 5402 5408 5415 5420 5429 5433 5439 5497 5502 5537 5553

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			5561 5609 5624 5672 5691 5734 5762 5892 5999 6002 6051 6068 6103 6107
stomach	Clontech	STO001	318 409 775 811 1107 1395 1959 2007 2019 2104 2429 2592 2683 2686 2782 2835 2913 2930 2960 3141 3150 3191 3271 3307 3358 3497 3704 3758 3899 3919 3936 3955 3959 3987 4149 4166 4220 4233 4247 4435 4497 4506 4536 4592 4779 4783 4815 4856 4867 4983 5002 5038 5159 5328 5365 5422 5498-5499 5515 5528 5530 5554 5567 5581 5588 5592 5594 5624 5669 5687 5722 5753 5760 5769 5772 5783 5982 6023 6050 6068 6111
thalamus	Clontech	THA002	69 456 653 778 798-799 1123 1362 1597 1628 1655 1731 1825 1930 1962 2024 2400 2402 2405 2421 2523 2602 2732-2733 2744 2782 2786 2835-2836 2900 2904 2967 3045 3092 3129 3134 3161 3164 3283 3366 3392 3409 3618 3680 3694 3747 3895 3915 3969 4031 4044 4192 4201 4214 4217 4303 4440 4456 4486 4537 4553 4560 4673 4678 4714 4757 4815 4824 4832 4847 4876 4888 5066 5069 5141 5165 5230-5231 5239 5245 5247 5260 5288 5290 5307 5310 5327-5328 5398-5399 5433 5435 5444 5480 5484-5485 5487 5491 5495 5499 5510 5519 5532 5548 5558 5563 5567 5583 5591 5619 5638 5698 5710 5717 5732 5755 5769 5790 5865 5890 5955 5961 6061 6085 6146 6177
thymus	Clontech	THM001	9 34 176 340-341 367 387 393 483 497 541 627 760 857 1030 1111 1115-1116 1157 1404 1426 1438 1538 1668 1781 1941 1959 1972 2115 2422 2530 2706 2712 2772 2782 2784 2793 2835 2879 2900 2904 2913 2926 2951 2990 2999 3013-3014 3051 3061-3062 3074 3079 3087 3119 3136 3164 3166 3177 3186 3199 3216 3236 3327 3334 3397 3402 3411 3415 3448 3538 3559 3572 3607- 3609 3617-3618 3691 3722 3738 3744 3747 3788 3844 3868 3878 3940 3944-3945 3960 3974 3980 4018 4045 4061 4166 4183 4195 4205-4207 4281 4303 4385 4422- 4423 4436 4440 4497 4500 4506 4533 4545 4609 4629 4674 4684 4769 4809 4830 4862 4869 4873 4938 4943 4964 5001 5038 5062 5073 5171 5224 5230 5239 5257 5266 5269 5275-5276 5279 5281-5282 5285 5287 5290 5305 5310-5312 5320 5323 5328 5330 5334 5365 5367 5370-5371 5385 5405 5407 5415 5417 5421-5422 5429 5431 5438-5439 5449 5465 5481 5485 5496 5499 5501 5504 5510 5515 5525 5530 5532 5536-5537 5549-5550 5555 5567-5568 5570-5571 5573 5580 5583 5594 5596 5606 5610 5613 5622 5637-5638 5641 5645-5646 5656 5665 5671 5684 5687 5692 5712 5729 5732-5733 5738 5752 5759 5765 5772-5773 5776 5844 5862 5889 5892 5934 5960 5982 5990 6011 6018 6042 6051 6053 6068 6088 6110 6168
thymus	Clontech	THMc02	5 9 22 28-29 32-34 36-38 40-41 44 46-47 51-52 65 69 97 127 172 293 367 499 501 541 629 638 647 649 684 729 734 774 779 785 798 821 823-826 878 884 922 954 1019 1030 1036 1061 1111 1115 1122 1129 1132 1163 1167- 1169 1171-1175 1302 1307 1345 1347 1421 1428 1449 1525 1544 1590 1596 1628 1638 1640 1648 1659 1683 1685-1688 1690-1693 1695-1700 1780-1781 1783 1796 1828 1842 1894 1916 1925 1928 1935 1954 1984 2068 2085 2098-2099 2413 2437 2453 2496 2499 2591 2607 2609 2658 2675 2681 2683 2694 2712 2746 2755-2757 2760-2761 2763 2765-2766 2782 2879 2883 2904 2926 2941 2943 2982 2999 3018 3084 3130 3134 3136 3146 3149-3150 3156 3162 3176 3189 3191 3203-3209 3211-

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PCT/US01/04941

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			3213 3327 3340 3357-3358 3364 3375 3435 3438-3445 3448 3542 3565 3588 3628 3671 3676 3721 3736 3738 3744 3749-3751 3762 3926 3943 3983 3988 4018 4037 4039-4040 4048 4061 4114 4117 4137 4142 4166 4172 4195 4206-4207 4209-4210 4215 4218 4237 4256-4257 4259-4260 4262-4264 4308 4335 4350 4398 4402 4409 4440 4450 4485 4497 4500 4505 4508 4514 4529 4533 4536 4538 4540 4548 4551 4553 4555-4558 4560 4572 4575 4624 4651 4656 4661 4672 4674 4692 4697-4698 4806 4809 4824 4826 4838 4870 4872-4873 4880 4883 4889-4893 4938 4969 4985 4993 5016-5017 5022 5029 5032 5038 5055 5066-5067 5072 5132 5147-5149 5157 5170 5172 5179-5180 5210 5213 5223 5225-5226 5229 5234 5238-5239 5246 5254 5257-5258 5262 5266 5269 5275 5277-5278 5281-5282 5290 5295 5305 5310 5319 5323 5328 5330 5334 5342 5360 5362 5370-5372 5388 5394 5396 5398-5399 5407-5408 5413 5415 5417 5420 5422 5429 5433 5436 5443 5448 5465 5480-5481 5484 5492 5496 5498-5499 5501 5504 5513 5515 5517 5521 5524-5525 5528 5532 5534 5537 5545 5549 5554-5555 5557 5568-5569 5573 5578 5580-5581 5583 5585 5587 5596 5609-5610 5612 5615-5617 5624-5625 5627 5633 5636-5637 5646 5660 5665 5668-5669 5673 5677 5680 5682 5685 5691 5693 5713 5722-5723 5732 5739 5742 5747 5750 5752 5762 5764 5767 5769 5772-5774 5786 5915 5934 5941 5943 5952 5964 5976 5981-5982 5985- 5987 5989 6000 6042 6050-6051 6069 6087 6093 6103 6146 6158 6169
thyroid gland	Clontech	THR001	12 20 38 69 137 164 307 311 330 332-337 439 456 532 536 659 713 716 721 772 775 781 785 899-900 922 931 934 942 944 951 958 1010 1076 1111 1113-1114 1128 1138 1182 1337-1339 1342-1343 1347 1388 1395 1417 1428 1461 1529 1531 1574 1628 1631 1645 1655-1656 1659 1668 1676 1755 1770 1780-1781 1842 1868-1870 1872- 1876 1887 1945 1959 1984 2011 2025 2032 2034 2040 2052 2074 2076-2077 2110 2218 2405 2515 2539 2544 2558 2599 2620 2627 2672 2681 2683 2694 2712 2725 2731 2739 2745 2762 2772 2775 2782 2835 2839 2879 2881 2900 2904 2907 2913 2916-2917 2926 2932 2963- 2965 2971 2979 2981 2985 2995 2999 3023 3050 3062 3136 3144 3146 3149 3161 3167 3171 3179 3186 3189- 3191 3199 3278 3287 3303 3307 3312 3314 3319 3324 3327 3333 3340 3358-3359 3368 3372 3390 3397 3402- 3405 3417 3440 3470 3485 3510 3532 3538 3558 3563- 3570 3595 3607 3609 3615 3618 3634 3692 3705 3714 3717 3729 3733 3739 3743-3744 3747 3762 3765 3823 3825 3844 3878 3880 3882 3889 3893 3895-3899 3901 3921 3927 3943-3944 3946 3959 3966 3971 3976 3981 4013 4018 4023 4032 4035-4037 4061 4142 4152 4165 4172 4198 4200 4206 4208-4209 4217 4229 4239 4244- 4245 4247 4268 4281 4299 4336 4342 4350 4367-4373 4378 4394 4404 4409 4412 4418-4419 4435-4436 4439- 4440 4449-4450 4482 4497 4501 4503 4515 4526 4533- 4537 4545 4548 4558-4559 4575 4599-4600 4609 4612 4624 4629 4632 4656 4671 4673 4730 4749 4759 4763 4780 4784 4788 4797 4809 4815 4827 4830 4832 4863- 4864 4873 4876 4881-4882 4884 4898 4904 4916 4938 4956 4966 4979 4981-4986 4993 5009 5013 5016 5025 5032 5038 5041 5061 5064 5143 5173 5183 5192 5196 5211 5213 5218 5224-5225 5228 5230-5231 5241 5246 5250 5254 5257 5259-5260 5262-5263 5265 5272 5281

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			5295-5296 5305 5311 5319 5323-5324 5326 5328 5330-5331 5354 5356 5364 5367 5370-5372 5377 5385 5390 5392 5396-5397 5400 5402-5403 5407 5409 5417 5421-5422 5426 5429 5432 5434 5438 5444 5448-5450 5452 5457-5458 5463 5480 5487 5489 5492-5495 5497 5499 5512-5513 5516-5517 5520 5525 5528 5530 5532 5535 5548 5555-5557 5560 5563 5567-5571 5573-5575 5580-5581 5583 5585 5587 5592 5594 5596 5601 5603 5607-5609 5612 5618 5620 5624 5632 5636 5645 5649 5665 5671 5674 5677 5680 5682 5687 5696 5716 5719-5720 5723-5725 5729 5732 5734-5735 5738 5741 5745 5747 5749 5753 5756-5757 5762 5765-5766 5772-5774 5776-5777 5783 5790 5802 5848 5851-5853 5866 5872 5884-5885 5887 5890 5937 5965 5967 5972 5976 6001-6002 6012 6033 6039 6042-6043 6046-6048 6051-6052 6057 6069 6085 6087 6098 6103 6106 6111 6152 6168 6176 6181
trachea	Clontech	TRC001	137 293 365 774 829 943 957-958 1030 1956 1959 1984 2058 2672 2692 2712 2782 2835 2911 2978 3023 3136 3140 3144 3161 3195 3277 3340 3358 3423 3523 3573-3574 3705 3762 3822 3839 3919 3943 3973 4043 4048 4165-4166 4185 4198 4536 4545 4553 4649 4815 5009 5038 5043 5218 5255 5281-5282 5288 5305 5364 5377 5398-5399 5407 5419 5422 5429 5438 5447 5483 5495 5497 5513 5525 5543 5551 5555 5573 5580 5594 5602 5608 5613 5619-5620 5638 5645 5692 5721 5738 5766 5790 5956 5974 6042 6062 6068 6101 6171
uterus	Clontech	UTR001	803 838 901 940 1061 1138 1388 1404 1527 1542 1628 1829 2030 2104 2683 2784 2835 2983 3093 3117 3146 3171-3172 3184 3191 3195 3277 3307 3358 3364 3402 3423 3448 3501 3563 3762 3844 3936 4066 4136 4192 4198 4371 4406 4449-4450 4500 4533 4703 4815 4830 4884 4991 5025 5038 5218 5254 5272 5290 5305 5374 5395 5407 5415 5422 5454 5493-5494 5497 5510 5513 5528 5549 5557 5567 5571 5574-5575 5580 5594 5601 5609-5610 5618 5620 5624 5638 5645 5654 5685 5696 5717 5727 5759 5765 5767 5772 5774-5775 5777 5866 5938 5972 6002 6053 6091 6103 6170

*The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

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TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3	AK023197	Homo sapiens	unnamed protein product	659	100
5	AF153062	Canis familiaris	type I collagen pre-pro-alpha1(I) chain	111	34
6	AB041228	Homo sapiens	G protein-coupled receptor TGR-1	297	98
7	Y28810	Homo sapiens	nn296_2 secreted protein.	65	91
8	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	299	76
9	Y65193	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1354.	131	53
14	AF315312	Homo sapiens	c-myc oncogene protein	223	91
15	AF315312	Homo sapiens	c-myc oncogene protein	205	82
18	U93563	Homo sapiens	putative p150	91	50
19	U43360	Peromyscus maniculatus	reverse transcriptase	110	48
20	D80009	Homo sapiens	KIAA0187	504	94
21	D88460	Homo sapiens	N-WASP	633	89
22	Y25426	Homo sapiens	Human SIGIRR protein.	434	100
23	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	113	71
25	AF003535	Homo sapiens	ORF2-like protein	67	33
29	AB012223	Canis familiaris	ORF2	73	58
32	AK022609	Homo sapiens	unnamed protein product	150	40
33	AF111848	Homo sapiens	PRO0529	148	38
37	AB012223	Canis familiaris	ORF2	99	39
38	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	75	63
40	L27428	Homo sapiens	reverse transcriptase	156	35
41	AF119851	Homo sapiens	PRO1722	99	90
43	AK021798	Homo sapiens	unnamed protein product	156	91
44	AF009668	multiple sclerosis associated retrovirus	polyprotein	162	33
46	X05472	Rattus norvegicus	ORF 3	97	53
47	AF090944	Homo sapiens	PRO0663	209	77
52	U09116	Homo sapiens	ORF2, encodes a reverse transcriptase homolog	82	32
59	U93568	Homo sapiens	putative p150	140	56
61	AF130051	Homo sapiens	PRO0898	195	66
66	AF003535	Homo sapiens	ORF2-like protein	54	80
70	AK026371	Homo sapiens	unnamed protein product	35	37
72	S80119	Rattus sp.	reverse transcriptase homolog	38	56
74	S80119	Rattus sp.	reverse transcriptase homolog	44	39
75	AF217521	Homo sapiens	uncharacterized bone marrow protein BM045	283	74
76	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	125	60
78	AF040639	Homo sapiens	aflatoxin B1-aldehyde reductase; AFAR	223	76
79	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	89	72
81	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	167	73
88	L27428	Homo sapiens	reverse transcriptase	259	40

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
89	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	171	56
90	AF130087	Homo sapiens	PRO2411	177	76
91	AJ000496	Rattus norvegicus	cyclic nucleotide-gated channel beta subunit	163	43
94	L24521	Homo sapiens	transformation-related protein	241	69
95	U15647	Mus musculus	reverse transcriptase	110	42
96	AF194537	Homo sapiens	NAG13	88	44
97	AF269133	Homo sapiens	novel interleukin receptor	384	100
100	S80119	Rattus sp.	reverse transcriptase homolog	193	63
105	AB004329	Rattus norvegicus	acetyl-CoA carboxylase	223	80
108	AF194537	Homo sapiens	NAG13	150	34
109	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	64
110	AF194537	Homo sapiens	NAG13	126	46
112	U88836	Homo sapiens	translational activator GCN1	183	61
114	W15092	Homo sapiens	Human protective protein cathepsin A.	168	96
116	Y12713	Mus musculus	gag polyprotein	291	65
119	AF194537	Homo sapiens	NAG13	92	38
120	AF130051	Homo sapiens	PRO0898	177	48
121	U93563	Homo sapiens	putative p150	124	44
122	L24521	Homo sapiens	transformation-related protein	90	73
123	AF130051	Homo sapiens	PRO0898	126	50
126	AF109907	Homo sapiens	S164	347	77
127	AJ388557	Canis familiaris	zinc finger protein	72	29
129	U93570	Homo sapiens	putative p150	152	39
130	U93570	Homo sapiens	putative p150	53	50
134	X13885	Nicotiana tabacum	extensin (AA 1-620)	138	30
135	AF119900	Homo sapiens	PRO2822	221	75
137	R95913	Homo sapiens	Neural thread protein.	255	62
142	X92485	Plasmodium vivax	pval	161	48
143	U93563	Homo sapiens	putative p150	121	57
144	AF119851	Homo sapiens	PRO1722	201	66
149	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	42	40
151	AF006514	Homo sapiens	CHD2	208	97
155	U93566	Homo sapiens	p40	46	34
158	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	75
161	Z68215	Caenorhabditis elegans	contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=82.1, E-value=3.7e-21, N=2; PF01484 (Nematode cuticle collagen N-terminal domain), Score=39.9, E-value=1.8e-08, N=1--cDNA EST yk69a6.5 comes from this gene--cDNA EST yk65h3.3 comes from this gene--cDNA EST yk59a5.5 comes from this gene--cDNA EST yk59e8.5 comes from this gene--cDNA EST yk99g9.5 comes from this gene--cDNA EST yk92g6.5	147	40

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			comes from this gene-cDNA EST yk584.5 comes from this gene-cDNA EST yk65h3.5 comes from this gene-cDNA EST yk446d12.3 comes from this gene-cDNA EST yk446d12.5 comes from this gene-cDNA EST yk234c11.3 comes from this gene-cDNA EST yk234c11.5 comes from this gene-cDNA EST yk302f5.5 comes from this gene		
164	L29029	Chlamydomonas reinhardtii	amino acid feature: Rod protein domain, aa 266 .. 468; amino acid feature: globular protein domain, aa 32 .. 265	150	31
166	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	51	76
167	Z48955	Didelphis virginiana	ORF-2, putative RT	104	41
169	A03758	Homo sapiens	serum albumin	519	91
170	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	157	70
174	U93569	Homo sapiens	putative p150	135	57
176	G03829	Homo sapiens	Human secreted protein, SEQ ID NO: 7910.	294	96
180	AK021764	Homo sapiens	unnamed protein product	82	54
181	LZ7428	Homo sapiens	reverse transcriptase	63	83
183	X05472	Rattus norvegicus	ORF 3	45	60
186	AF090942	Homo sapiens	PRO0657	65	57
187	Y87330	Homo sapiens	Human signal peptide containing protein HSPP-107 SEQ ID NO:107.	171	94
188	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	136	63
190	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	38	39
191	D84391	Mus musculus	reverse transcriptase	144	52
193	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	124	76
194	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	132	69
196	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	65	68
199	U70935	Peromyscus maniculatus	reverse transcriptase	104	52
200	M13100	Rattus norvegicus	unknown protein	62	91
201	U93569	Homo sapiens	putative p150	94	51
202	L23545	Homo sapiens	putative	59	42
203	U93563	Homo sapiens	putative p150	255	36
205	AF194537	Homo sapiens	NAG13	106	45
206	Y36156	Homo sapiens	Human secreted protein #28.	48	81
209	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	199	45
212	Y36156	Homo sapiens	Human secreted protein #28.	75	80

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
215	AK023542	Homo sapiens	unnamed protein product	108	46
217	U93564	Homo sapiens	putative p150	166	38
218	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	218	60
219	U43360	Peromyscus maniculatus	reverse transcriptase	171	40
220	AC006145	Homo sapiens	calcium channel; match to P54289 (PID:g1705852)	195	92
223	G03628	Homo sapiens	Human secreted protein, SEQ ID NO: 7709.	70	59
226	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	51	57
228	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	49	41
229	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	69	63
230	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	215	71
232	M13100	Rattus norvegicus	unknown protein	81	58
233	U15647	Mus musculus	reverse transcriptase	135	44
235	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	55	78
238	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	148	50
239	AF119851	Homo sapiens	PRO1722	68	77
240	U93563	Homo sapiens	putative p150	134	47
244	M13100	Rattus norvegicus	unknown protein	82	43
248	X61296	Rattus norvegicus	open reading frame 2	75	40
252	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	97	70
254	AF130089	Homo sapiens	PRO2550	145	53
256	M10987	Bovine leukemia virus	gag polyprotein	51	50
257	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	188	64
261	AF194537	Homo sapiens	NAG13	63	51
264	AF130079	Homo sapiens	PRO2852	81	60
265	U93569	Homo sapiens	putative p150	385	52
267	AF016099	Mus musculus	endonuclease/reverse transcriptase	123	36
270	U87607	Rattus norvegicus	putative RNA binding protein 1	81	51
271	U93565	Homo sapiens	putative p150	125	67
272	AK022550	Homo sapiens	unnamed protein product	105	38
284	L24521	Homo sapiens	transformation-related protein	46	64
286	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	288	67
290	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	101	60
293	AF090942	Homo sapiens	PRO0657	59	64
297	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	320	71
301	U93568	Homo sapiens	p40	96	45
302	U93565	Homo sapiens	putative p150	127	39
304	AB012223	Canis familiaris	ORF2	136	32
305	AF003535	Homo sapiens	ORF2-like protein	131	46

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
395	U90550	Homo sapiens	butyrophilin	100	63
396	U93569	Homo sapiens	putative p150	76	48
397	AF156550	Mus musculus	putative E1-E2 ATPase	250	43
401	AF065389	Homo sapiens	tetraspan NET-4	353	78
402	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	739	65
404	AL157473	Homo sapiens	hypothetical protein	187	74
405	M97501	Homo sapiens	cytoplasmic linker protein-170 alpha-2	158	100
408	M18247	Feline leukemia virus	gag-pol precursor polypeptide pPr80	42	64
409	AL139377	Homo sapiens	bA251J8.1.1 (novel protein, isoform 1)	561	99
410	U93564	Homo sapiens	putative p150	181	40
411	AF194537	Homo sapiens	NAG13	37	39
416	M19503	Homo sapiens	ORF1; putative	117	45
417	AF156550	Mus musculus	putative E1-E2 ATPase	346	47
421	AB012223	Canis familiaris	ORF2	114	34
422	U93565	Homo sapiens	putative p150	59	32
423	AF130089	Homo sapiens	PRO2550	151	51
424	AF130089	Homo sapiens	PRO2550	151	51
425	G03628	Homo sapiens	Human secreted protein, SEQ ID NO: 7709	70	59
426	AF020351	Homo sapiens	NADH:ubiquinone oxidoreductase 18 kDa IP subunit	122	96
430	Y85573	Homo sapiens	His-UNC-53/3 fragment/GFP fusion insert of plasmid pGI3303	313	72
431	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	147	56
432	D70831	Homo sapiens	Zinc-finger protein	146	69
433	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	150	49
434	X15311	Woolly monkey sarcoma virus	reverse transcriptase (476 AA)	183	41
435	M15805	Feline sarcoma virus	gag-abl-pol fusion polypeptide	189	42
437	W48351	Homo sapiens	Human breast cancer related protein BCRB2	95	51
438	U97497	Homo sapiens	butyrophilin	315	95
442	X61296	Rattus norvegicus	open reading frame 2	75	40
443	X61296	Rattus norvegicus	open reading frame 2	75	40
444	AF132944	Homo sapiens	CGI-10 protein	174	67
445	Y70751	Homo sapiens	Human tyrosine kinase receptor Flt1	35	30
449	AF003535	Homo sapiens	ORF2-like protein	37	57
450	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284	47	57
451	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284	47	57
452	U93564	Homo sapiens	putative p150	44	29
453	X61296	Rattus norvegicus	open reading frame 2	104	62
456	AK025863	Homo sapiens	unnamed protein product	85	93
457	AK000385	Homo sapiens	unnamed protein product	280	65
459	M13100	Rattus	unknown protein	102	41

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		norvegicus			
462	U93565	Homo sapiens	putative p150	48	33
466	AF149770	Homo sapiens	sentrin/SUMO-specific protease	268	89
469	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	262	78
472	AB012223	Canis familiaris	ORF2	159	46
475	AF130089	Homo sapiens	PRO2550	79	48
476	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	182	66
480	U70935	Peromyscus maniculatus	reverse transcriptase	104	52
483	AF130089	Homo sapiens	PRO2550	114	51
486	AF130052	Homo sapiens	PRO0956	111	57
487	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	114	50
489	AC006145	Homo sapiens	calcium channel; match to P54289 (PID:g1705852)	195	92
493	U93563	Homo sapiens	putative p150	126	46
495	X63526	Homo sapiens	homologue to elongation factor 1-gamma from A.salina	282	82
496	AK024718	Homo sapiens	unnamed protein product	606	95
497	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	130	59
501	U37351	Mus musculus	Paneth cell enhanced expression PCEE	523	91
504	U93563	Homo sapiens	putative p150	85	43
505	L27428	Homo sapiens	reverse transcriptase	39	53
506	U93567	Homo sapiens	putative p150	54	46
509	D88152	Homo sapiens	acetyl-coenzyme A transporter	52	91
512	AL031349	Schizosaccharomyces pombe	putative vesicular transport protein	210	30
514	M13100	Rattus norvegicus	unknown protein	181	42
521	W27653	Homo sapiens	Secreted protein AS32.	44	33
524	M12140	Homo sapiens	envelope protein	71	68
525	U95090	Homo sapiens	F19541_1	212	87
526	AB033109	Homo sapiens	KIAA1283 protein	234	92
530	Y01167	Homo sapiens	Polypeptide fragment encoded by gene 10.	536	82
531	AF016099	Mus musculus	endonuclease/reverse transcriptase	196	42
536	D42063	Homo sapiens	RanBP2 (Ran-binding protein 2)	400	93
538	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	88	58
539	AF130079	Homo sapiens	PRO2852	224	62
540	AC006020	Homo sapiens	lysine ketoglutarate reductase/saccharopine dehydrogenase	1024	99
541	AF064243	Homo sapiens	intersectin short form	74	46
543	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	83	46
545	AF143723	Homo sapiens	heat shock protein HSP60	278	81
546	AF130052	Homo sapiens	PRO0956	51	33
548	AF033260	porcine endogenous type C retrovirus	reverse transcriptase	129	48
552	X83413	Human herpesvirus 6	U88	205	53

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SEQ ID NO.	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
559	U15647	Mus musculus	reverse transcriptase	142	37
561	U38473	Escherichia coli	putative glycosyl transferase	144	96
567	U93572	Homo sapiens	putative p150	191	43
569	D90835	Escherichia coli	Porin OmpC	197	97
570	U93572	Homo sapiens	putative p150	112	54
572	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	94	62
577	AB012223	Canis familiaris	ORF2	74	24
583	AF043636	Plasmodium chabaudi	circumsporozoite protein	244	55
590	X65165	Volvox carteri	extensin	178	43
591	D90809	Escherichia coli	Adhesin AIDA-I precursor.	72	82
597	U82664	Escherichia coli	Hha protein	180	56
598	D90868	Escherichia coli	PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EIIFRU).	587	87
599	D90892	Escherichia coli	ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE-TRNA LIGASE) (ALARS).	550	68
600	AE000116	Escherichia coli K12	probable ATP-dependent RNA helicase	674	81
601	AB012223	Canis familiaris	ORF2	74	24
606	U93568	Homo sapiens	putative p150	109	35
607	AB012223	Canis familiaris	ORF2	145	36
608	AB012223	Canis familiaris	ORF2	78	34
609	S62928	Homo sapiens	PRB1M protein precursor	159	36
614	AB012223	Canis familiaris	ORF2	74	24
617	M64793	Rattus norvegicus	salivary proline-rich protein	146	33
618	AF039916	Homo sapiens	CD39L2	304	70
620	AF013215	Bos taurus	ribosomal protein S2	53	70
625	G02019	Homo sapiens	Human secreted protein, SEQ ID NO: 6100.	338	100
627	AF181985	Homo sapiens	serine/threonine kinase	597	82
628	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	342	67
636	AF076183	Rattus norvegicus	cytosolic sorting protein PACS-1a	423	63
645	AB004885	Homo sapiens	PKU-beta	117	61
649	U70671	Homo sapiens	ataxin-2 related protein	592	89
650	AK025974	Homo sapiens	unnamed protein product	509	70
651	AK022291	Homo sapiens	unnamed protein product	556	90
654	AC004983	Homo sapiens	similar to PID:g3877944	125	88
655	M27877	Homo sapiens	HPF1 protein	615	65
657	AK026448	Homo sapiens	unnamed protein product	129	100
659	AK026182	Homo sapiens	unnamed protein product	526	100
667	AK023277	Homo sapiens	unnamed protein product	355	98

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
668	AF104402	Rattus norvegicus	syndapin 1	482	90
671	U93563	Homo sapiens	putative p150	124	45
672	AF274863	Homo sapiens	secretory pathway component Sec3 IB-1	131	96
678	S80119	Rattus sp.	reverse transcriptase homolog	274	58
679	M24898	Homo sapiens	triiodothyronine receptor	348	57
681	U75930	Orgyia pseudotsugata nuclear polyhedrosis virus	unknown	150	36
682	AF119860	Homo sapiens	PRO2014	85	51
683	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	84	65
685	AF243044	Homo sapiens	ECSIT	260	43
686	X15879	Homo sapiens	precursor polypeptide (AA -19 to 237)	171	51
687	AB020640	Homo sapiens	KIAA0833 protein	558	88
690	AB002317	Homo sapiens	KIAA0319	283	96
691	AK023542	Homo sapiens	unnamed protein product	152	52
692	AJ245709	Homo sapiens	Akt-3 protein	194	100
693	AF216805	Rattus norvegicus	nuclear matrix transcription factor	402	97
694	AL031717	Homo sapiens	C361A3.1 (JNK/SAPK-associated protein-1)	645	100
696	AB033057	Homo sapiens	KIAA1231 protein	611	89
698	Y02168	Homo sapiens	A facilitative glucose transporter protein GLUT8.	499	79
699	AL161931	Homo sapiens	bA1021O19.1 (zinc finger protein 33a (KOX 31))	99	48
703	AF251038	Homo sapiens	GAP-like protein	794	80
706	J03203	Plasmodium brasilianum	circumsporozoite protein	278	47
707	AK000555	Homo sapiens	unnamed protein product	326	56
711	U85707	Homo sapiens	leukemogenic homolog protein	754	89
713	D45021	Homo sapiens	rab GDI alpha	363	88
716	U69263	Homo sapiens	matrilin-2 precursor	277	95
717	X83413	Human herpesvirus 6	U88	170	49
721	AF009329	Rattus norvegicus	enhancer-of-split and hairy-related protein 1	94	66
722	AL390114	Leishmania major	extremely cysteine/valine rich protein	168	42
723	AL390114	Leishmania major	extremely cysteine/valine rich protein	231	44
724	AL390114	Leishmania major	extremely cysteine/valine rich protein	205	40
726	AB011137	Homo sapiens	KIAA0565 protein	109	40
727	G02219	Homo sapiens	Human secreted protein, SEQ ID NO: 6300.	167	97
728	AJ238248	Homo sapiens	centaurin beta2	85	70
729	AJ132948	Homo sapiens	rfi7 protein	399	80
730	Y77663	Homo sapiens	Human FKHSf polypeptide.	369	68
731	AB046852	Homo sapiens	KIAA1632 protein	375	78
735	A67510	Mus musculus	MUS MUSCULUS GENOMIC DNA CONTAINING N ALLELE OF FV1 GENE.	113	36
736	AF016099	Mus musculus	endonuclease/reverse transcriptase	61	35

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
739	U68138	Homo sapiens	PSD-95	410	72
740	Y73858	Homo sapiens	Human prostate tumor EST fragment derived protein #45.	646	93
741	Y15197	Mus musculus	microtubule-associated protein, MAP-115	42	26
742	W78145	Homo sapiens	Human secreted protein encoded by gene 20 clone HSKZE52.	396	67
743	AK000538	Homo sapiens	unnamed protein product	352	96
744	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	504	98
746	Y23330	Homo sapiens	Human tumour suppressor (kismet) protein.	280	96
747	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	96	38
748	AB046632	Macaca fascicularis	unnamed protein product	517	82
754	M12100	Mus musculus	proline-rich protein MP-3	151	37
755	M63819	Plasmodium falciparum	malaria antigen	122	50
760	AF089750	Homo sapiens	flotillin-1	416	94
761	AL390114	Leishmania major	extremely cysteine/valine rich protein	189	43
765	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	105	50
767	Y51611	Homo sapiens	Human HSGT1 protein.	752	91
768	AF274863	Homo sapiens	secretory pathway component Sec31B-1	131	96
769	AJ245587	Homo sapiens	Kruppel-type zinc finger	195	63
770	AJ245587	Homo sapiens	Kruppel-type zinc finger	237	42
772	AF112221	Homo sapiens	rap2 interacting protein x	59	100
773	U78521	Homo sapiens	immunophilin homolog ARA9	96	80
774	W60046	Homo sapiens	Human TNF receptor related splice variant 1 (TR2-SV1) protein.	123	36
778	AK022609	Homo sapiens	unnamed protein product	154	34
780	Y02100	Homo sapiens	A multifunctional protein of the invention.	343	85
781	AF123534	Homo sapiens	nucleolar protein NOP5/NOP58	570	90
782	B06334	Homo sapiens	Human subtilisin-kexin isoenzyme 1.	292	94
783	AF095446	Gallus gallus	syndesmos	653	84
785	AF201390	Mus musculus	p300 transcriptional cofactor JMY	207	42
786	AF130089	Homo sapiens	PRO2550	98	55
788	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	59	58
791	U93565	Homo sapiens	putative p150	116	78
792	AB009672	Homo sapiens	MDC3	698	84
795	AF187980	Drosophila melanogaster	Partner of Paired	385	59
796	AF032668	Rattus norvegicus	rsec15	320	89
798	D45131	Homo sapiens	basigin	540	82
801	AK001403	Homo sapiens	unnamed protein product	660	99
804	U93570	Homo sapiens	putative p150	181	41
806	AK026015	Homo sapiens	unnamed protein product	316	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
807	X56044	Mus musculus	protein Hif9C	36	31
810	AK024644	Homo sapiens	unnamed protein product	228	97
811	AF200187	cercopithecine herpesvirus 15	EBNA2-like protein	89	70
812	AK001441	Homo sapiens	unnamed protein product	438	88
813	U83913	Mus musculus	proliferation potential-related protein	490	54
814	AF116910	Homo sapiens	putative ribonuclease III	604	89
816	U93563	Homo sapiens	putative p150	205	49
823	AF164615	Homo sapiens	Gag-Pro-Pol protein	41	39
830	AK023542	Homo sapiens	unnamed protein product	144	53
834	W83947	Homo sapiens	Human secreted protein from gene 17 clone HPFDU90.	263	97
836	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	229	71
837	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	87	61
840	X81420	Homo sapiens	hair type II basic keratin	87	93
843	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	181	63
846	M13100	Rattus norvegicus	unknown protein	36	64
848	U83303	Homo sapiens	line-1 reverse transcriptase	75	53
850	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	89	85
851	AF098533	Homo sapiens	RAD17 isoform 3	239	61
853	AF118090	Homo sapiens	PRO2044	251	87
856	AK022542	Homo sapiens	unnamed protein product	215	64
858	U22815	Homo sapiens	LAR-interacting protein 1a	249	81
861	D86982	Homo sapiens	similar to human ankyrin 1(S08275)	200	53
865	Z19092	Oryctolagus cuniculus	trichohyalin	160	39
868	AF127506	Homo sapiens	adenomatosis polyposis coli tumor suppressor	223	100
869	Y36203	Homo sapiens	Human secreted protein #75.	136	68
873	U93569	Homo sapiens	putative p150	170	58
874	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	183	62
876	AF194537	Homo sapiens	NAG13	49	69
877	AL121601	Homo sapiens	dJ315G1.2 (apoptosis inhibitor 3 (XIAP, HILP))	192	64
878	X75316	Mus musculus	SEB4	41	100
886	AF092094	Homo sapiens	AP-4 adaptor complex beta4 subunit	177	92
887	AF084830	Homo sapiens	two pore domain K+ channel; TASK-2	305	100
888	W29471	Homo sapiens	pANCA-reactive fragment of human histone H1S-2.	69	42
889	AE003908	Xylella fastidiosa	hypothetical protein	160	33
891	S80119	Rattus sp.	reverse transcriptase homolog	162	58
892	AF119851	Homo sapiens	PRO1722	53	83
894	AL3359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	164	58
897	AC007369	Arabidopsis thaliana	Similar to RNA helicases	157	42
899	U15647	Mus musculus	reverse transcriptase	119	74

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
901	M36501	Homo sapiens	alpha-2-macroglobulin	46	64
903	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	45	69
904	S80864	Homo sapiens	cytochrome c-like polypeptide	165	62
907	Y17832	Human endogenous retrovirus K	pol protein	194	60
908	AF194537	Homo sapiens	NAG13	49	69
910	AF167706	Homo sapiens	cysteine-rich repeat-containing protein S52 precursor	1876	100
912	U38904	Homo sapiens	zinc finger protein C2H2-25	207	75
913	AB018296	Homo sapiens	KIAA0753 protein	243	97
914	U80018	Homo sapiens	kidney and liver proline oxidase 1	241	100
916	AF064729	Homo sapiens	RAN binding protein 16	698	80
918	U93569	Homo sapiens	putative p150	84	36
919	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	45	69
920	AF151034	Homo sapiens	HSPC200	159	87
922	AF161426	Homo sapiens	HSPC308	279	87
923	U40490	Homo sapiens	nicotinamide nucleotide transhydrogenase	162	97
924	Y79507	Homo sapiens	Human carbohydrate-associated protein CRBAP-3.	74	68
926	AF130089	Homo sapiens	PRO2550	244	82
927	AF142328	Homo sapiens	transcription factor IIC90	70	82
929	M36067	Homo sapiens	DNA ligase 1	53	36
931	AK026417	Homo sapiens	unnamed protein product	952	79
932	AC003682	Homo sapiens	R28830_1	324	64
933	U67988	Homo sapiens	guanylate kinase associated protein	292	87
934	L00974	Homo sapiens	'SP40,40'	152	55
936	U94831	Homo sapiens	multispanning membrane protein	306	65
937	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	57	44
939	Y84809	Homo sapiens	A human cadherin-like asymmetry protein-1 (Clasp-1).	347	62
940	AF293384	Homo sapiens	PLIC-1	373	96
943	D16480	Homo sapiens	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein	228	85
944	AF049885	Homo sapiens	Arg/Abi-interacting protein ArgBP2b	258	84
949	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone H1DAD22.	206	58
950	AB011792	Homo sapiens	extracellular matrix protein	231	95
951	Z24725	Homo sapiens	mitogen inducible gene mig-2	62	100
953	AF003535	Homo sapiens	ORF2-like protein	90	39
956	AL353625	Homo sapiens	bA288H12.1 (insulin-like growth factor 2 receptor)	360	81
957	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	71	45
958	AF288207	Homo sapiens	cysteinyl-tRNA synthetase	262	100
963	M12987	Plasmid F	Protein A	785	90
964	AB007644	Arabidopsis thaliana	contains similarity to phytoeyanin/early nodulin-like protein-gene_id:K19P17.3	171	36

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
966	X60200	Escherichia coli	transposase	91	100
967	AF009205	Homo sapiens	unknown	99	62
968	U14003	Escherichia coli	ORF_o281	206	97
969	X02164	Escherichia coli	pot. PBP 1A	527	95
972	D38582	Escherichia coli	DinP	568	91
973	AF242208	Escherichia coli	putative enzyme	156	93
975	U14003	Escherichia coli	ORF_o761	400	85
976	L19201	Escherichia coli	6-phosphofructokinase	249	88
979	X04619	Escherichia coli	A protein (AA 1-388)	192	75
980	M38287	Escherichia coli	RNA polymerase beta subunit (EC 2.7.7.6)	446	90
991	X06791	Escherichia coli	maltodextrin phosphorylase	214	97
993	X13065	Bacteriophage phi-80	cl gene (AA 1 - 236)	270	83
994	AE000276	Escherichia coli K12	orf, hypothetical protein	38	100
995	Y07714	Escherichia coli	spheroplast protein y	162	94
1000	D90877	Escherichia coli	FORMATE HYDROGENLYASE TRANSCRIPTIONAL ACTIVATOR	930	96
1003	M12987	Plasmid F	Protein D	84	94
1008	D90850	Escherichia coli	Probable nitrate reductase (EC 1.7.99.4)	279	100
1009	AE000303	Escherichia coli K12	putative oxidoreductase	177	52
1010	W19347	Homo sapiens	Human filamin-like beta 7 integrin binding protein FLP-1	191	77
1011	U28377	Escherichia coli	ORF_f848	307	91
1012	AB000275	Homo sapiens	DAP-2	243	63
1013	Z14020	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	92	54
1014	U28377	Escherichia coli	ORF_f848	170	100
1016	AF119817	Homo sapiens	discs, large (Drosophila) homolog-associated protein 2	231	93
1017	AC003113	Arabidopsis thaliana	F24O1.6	149	55
1019	AL162458	Homo sapiens	bA465L10.2 (novel C2H2 type zinc finger protein similar to chicken FZF-1)	58	50
1020	U20897	Homo sapiens	melanoma ubiquitous mutated protein	41	100
1021	M13577	Homo sapiens	myelin basic protein	493	89
1025	AB033109	Homo sapiens	KIAA1283 protein	833	96
1026	AF038007	Homo sapiens	FIC1	276	55
1028	AF157634	Homo sapiens	collapsin response mediator protein-5	231	91

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SEQ ID NO.	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1030	AF067804	Homo sapiens	HDCMC04P	129	62
1032	AL096768	Homo sapiens	dJ858B16.1 (KIAA0542 (isoform 2))	39	46
1033	AF193613	Homo sapiens	cell recognition molecule Caspr2	168	48
1034	AL117352	Homo sapiens	dJ876B10.2 (novel protein (ortholog of rat EXO84))	248	92
1036	AL031721	Homo sapiens	c399E4.1 (similar to D.melanogaster unkempt protein.)	193	91
1037	AF053356	Homo sapiens	leucin rich neuronal protein	365	41
1038	U93563	Homo sapiens	putative p150	63	40
1039	Y17832	Human endogenous retrovirus K	env protein	291	61
1040	AJ011414	Homo sapiens	plexin-B1/SEP receptor	598	90
1041	AJ011414	Homo sapiens	plexin-B1/SEP receptor	494	86
1042	L37380	Rattus norvegicus	apical endosomal glycoprotein	176	50
1043	AB030505	Mus musculus	UBE-1c2	114	80
1045	AC074331	Homo sapiens	ZNF225	422	75
1046	AB020684	Homo sapiens	KIAA0877 protein	114	51
1048	AF056618	Homo sapiens	BWSCR2 associated zinc-finger protein BAZ2	255	98
1049	L26335	Cavia porcellus	zinc finger protein	688	90
1051	AF040247	Homo sapiens	erythroid differentiation-related factor 1	186	83
1052	M27877	Homo sapiens	HPF1 protein	477	66
1053	U62325	Homo sapiens	FE65-like protein	561	89
1054	AF149046	Homo sapiens	Sex comb on midleg homolog 1 isoform 2	323	75
1055	AK022609	Homo sapiens	unnamed protein product	137	44
1057	AJ277291	Homo sapiens	HELG protein	508	81
1058	D87073	Homo sapiens	similar to Human zinc finger protein(ZNF142)	217	41
1059	AL109915	Homo sapiens	dJ120N9.1 (KIAA0656 protein (similar to clathrin assembly lymphoid myeloid leukemia protein (CALM)))	406	68
1062	AF040247	Homo sapiens	erythroid differentiation-related factor 1	467	95
1063	X76556	Homo sapiens	CAB3b	280	94
1064	AP001745	Homo sapiens	similar to zinc finger 5 protein	674	82
1065	Y73346	Homo sapiens	HTRM clone 619699 protein sequence.	67	57
1067	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	306	88
1068	AB033118	Homo sapiens	KIAA1292 protein	647	88
1070	AF155819	Mus musculus	doublecortin-like kinase	198	61
1071	AK000267	Homo sapiens	unnamed protein product	228	100
1072	AC009399	Homo sapiens	KIAA0998	661	99
1075	AF113751	Mus musculus	nuclear pore membrane glycoprotein POM210	356	80
1076	AF273042	Homo sapiens	CTCL tumor antigen sel-1	288	84
1077	AF068623	Homo sapiens	mineralocorticoid receptor	269	77
1080	X56805	Gallus gallus	procKr2	251	43
1081	D10627	Mus musculus	zinc finger protein	344	61
1082	AB020698	Homo sapiens	KIAA0891 protein	268	96
1083	Y08200	Homo sapiens	rab geranylgeranyl transferase	198	90

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1085	U79660	Homo sapiens	Treacher Collins syndrome	342	75
1086	AF182213	Mus musculus	microtubule-associated protein MAP1A	427	67
1088	AJ242501	Homo sapiens	E-MAP-115-95	246	44
1089	D45210	Mus musculus	zinc finger protein	395	61
1090	L31881	Homo sapiens	nuclear factor 1-X	449	92
1091	AL390114	Leishmania major	extremely cysteine/valine rich protein	140	37
1092	U03975	Tripanneustes gratilla	dynein heavy chain isotype 6	59	55
1093	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	147	72
1094	AB029482	Mus musculus	JNK-binding protein JNKBP1	496	86
1095	AE003798	Drosophila melanogaster	CG15084 gene product	104	36
1096	Y44559	Homo sapiens	Human Rhotekin protein.	265	77
1098	X52533	Mus musculus	zinc finger protein (AA 1-411)	127	34
1099	AF208227	Homo sapiens	transcriptional coactivator AIB3	317	58
1101	M83679	Rattus norvegicus	RAB15	143	100
1102	AC007787	AA 187-502	NFI-X3=transcription factor	424	75
1104	U22815	Homo sapiens	LAR-interacting protein 1a	293	67
1105	Y94963	Homo sapiens	Human secreted protein clone nf56_3 protein sequence SEQ ID NO:132.	430	81
1106	AF015037	Oryctolagus cuniculus	endooligopeptidase A related protein; EOFA related protein	404	84
1107	AF217226	Homo sapiens	zinc finger protein ZNF286	320	47
1108	AB001517	Homo sapiens	PWP2 protein	200	80
1111	Y18537	Homo sapiens	human leucocyte antigen C	384	92
1112	Z50150	Homo sapiens	tyrosine kinase activator protein 1 (TKA-1)	581	83
1113	AF022815	Homo sapiens	proteasome subunit XAPC7	74	87
1114	Y13047	Homo sapiens	glutathione transferase A4-4	538	92
1115	AJ289118	Homo sapiens	CD1E antigen, isoform 8	44	70
1116	AL049824	Homo sapiens	dJ117L23.1 (Cyclophilin 33 (Peptidyl-prolyl cis-trans isomerase))	644	93
1118	AF141347	Homo sapiens	alpha-tubulin	48	100
1119	AJ133798	Homo sapiens	copine VII protein	246	54
1120	AF034198	Homo sapiens	IGSF1	480	94
1121	AE000163	Escherichia coli K12	putative transport	524	80
1122	AB040893	Homo sapiens	KIAA1460 protein	241	92
1123	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	210	78
1124	U83192	Homo sapiens	post-synaptic density protein 95	563	84
1126	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	142	60
1127	AB015348	Homo sapiens	HRHFB2060	599	96
1128	AF077207	Homo sapiens	HSPC021	640	90
1129	AF243044	Homo sapiens	ECST1	69	86
1130	AF016903	Homo sapiens	agrin precursor	271	75
1131	AF257319	Homo sapiens	SH3-containing protein SH3GLB2	713	69
1132	X64300	Oryctolagus cuniculus	cardiac calcium channel beta-subunit CaB3	480	89
1134	AF275816	Homo sapiens	PR-domain containing protein 9	74	64
1135	AF216389	Homo sapiens	semaphorin Rs	540	86

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1136	Z21707	Homo sapiens	polypeptide	309	71
1138	L28010	Homo sapiens	HnRNP F protein	179	96
1139	Y53005	Homo sapiens	Human secreted protein clone pm749.8 protein sequence SEQ ID NO: 16.	640	99
1142	M23725	Homo sapiens	M2-type pyruvate kinase	402	69
1143	L07955	Bos taurus	factor activating exoenzyme S	447	82
1144	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	156	62
1145	AF219114	Homo sapiens	chromatin remodelling factor SWI11Alpha	625	83
1146	AF194537	Homo sapiens	NAG13	102	61
1147	X82835	Homo sapiens	sodium channel alpha subunit	689	99
1155	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	217	72
1156	AF038995	Mus musculus	putative RNA helicase RCK.	212	62
1157	AF194537	Homo sapiens	NAG13	293	67
1164	U83303	Homo sapiens	line-1 reverse transcriptase	151	41
1167	AF035191	Homo sapiens	nuclear autoantigenic sperm protein autosomal variant	163	89
1172	D50683	Homo sapiens	TGF-beta1R alpha	614	86
1181	M12140	Homo sapiens	envelope protein	216	50
1182	AB020629	Homo sapiens	K1AA0822 protein	194	100
1183	L27428	Homo sapiens	reverse transcriptase	152	43
1184	AF003535	Homo sapiens	ORF2-like protein	158	51
1185	AE000375	Escherichia coli K12	putative actin	298	88
1187	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	93	73
1188	U36753	Homo sapiens	protease-activated receptor 2	168	66
1191	U15647	Mus musculus	reverse transcriptase	195	56
1194	AF025374	Homo sapiens	TIRC7	267	96
1202	M12140	Homo sapiens	envelope protein	295	44
1211	M93665	Bos taurus	casein kinase II alpha subunit	431	82
1212	X17025	Homo sapiens	homologue of yeast IPP isomerase	177	66
1217	U75916	Rattus norvegicus	zonula occludens 2 protein	201	72
1218	AB046048	Macaca fascicularis	unnamed portein product	115	68
1219	U93563	Homo sapiens	putative p150	157	39
1220	S80119	Rattus sp.	reverse transcriptase homolog	172	53
1221	Y34125	Homo sapiens	Human potassium channel K+Hnov27.	241	88
1222	AF030339	Homo sapiens	VESPR	296	86
1225	AF054502	Homo sapiens	latent transforming growth factor-beta binding protein 4	349	84
1226	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	116	77
1227	W47029	Homo sapiens	Human N-proteinase (70 kDa short form).	515	95
1230	AF090942	Homo sapiens	PRO0657	206	69
1233	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	180	70
1235	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	64	69
1240	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	112	64

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1243	U93574	Homo sapiens	putative p150	156	38
1246	U93570	Homo sapiens	p40	183	59
1247	R32563	Homo sapiens	HSA.	544	89
1248	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	606	94
1249	AF251146	Ovis aries	alpha-tubulin 1	546	86
1250	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	167	69
1251	U87607	Rattus norvegicus	putative RNA binding protein 1	234	41
1252	AF130089	Homo sapiens	PRO2550	205	61
1253	W58701	Homo sapiens	Human ST-2 partial sequence.	434	100
1255	U93567	Homo sapiens	putative p150	221	60
1256	AF072508	Homo sapiens	envelope protein	250	42
1261	AL035456	Homo sapiens	dJ1099D15.1 (A putative DNAJ protein)	277	83
1274	B01372	Homo sapiens	Neuron-associated protein.	205	75
1276	AF080234	Homo sapiens	polymerase	287	65
1278	Y36156	Homo sapiens	Human secreted protein #28.	103	47
1280	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	213	68
1282	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	217	76
1283	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	197	73
1284	AK023140	Homo sapiens	unnamed protein product	37	42
1291	AF308601	Homo sapiens	NOTCH 2	238	97
1292	AF072718	Homo sapiens	Key-1A6 protein	268	56
1293	AC005550	Homo sapiens	homeobox protein mox-2; match to P50222 (PID:g1709079)	597	82
1294	L27428	Homo sapiens	reverse transcriptase	275	52
1295	AF217374	Acanthaster planci	cytochrome oxidase subunit I	162	64
1299	AF194537	Homo sapiens	NAG13	180	46
1300	AF194537	Homo sapiens	NAG13	178	51
1301	AF194537	Homo sapiens	NAG13	174	51
1303	Z13007	Ovis aries	TCR gamma	197	42
1304	U93567	Homo sapiens	putative p150	132	46
1305	U93566	Homo sapiens	p40	149	49
1306	U93569	Homo sapiens	putative p150	317	66
1307	U83303	Homo sapiens	line-1 reverse transcriptase	151	41
1308	M59807	Homo sapiens	putative	398	71
1318	AF302773	Homo sapiens	ninein-Ln isoform	166	45
1319	Y17832	Human endogenous retrovirus K	env protein	338	54
1323	X98032	Homo sapiens	isoform I	369	60
1328	AL390114	Leishmania major	extremely cysteine/valine rich protein	156	50
1336	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	153	84
1339	AF235100	Homo sapiens	matrix protein for thyroid hormone synthesis	526	79
1342	X62048	Homo sapiens	Wee1 Hu	524	85
1343	U49974	Homo sapiens	mariner transposase	246	81
1346	S80119	Rattus sp.	reverse transcriptase homolog	163	53
1347	L04490	Homo sapiens	NADH dehydrogenase	832	84

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			(ubiquinone)		
1348	L11672	Homo sapiens	zinc finger protein	199	56
1351	Y79211	Homo sapiens	Human transferase TRNSFS-3.	319	100
1359	M16961	Homo sapiens	alpha-2-HS-glycoprotein	572	97
1360	R71333	Homo sapiens	Deduced sequence encoded by Wilson's disease gene cDNA.	488	96
1361	AF070598	Homo sapiens	ABC transporter	179	71
1363	AF003535	Homo sapiens	ORF2-like protein	183	54
1364	U05340	Homo sapiens	p55CDC	583	91
1365	Y18097	Homo sapiens	Human Sel-IL protein sequence.	253	72
1366	AB040893	Homo sapiens	KIAA1460 protein	269	78
1367	D63880	Homo sapiens	KIAA0159 gene product is related to yeast protein L8479.14.	217	75
1368	U84401	Homo sapiens	smoothened	443	98
1369	AF072506	Homo sapiens	envelope protein precursor	548	88
1370	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	60	54
1372	AB019435	Homo sapiens	phospholipase	549	87
1377	M63014	Homo sapiens	serum paraoxonase	148	50
1378	V01201	Simian sarcoma virus	coding sequence of pol	246	56
1379	L19297	Homo sapiens	carbonic anhydrase V	341	100
1380	AF121255	Homo sapiens	protein translation initiation factor 2C2; EIF2C2	208	90
1381	L38820	Homo sapiens	CD1D antigen	545	82
1386	X65019	Homo sapiens	interleukin-1B converting enzyme	577	94
1387	Z97074	Homo sapiens	p40	481	81
1388	D23660	Homo sapiens	ribosomal protein	565	86
1392	Z75536	Caenorhabditis elegans	contains similarity to Pfam domain: PF00226 (DnaJ domain), Score=44.2, E-value=9.7e-10, N=1-cDNA EST yk250d6.5 comes from this gene-cDNA EST yk398h12.5 comes from this gene	180	41
1393	AF143536	Homo sapiens	colon cancer-associated protein Mic1	477	79
1397	AF112227	Homo sapiens	TDE homolog	270	89
1402	W88461	Homo sapiens	Human 7-transmembrane receptor HEOAD54 polypeptide.	510	95
1404	AB047600	Macaca fascicularis	hypothetical protein	67	66
1405	AF121141	Homo sapiens	endocrine regulator	363	71
1406	Y73363	Homo sapiens	HTRM clone 2762174 protein sequence.	215	46
1408	U93574	Homo sapiens	putative p150	181	39
1413	X16356	Homo sapiens	TM3-CEA protein	279	45
1415	U16844	Simian SRV-like type D retrovirus	envelope protein gp20E	199	37
1416	D14497	Homo sapiens	proto-oncogene protein	405	88
1417	AB011158	Homo sapiens	KIAA0586 protein	373	97
1421	U95006	Homo sapiens	D9 splice variant A	145	100
1422	G00542	Homo sapiens	Human secreted protein, SEQ	47	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 4623.		
1423	U55772	Mus musculus	p170 phosphatidylinositol 3-kinase	172	70
1424	D63998	Homo sapiens	golgi alpha-mannosidase II	185	83
1425	A1035659	Homo sapiens	dj979N1.3 (novel protein)	305	49
1426	AF016099	Mus musculus	endonuclease/reverse transcriptase	168	36
1427	AK027124	Homo sapiens	unnamed protein product	613	96
1428	AF068227	Homo sapiens	putative transmembrane protein	335	91
1431	Z47552	Homo sapiens	flavin-containing monooxygenase 3 (FMO3)	539	87
1435	L11932	Homo sapiens	serine hydroxymethyltransferase	185	75
1438	AK023550	Homo sapiens	unnamed protein product	161	93
1441	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	89	84
1442	M27819	Homo sapiens	anion exchange protein 1	215	97
1444	AF119851	Homo sapiens	PRO1722	174	68
1450	X12662	Homo sapiens	arginase	158	64
1452	AF178669	Rattus norvegicus	p34	147	78
1453	A22096	Homo sapiens	plasminogen	638	85
1456	U60269	Homo sapiens	putative envelope protein;orf similar to env of Type A and Type B retroviruses and to class II HERVs	348	65
1458	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	259	94
1459	AJ132949	Homo sapiens	rfg5 protein	51	75
1460	S75295	Homo sapiens	nucleoprotein interactor 1, NPI-1=SRP1 homolog	1022	98
1461	AF174601	Homo sapiens	F-box protein Fbx21	176	94
1462	U60803	Homo sapiens	clathrin heavy chain 2	285	80
1466	AF108420	Takifugu rubripes	l-aminocyclopropane-carboxylate synthase	181	41
1467	L10986	Caenorhabditis elegans	putative	213	35
1469	AB049837	Macaca fascicularis	hypothetical protein	425	84
1471	AF164614	Homo sapiens	Gag-Pro-Pol protein	76	41
1475	AF010406	Ovis aries	cytochrome c-oxidase subunit 2	166	59
1478	AF010406	Ovis aries	cytochrome c-oxidase subunit 2	179	64
1480	AE000430	Escherichia coli K12	putative cellulose synthase	555	91
1484	U82664	Escherichia coli	similar to M. jannaschii MG372	573	85
1487	X97452	Escherichia coli	paaA	532	93
1488	AF009205	Homo sapiens	unknown	196	86
1490	D90741	Escherichia coli	MdoG protein.	156	84
1492	AB002292	Homo sapiens	KIAA0294	172	83
1494	M62747	Escherichia coli	RNase E	467	89
1498	U28377	Escherichia coli	ORF f288	225	83
1499	X72298	Escherichia coli	member of cooF family containing 4Fe/4S iron sulfur centre	280	85

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1501	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	156	65
1502	M27058	Escherichia coli	anaerobic class I fumarase (EC 4.2.1.2)	152	77
1505	D90702	Escherichia coli	Citrate lyase alpha chain (acyl lyase subunit) (citF) homolog	442	85
1507	X04619	Escherichia coli	A protein (AA 1-388)	175	86
1509	J03795	Escherichia coli	herC protein	295	80
1510	AE000467	Escherichia coli K12	heat shock protein hslVU, ATPase subunit, homologous to chaperones	420	85
1524	AL138641	Arabidopsis thaliana	putative protein	256	45
1525	S65762	Homo sapiens	beta-fodrin	643	93
1526	AF206329	Mus musculus	polydrom protein	524	83
1527	AF038441	Homo sapiens	phospholipase D2	224	100
1528	AF145710	Homo sapiens	calcium/calmodulin-dependent protein kinase II alpha subunit	595	83
1531	AF022795	Homo sapiens	TGF beta receptor associated protein-1	596	87
1534	W59357	Homo sapiens	Human retinal degeneration B1 polypeptide (hrdgB1).	681	95
1536	Y73387	Homo sapiens	HTRM clone 3340290 protein sequence.	64	92
1537	AJ132948	Homo sapiens	rfg7 protein	581	91
1538	M17885	Homo sapiens	acidic ribosomal phosphoprotein (P0)	593	87
1541	AL359061	Homo sapiens	KIAA1199 hypothetical protein	263	60
1543	AL117354	Homo sapiens	dJ976O13.1 (CGI-100 protein)	466	91
1545	AK023136	Homo sapiens	unnamed protein product	299	93
1550	AE003620	Drosophila melanogaster	CG7810 gene product	157	50
1551	AF062655	Mus musculus	plenty-of-prolines-101; POP101; SH3-philo-protein	557	92
1552	AL390114	Leishmania major	extremely cysteine/valine rich protein	195	48
1553	Y44905	Homo sapiens	Human potassium channel molecule ERG-LP2 partial protein.	595	94
1558	AF132021	Homo sapiens	myosin X	674	95
1567	AJ272269	Homo sapiens	zinc-binding protein	291	40
1568	AF207702	Homo sapiens	homeodomain-interacting protein kinase 2	502	71
1569	R41333	Homo sapiens	113 kD ISGF-3alpha.	335	85
1571	AF264780	Homo sapiens	sporulation-induced transcript 4-associated protein SAPLb	478	94
1572	AF217411	Homo sapiens	neuroigin 3 isoform HNL3	651	94
1573	A21577	Homo sapiens	blood plasma component having a biological activity of inhibiting cytolysis mediated by a cytolytic protein	539	79
1574	U47924	Homo sapiens	isopeptidase T	593	87
1575	X05236	Homo sapiens	aldolase A (AA 1-364)	605	92
1576	AB046775	Homo sapiens	KIAA1555 protein	591	86
1578	U87223	Homo sapiens	contactin associated protein	37	35
1579	AL359782	Trypanosoma brucei	possible (hvh-6) u1102, variant a dna, complete virion genome.	156	53

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1580	AF294790	Mus musculus	RING-finger protein MURF	358	84
1584	AB033615	Mus musculus	phospholipase C-L2	398	56
1585	AL132654	Homo sapiens	dJ450M14.2 (novel protein similar to KIAA0188, KIAA0249 and yeast SMP2)	534	96
1587	U17474	Homo sapiens	autoantigen	355	76
1588	AB019435	Homo sapiens	phospholipase	174	88
1589	AF119851	Homo sapiens	PRO1722	165	73
1591	W64469	Homo sapiens	Human secreted protein from clone CW795_2	157	57
1593	AK023397	Homo sapiens	unnamed protein product	611	96
1595	AB046020	Macaca fascicularis	unnamed protein product	404	96
1597	Y21011	Homo sapiens	Human glial fibrillary acidic protein GFAP mutant fragment 20.	420	98
1598	X95808	Homo sapiens	X-linked mental retardation candidate gene	386	87
1603	W85472	Homo sapiens	PS118 protein encoded by consensus sequence.	450	97
1605	AK000267	Homo sapiens	unnamed protein product	246	95
1606	Y10929	Homo sapiens	kruppel-type zinc finger protein	557	79
1607	AL445192	Homo sapiens	bA269H4.1 (KIAA1415, similar to T-Lymphoma invasion and metastasis inducing protein 1)	519	85
1608	AF076929	Homo sapiens	synphilin 1	612	93
1609	AF007833	Homo sapiens	kruppel-related zinc finger protein hckRox	711	82
1610	X99688	Homo sapiens	TYL	349	58
1612	AK027092	Homo sapiens	unnamed protein product	173	66
1613	AJ011654	Homo sapiens	triple LIM domain protein	380	67
1614	Z97630	Homo sapiens	dJ466N1.2 (glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase))	198	51
1615	Y17833	Human endogenous retrovirus K	env protein	264	43
1616	AB046029	Macaca fascicularis	unnamed protein product	635	94
1619	AF194537	Homo sapiens	NAG13	285	60
1620	AB002375	Homo sapiens	KIAA0377	158	73
1621	Y11618	Homo sapiens	Human 5' EST secreted protein SEQ ID NO:270.	482	88
1622	AF274863	Homo sapiens	secretory pathway component Sec31B-1	335	98
1623	X76858	Mus musculus	DNA binding protein	139	33
1624	L14851	Rattus norvegicus	neurexin III-alpha	740	80
1627	AC004549	Homo sapiens	TXBP151	384	83
1628	X05236	Homo sapiens	aldolase A (AA 1-364)	385	88
1630	Y99653	Homo sapiens	Human GTPase associated protein-4.	634	92
1631	Y00281	Homo sapiens	precursor	638	94
1632	M64982	Homo sapiens	common fibrinogen alpha chain	530	78
1633	M20022	Homo sapiens	HLA-E class I protein precursor	598	84
1634	X53827	Bos taurus	79KDa heat shock cognate protein	521	89

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1635	U05875	Homo sapiens	AF-1	702	89
1636	M95178	Homo sapiens	alpha-actinin	642	88
1637	U81031	Homo sapiens	OS9	324	92
1640	X86901	Homo sapiens	alpha-spectrin	400	90
1641	AF071172	Homo sapiens	HERC2	270	87
1642	D78012	Homo sapiens	dihydropyrimidinase related protein-1	601	87
1643	AB042824	Homo sapiens	DNA helicase recQ5 beta	681	97
1645	X97442	Homo sapiens	transmembrane protein	618	90
1646	AF003535	Homo sapiens	ORF2-like protein	153	46
1648	M64925	Homo sapiens	erythrocyte p55	643	91
1649	S69232	Homo sapiens	electron transfer flavoprotein-ubiquinone oxidoreductase, ETF-QO [EC 1.5.5.1]	188	86
1650	AF081484	Homo sapiens	alpha-tubulin isoform 1	646	92
1654	AX045409	synthetic construct	OP1	522	84
1655	S45936	Homo sapiens	HTS1	683	93
1656	U50330	Homo sapiens	procollagen C-proteinase	815	95
1657	S80119	Rattus sp.	reverse transcriptase homolog	223	45
1659	D63475	Homo sapiens	product is related to clathrin-associated protein.	631	91
1661	X52897	Homo sapiens	A1S9 protein (AA 1-803)	589	84
1662	Y48611	Homo sapiens	Human breast tumour-associated protein 72.	429	90
1663	AB019602	Homo sapiens	IDN3-B	469	74
1665	X52625	Rattus norvegicus	cytosolic 3-hydroxy 3-methylglutaryl coenzyme A synthase (AA 1-520)	210	67
1666	X80692	Homo sapiens	p97mapk	533	82
1667	AF093680	Homo sapiens	transcription factor IIB	624	88
1668	U14990	Homo sapiens	ribosomal protein S3	656	93
1669	Z49939	Saccharomyces cerevisiae	Rrp5p	335	50
1670	AC002550	Homo sapiens	Unknown gene product	509	85
1671	W29639	Homo sapiens	Human secreted protein CG99_2.	754	96
1672	AF081484	Homo sapiens	alpha-tubulin isoform 1	950	100
1673	U77415	Mus musculus	Bop1	1707	89
1674	AF081484	Homo sapiens	alpha-tubulin isoform 1	720	97
1675	AL110271	Homo sapiens	hypothetical protein	172	96
1676	AF190579	Ovis aries	ribosomal protein L32	270	94
1677	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	67	75
1678	W97778	Homo sapiens	Lens epithelial cell derived growth factor C-terminal polypeptide.	176	83
1681	AK000385	Homo sapiens	unnamed protein product	165	82
1682	AF118086	Homo sapiens	PRO1992	148	71
1683	D25538	Homo sapiens	KIAA0037	156	76
1684	AL096857	Homo sapiens	hypothetical protein	393	86
1688	AF090942	Homo sapiens	PRO0657	154	47
1689	AL096857	Homo sapiens	hypothetical protein	398	85
1690	AL096857	Homo sapiens	hypothetical protein	293	100
1692	X01469	Plasmodium falciparum	histidine-rich protein	237	37
1693	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	149	47

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1694	G00962	Homo sapiens	Human secreted protein, SEQ ID NO: 5043.	317	98
1696	AF061935	Homo sapiens	HIV-1 Vpr-binding protein	173	78
1698	AK023121	Homo sapiens	unnamed protein product	129	67
1699	AL049843	Homo sapiens	dJ392M17.3 (KIAA0349 protein)	204	97
1702	AJ238248	Homo sapiens	centaurin beta2	37	33
1704	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	85	54
1705	M97886	Canis familiaris	adenylyl cyclase	455	100
1706	W80369	Homo sapiens	A human interferon-alpha-induced protein.	912	99
1707	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	145	70
1713	AF055995	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP100	310	96
1714	L19704	Homo sapiens	alternative first exon	239	97
1715	AF229255	Rattus norvegicus	delta Kalirin-7	163	80
1719	X76132	Homo sapiens	tumour suppressor	177	100
1720	AB020629	Homo sapiens	KIAA0822 protein	208	70
1721	AC006930	Homo sapiens	R33423.1	269	92
1726	AF159615	Homo sapiens	FGF receptor activating protein 1	242	77
1728	AB024445	Mus musculus	junctophilin type 1	554	99
1729	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	204	57
1731	W80369	Homo sapiens	A human interferon-alpha-induced protein.	809	98
1733	Y82704	Homo sapiens	Human glucose-dependent insulinotropic peptide receptor protein sequence.	44	40
1734	Y59748	Homo sapiens	Human normal ovarian tissue derived protein 25.	223	100
1739	Y13247	Homo sapiens	FB19 protein	730	97
1740	M74178	Homo sapiens	hepatocyte growth factor-like protein	538	95
1741	AL021571	Caenorhabditis elegans	predicted using GeneFinder	189	52
1742	AL021571	Caenorhabditis elegans	predicted using GeneFinder	205	53
1743	L38486	Homo sapiens	microfibril-associated glycoprotein 4	745	100
1744	X00198	Homo sapiens	myc protein (aa 253-439) (17 is 2nd base in codon)	245	86
1745	X66865	Bos taurus	guanylate cyclase	159	88
1747	U49058	Rattus norvegicus	rA4	172	54
1752	AF261917	Homo sapiens	RNA helicase II/Gu protein	180	61
1753	Y00724	Homo sapiens	prepro-alpha-2 chain	218	100
1754	AJ243835	Ctenopharyngodon idella	delta-9-desaturase	401	78
1755	U76618	Mus musculus	N-RAP	408	88
1756	Y57884	Homo sapiens	Human transmembrane protein HTMPN-8.	167	89
1758	AF229067	Homo sapiens	PADI-H protein	150	68
1759	M33475	Saguinus oedipus	MHC class IA protein precursor	421	79
1760	U93565	Homo sapiens	putative p150	208	64

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1761	X85018	Homo sapiens	UDP-GalNAc:polypeptide N-acetylglucosaminyl transferase	221	100
1762	AB020663	Homo sapiens	KIAA0856 protein	182	100
1765	R39472	Homo sapiens	HSA-vWF(470-713) fusion protein.	394	96
1766	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	561	88
1767	M10014	Homo sapiens	fibrinogen gamma-prime chain	595	86
1768	AL022313	Homo sapiens	dJ1119A7.2 (eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD) (EIF3-P66))	478	75
1770	D55654	Homo sapiens	cytosolic malate dehydrogenase	249	98
1779	D84430	Homo sapiens	phenylalanyl tRNA synthetase	461	95
1780	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	426	95
1781	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	580	96
1782	A00279	synthetic construct	Human serum albumin	556	89
1783	U81002	Homo sapiens	TRAF4 associated factor 1	185	94
1785	AF130089	Homo sapiens	PRO2550	39	75
1786	W30600	Homo sapiens	Human type V adenylyl cyclase protein sequence.	689	100
1787	AY004226	Homo sapiens	betaV spectrin isoform sigma3	684	96
1789	M86917	Homo sapiens	oxysterol-binding protein	390	74
1791	Y13386	Homo sapiens	Amino acid sequence of protein PRO247.	492	85
1792	A14656	synthetic construct	protein antigen	291	84
1795	U95090	Homo sapiens	F19541_1	160	89
1796	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	250	67
1799	U93565	Homo sapiens	putative p150	47	30
1806	AB021644	Homo sapiens	gonadotropin inducible transcription repressor-4	181	60
1809	W40054	Homo sapiens	P300/CBP-associated transcriptional cofactor P/CAF C-terminus.	167	79
1811	AC006528	Arabidopsis thaliana	putative DNA replication licensing factor	257	77
1815	AF155132	Homo sapiens	FOXJ2 forkhead factor	415	100
1821	AF119851	Homo sapiens	PRO1722	109	47
1825	AF235097	Homo sapiens	Hb2E	364	78
1829	AB021660	Homo sapiens	carbonic anhydrase VB	221	93
1830	AK022360	Homo sapiens	unnamed protein product	433	82
1831	W61534	Homo sapiens	Homo sapiens P-TEN tumour suppressor.	243	78
1835	AB040457	Homo sapiens	NCBE	645	100
1836	U49055	Rattus norvegicus	ra8	525	93
1838	L02543	Bos taurus	nicotinamide nucleotide transhydrogenase	274	100
1841	AF119851	Homo sapiens	PRO1722	85	76
1842	U66616	Homo sapiens	SWI/SNF complex 170 kDa subunit	1000	93
1844	Z12842	Oryctolagus	protein of unknown function	299	78

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		cuniculus			
1845	Z12842	Oryctolagus cuniculus	protein of unknown function	299	78
1846	AL138972	Unknown	/prediction=(method:"genscan", version:"1.0", score:"119.22"); /prediction=(method:	212	35
1847	AC006644	Caenorhabditis elegans	similar to Saccharomyces cerevisiae SSM4 protein (PID:g505184)	487	48
1848	D89729	Homo sapiens	CRM1 protein	210	91
1849	AK001858	Homo sapiens	unnamed protein product	311	86
1850	AE000463	Escherichia coli K12	putative glycosidase	254	100
1852	AE000463	Escherichia coli K12	putative glycosidase	254	100
1854	AE000463	Escherichia coli K12	putative glycosidase	254	100
1855	AE000463	Escherichia coli K12	putative glycosidase	254	100
1856	Y11484	Homo sapiens	phosphoenolpyruvate carboxykinase (GTP)	353	76
1857	AK001691	Homo sapiens	unnamed protein product	210	95
1858	D31764	Homo sapiens	KIAA0064	1262	100
1860	AB018580	Homo sapiens	hluPGFS	154	73
1863	AF153679	Homo sapiens	malonyl-CoA decarboxylase	261	96
1864	AF153679	Homo sapiens	malonyl-CoA decarboxylase	261	96
1866	G01034	Homo sapiens	Human secreted protein, SEQ ID NO: 5115.	159	56
1869	AC007228	Homo sapiens	BC37295.1	725	100
1870	Y02376	Homo sapiens	Polypeptide identified by the signal sequence trap method.	171	100
1872	AF109907	Homo sapiens	S171	890	100
1873	AB023203	Homo sapiens	KIAA0986 protein	622	92
1874	X95325	Homo sapiens	DNA-binding protein	166	94
1875	AF272390	Homo sapiens	myosin 5c; myosin Vc	200	95
1877	AF176832	Homo sapiens	low density lipoprotein receptor related protein-deleted in tumor	595	100
1878	X78801	Gallus gallus	ovomacroglobulin, ovostatin	319	31
1880	AF093097	Homo sapiens	putative RNA-binding protein Q99	155	93
1881	W75051	Homo sapiens	Fragment of human secreted protein encoded by gene 153.	177	100
1882	X55544	Homo sapiens	TREB protein	547	83
1885	AF216833	Homo sapiens	M-ABC2 protein	324	87
1886	AF178948	Homo sapiens	TALE homeobox protein Meis2a	583	100
1887	D42054	Homo sapiens	KIAA0092 gene product is distantly related to smooth muscle myosin.	396	100
1889	AL022165	Homo sapiens	dJ71L16.5 (KIAA0267 LIKE putative Na(+)/H(+) exchanger)	568	97
1891	AF033116	Mus musculus	Smad interacting protein 1	328	98
1893	AB029005	Homo sapiens	KIAA1082 protein	346	91
1894	AB029005	Homo sapiens	KIAA1082 protein	950	100
1896	U49974	Homo sapiens	mariner transposase	398	77
1897	AP001660	Homo sapiens	putative gene, multidrug resistance associated protein like	436	97

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1898	U22325	Mus musculus	Fgd1	266	97
1900	AB037675	Homo sapiens	PEST-containing nuclear protein	758	100
1902	AC003007	Homo sapiens	Unknown gene product (partial)	191	74
1904	AF064729	Homo sapiens	RAN binding protein 16	782	100
1906	AF283991	Homo sapiens	(N6-adenosine)-methyltransferase	676	96
1908	Y31237	Homo sapiens	Human Apo B protein fragment.	1497	100
1909	B12453	Homo sapiens	Human HNRCR protein SEQ ID NO:20.	203	74
1910	D45132	Homo sapiens	zinc-finger DNA-binding protein	97	54
1911	AB050502	Homo sapiens	vascular adhesion protein-1	456	86
1912	D64000	Synechocystis sp.	hypothetical protein	44	45
1913	AF070598	Homo sapiens	ABC transporter	496	100
1917	AF151840	Homo sapiens	CGI-82 protein	481	100
1920	AF273047	Homo sapiens	CTCL tumor antigen se20-7	208	97
1921	P90387	Homo sapiens (Human)	N-terminal of human serum albumin polypeptide.	178	97
1922	U02313	Mus musculus	protein kinase	1422	82
1924	U18374	Rattus norvegicus	farnesoid X activated receptor	147	100
1925	U35113	Homo sapiens	metastasis-associated gene	1380	81
1928	U29725	Homo sapiens	BMK1 alpha kinase	42	42
1929	A014404	Homo sapiens	kinesin-like protein RBKIN2	297	98
1930	U85193	Homo sapiens	nuclear factor I-B2	566	100
1931	D64000	Synechocystis sp.	hypothetical protein	43	45
1934	M64934	Homo sapiens	kell blood group protein	217	97
1935	U35113	Homo sapiens	metastasis-associated gene	512	59
1936	Z49878	Homo sapiens	guanidinoacetate N-methyltransferase	267	85
1937	U35113	Homo sapiens	metastasis-associated gene	167	49
1938	U97001	Caenorhabditis elegans	similar to Schizosaccharomyces pombe 4-nitrophenylphosphatase (PNPPASE) (GB:X62722, NID:g5005)	292	51
1939	U95000	Homo sapiens	hyd protein	845	94
1940	AC006042	Homo sapiens	supported by human ESTs AI681256.1(NID:g4891438),N 32168.1(NID:g1152567), and genscan	256	82
1941	AF301013	Homo sapiens	regulator of nonsense transcripts 2	362	98
1942	U12728	Homo sapiens	hCRMP-1	259	96
1943	D21102	Homo sapiens	prolyl endopeptidase	163	96
1946	AB011155	Homo sapiens	KIAA0583 protein	2017	100
1947	AF118090	Homo sapiens	PRO2044	203	97
1948	AF130089	Homo sapiens	PRO2550	227	66
1951	U51336	Homo sapiens	inositol 1,3,4-trisphosphate 5/6-kinase	169	100
1952	W56766	Homo sapiens	Homo sapiens LexA-PS-1 fusion protein.	168	100
1956	AF117210	Homo sapiens	host cell factor 2	582	91
1957	D21102	Homo sapiens	prolyl endopeptidase	163	96
1959	AJ276485	Homo sapiens	integral membrane transporter	189	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			protein		
1960	B12453	Homo sapiens	Human HNRCR protein SEQ ID NO:20.	179	57
1961	AF094519	Mus musculus	diaphanous-related formin; p134 mDia2	478	76
1963	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	175	80
1964	X65019	Homo sapiens	interleukin-1B converting enzyme	581	92
1970	AF257660	Sus scrofa	crocalbin-like protein	344	96
1971	AF169035	Homo sapiens	protein kinase	172	96
1973	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	151	78
1974	AE003820	Drosophila melanogaster	CG13320 gene product	168	41
1975	U57796	Homo sapiens	zinc finger protein	505	72
1976	U16296	Homo sapiens	TIAMI protein	189	97
1979	W73629	Homo sapiens	Human secreted protein clone cd265_11.	200	97
1984	D87438	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	183	97
1985	D84430	Homo sapiens	phenylalanyl tRNA synthetase	525	89
1987	W93828	Homo sapiens	Human GUS protein fragment.	228	86
1989	AJ271736	Homo sapiens	hypothetical protein	150	87
1993	W54083	Homo sapiens	Homo sapiens BARD1 Pdelta1140-1160 sequence.	181	92
1994	AL359617	Homo sapiens	hypothetical protein	614	97
1996	A210818	Homo sapiens	SWAP-70	194	100
1997	D14849	Mus musculus	meiosis-specific nuclear structural protein 1	497	86
1998	U97001	Caenorhabditis elegans	similar to Schizosaccharomyces pombe 4-nitrophenylphosphatase (PNPPASE) (GB:X62722, NID:g5005)	299	53
1999	W97778	Homo sapiens	Lens epithelial cell derived growth factor C-terminal polypeptide.	195	90
2000	AB029039	Homo sapiens	KIAA1116 protein	281	94
2002	U73199	Mus musculus	Rho-guanine nucleotide exchange factor	281	59
2008	D86982	Homo sapiens	similar to human ankyrin 1(S08275)	613	100
2009	B25777	Homo sapiens	Human secreted protein SEQ ID #89.	617	98
2011	AF051850	Homo sapiens	supervillin	158	96
2012	AF117888	Homo sapiens	myosin-IXa	164	91
2014	AJ132591	Homo sapiens	zinc finger protein	626	95
2015	AB033098	Homo sapiens	KIAA1272 protein	323	90
2017	U17278	Homo sapiens	hCRMP-1	212	89
2018	M26268	Homo sapiens	lecithin:cholesterol acyltransferase precursor	169	96
2019	U49719	Homo sapiens	hydroxymethylglutaryl-CoA lyase	222	100
2020	U80735	Homo sapiens	CAGF28	577	97
2021	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	149	72
2023	AJ010232	Homo sapiens	RET finger protein-like 3	167	57

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2024	U06631	Homo sapiens	homologous to mouse gene PC326:GenBank Accession Number M95564	249	94
2025	AF119845	Homo sapiens	PRO1304	602	100
2026	AK021815	Homo sapiens	unnamed protein product	567	92
2027	AC007228	Homo sapiens	BC37295_1	176	100
2030	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	549	95
2032	AJ252060	Homo sapiens	TRABID protein	88	70
2033	U58088	Homo sapiens	Hs-CUL-2	166	77
2034	U50078	Homo sapiens	p532	211	100
2037	AF164611	Homo sapiens	Gag-Pro-Pol-Env protein	252	67
2038	AE003603	Drosophila melanogaster	CG10233 gene product	148	41
2040	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	293	96
2041	U72742	Oryctolagus cuniculus	UDP-glucuronosyltransferase	202	86
2042	M95724	Homo sapiens	centromere autoantigen C	171	100
2043	AB046825	Homo sapiens	KIAA1605 protein	160	93
2044	AB029089	Oryctolagus cuniculus	eukaryotic polypeptide chain release factor 1	263	87
2045	AJ010232	Homo sapiens	RET finger protein-like 3	167	57
2046	L28956	Mus musculus	CTP:phosphocholine cytidyltransferase	244	92
2048	AF012281	Homo sapiens	PDZ domain containing-protein; PDZK1	180	75
2049	AL133174	Homo sapiens	dJ470L14.1.1 (Isoform 1 of chromosome segregation 1 (yeast homolog)-like (CSE1L))	174	100
2051	U47741	Homo sapiens	CREB-binding protein	342	100
2052	AF047042	Homo sapiens	citrate synthase	335	90
2053	L40631	Mus musculus	ankyrin 3	146	75
2055	AB012223	Canis familiaris	ORF2	158	65
2057	AC006528	Arabidopsis thaliana	putative DNA replication licensing factor	257	77
2058	AK026262	Homo sapiens	unnamed protein product	750	100
2062	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	149	72
2065	AF025794	Homo sapiens	methionine synthase reductase	181	97
2066	AF151803	Homo sapiens	CGI-45 protein	621	84
2067	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	150	55
2074	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1))	161	90
2076	AF257305	Homo sapiens	ASH1	639	100
2077	AF165517	Homo sapiens	17-beta-hydroxysteroid dehydrogenase type VII	55	90
2079	U32519	Homo sapiens	GAP SH3 binding protein	208	90
2081	AB012223	Canis familiaris	ORF2	158	65
2082	M32082	Homo sapiens	phosphoribosylglycinamide formyltransferase	212	91
2083	Z24725	Homo sapiens	mitogen inducible gene mig-2	229	100
2084	M75106	Homo sapiens	prepro-plasma carboxypeptidase B	789	99
2085	AL080243	Homo sapiens	E1A binding protein p300; match: proteins: Sw Q09472	763	98

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			Sw:Q92793 Sw:P45481 Wp:CE00571 Wp:CE21117 Tr:O01368 Wp:CE08356 Wp:CE00570 Wp:CE08453 Tr:O44076		
2086	AL022165	Homo sapiens	dJ71L16.5 (KIAA0267 LIKE putative Na(+)/H(+) exchanger)	566	94
2087	AC007228	Homo sapiens	BC37295_1	166	100
2089	L02897	Canis familiaris	beta-spectrin	35	46
2090	AL355178	Homo sapiens	dJ947L8.1.5 (novel CUB domain protein)	233	70
2092	AL022165	Homo sapiens	dJ71L16.5 (KIAA0267 LIKE putative Na(+)/H(+) exchanger)	614	100
2097	AF124145	Homo sapiens	autocrine motility factor receptor	548	98
2099	Y78795	Homo sapiens	Human antizucal-2 (AZ-2) amino acid sequence.	609	92
2102	AB023218	Homo sapiens	KIAA1001 protein	162	96
2103	D28483	Homo sapiens	SCR3	152	100
2105	Y25426	Homo sapiens	Human SIGIRR protein.	542	99
2106	AF116645	Homo sapiens	PRO1708	158	71
2107	AK023084	Homo sapiens	unnamed protein product	564	84
2108	AY008372	Homo sapiens	oxysterol binding protein-related protein 3	945	99
2109	X61296	Rattus norvegicus	open reading frame 2	163	37
2110	AC003007	Homo sapiens	Unknown gene product (partial)	191	74
2112	AB019987	Homo sapiens	chromosome-associated polypeptide-C	63	100
2113	D87451	Homo sapiens	Contains C3HC4 type zinc finger signature	494	81
2115	X64728	Homo sapiens	hCHML	825	100
2117	AC002080	Homo sapiens	receptor protein tyrosine kinase	691	99
2121	L16876	Homo sapiens	cytochrome P-450C18	511	86
2122	AB002366	Homo sapiens	KIAA0368	1023	100
2125	Y94928	Homo sapiens	Human secreted protein clone pg195_1 protein sequence SEQ ID NO:62.	423	73
2126	AF027770	Mycobacterium smegmatis	unknown	183	36
2128	M12987	Plasmid F	Protein A	490	86
2129	D90807	Escherichia coli	ORF ID: o317#1; similar to	698	95
2130	X60200	Escherichia coli	transposase	186	71
2132	AE000278	Escherichia coli K12	putative resistance protein	555	92
2135	AF009205	Homo sapiens	unknown	206	86
2136	M60916	Escherichia coli	cytidine deaminase	232	100
2137	AB002292	Homo sapiens	KIAA0294	217	79
2138	X01653	Escherichia coli	adenylate cyclase	192	93
2139	AF009205	Homo sapiens	unknown	191	92
2140	AF009205	Homo sapiens	unknown	182	90
2141	M12987	Plasmid F	Protein A	297	98
2142	D90699	Escherichia coli	Bacteriophage n4 adsorption inner membrane protein NfrB.	501	82
2144	L25859	Escherichia coli	cydD	274	91

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		coli			
2145	U14003	Escherichia coli	fumarate reductase, flavoprotein subunit	565	83
2148	AF009205	Homo sapiens	unknown	155	82
2149	X04619	Escherichia coli	A protein (AA 1-388)	244	95
2150	D90884	Escherichia coli	BENZENE 1,2-DIOXYGENASE BETA SUBUNIT (EC 1.14.12.3) (P2 SUBUNIT).	546	87
2151	X06331	Escherichia coli	leucyl-tRNA synthetase	173	100
2152	AF064539	Bacteriophage N15	gp5	510	89
2153	X69182	Escherichia coli	deoxyribodipyrimidine photolyase	185	97
2156	M20791	Escherichia coli	secA protein	535	93
2157	AF228498	Escherichia coli	KbaZ	160	100
2161	AE000458	Escherichia coli K12	ATP-dependent DNA helicase	415	90
2162	U28377	Escherichia coli	ORF_1848	171	100
2163	U00006	Escherichia coli	No definition line found	310	76
2166	D90757	Escherichia coli	Respiratory nitrate reductase 1 alpha chain (EC 1.7.99.4).	226	91
2167	D90769	Escherichia coli	ATH1 protein.	254	96
2168	X03895	Escherichia coli	UDP-sugar hydrolase	554	92
2171	U18997	Escherichia coli	glucose-1-phosphate adenylyltransferase	195	97
2172	M63939	Escherichia coli	transfer RNA-guanine transglycosylase	542	91
2175	X68301	Escherichia coli	NADH dehydrogenase I, subunit nuoC	164	96
2176	U00039	Escherichia coli	No definition line found	484	93
2177	U00039	Escherichia coli	No definition line found	194	94
2178	D90721	Escherichia coli	Hypothetical 67.7 kd protein CY02B10.18C.	168	100
2179	X66086	Escherichia coli	pyridine nucleotide transhydrogenase	508	91
2180	X69089	Homo sapiens	165kD protein	234	88
2181	AF233324	Salmonella typhimurium LT2	97% identity with amino acids 1-317 of E. coli putative ATP-dependent RNA helicase (RHLB) (SP:P24229); contains similarity to Pfam family PF00270 (DEAD/DEAH box helicase), score=186.5, E=4.6e-58, N=1	258	87
2182	X04619	Escherichia coli	A protein (AA 1-388)	157	86
2183	AF009205	Homo sapiens	unknown	155	82
2185	D90393	Escherichia coli	PhoQ protein	597	97

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SEQ ID NO.	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		coli			
2187	X14152	Escherichia coli	SrmB protein	240	95
2188	M10101	Escherichia coli	IMP dehydrogenase	216	91
2189	D90791	Escherichia coli	ORF_ID:o280#4; similar to	589	93
2190	Z21844	Escherichia coli	adenylyl-transferase	541	93
2192	X04306	Escherichia coli	3-dehydroquinase (aa 1-240)	307	85
2193	U14336	Citrobacter freundii	6-phosphogluconate dehydrogenase	545	93
2195	X14430	Escherichia coli	ORF A gene product (AA 1 - 179)	514	88
2197	K00985	Escherichia coli	DNA polymerase III epsilon subunit	272	98
2198	M83316	Escherichia coli	pppGpp phosphohydrolase	207	95
2199	V00371	Escherichia coli	tryptophanyl-tRNA synthetase	183	90
2201	X04341	Escherichia coli	gyrase B (AA 1-804)	552	92
2203	D90747	Escherichia coli	Transcription-repair coupling protein mfd	183	97
2204	AE000351	Escherichia coli K12	orf, hypothetical protein	512	91
2205	D90795	Escherichia coli	Pectinase gene transcriptional regulator.	199	97
2206	Y09439	Escherichia coli	UUP protein	490	88
2207	AF238234	Entamoeba histolytica	diaphanous protein	167	44
2210	L10328	Escherichia coli	f445	492	83
2212	AF009204	Homo sapiens	PSD-95/SAP90-associated protein-2	210	95
2214	U82664	Escherichia coli	similar to M. fervidus malate dehydrogenase	551	93
2215	D90864	Escherichia coli	OUTER MEMBRANE USHER PROTEIN PAPC PRECURSOR.	193	100
2216	M12987	Plasmid F	Protein A	298	94
2218	AB002292	Homo sapiens	KIAA0294	542	99
2219	U00008	Escherichia coli	yejK	201	79
2220	U28379	Escherichia coli	ORF_f254	145	83
2221	U18997	Escherichia coli	ORF_o462	202	93
2223	U18997	Escherichia coli	ORF_o388	205	97
2225	D90843	Escherichia coli	Phosphomannomutase (EC 5.4.2.8) (PMM).	481	83
2227	D90701	Escherichia coli	ORF_ID:o166#4	538	91
2229	D90835	Escherichia coli	Porin OmpC	159	91
2230	AE000115	Escherichia coli	survival protein	241	95

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		coli K12			
2231	U14003	Escherichia coli	phosphotransferase system trehalose permease	175	91
2233	X02307	Escherichia coli	aspartase	518	94
2234	J05492	Escherichia coli	cytochrome o ubiquinol oxidase C subunit	155	91
2235	D90741	Escherichia coli	Novobiocin resistance-related protein Nov	218	97
2237	D90747	Escherichia coli	Transcription-repair coupling protein mfd	216	93
2238	X04619	Escherichia coli	A protein (AA 1-388)	221	79
2240	D90733	Escherichia coli	Lon protease (lon) homolog	529	90
2241	AF009205	Homo sapiens	unknown	197	95
2242	AF009205	Homo sapiens	unknown	233	95
2244	X16584	Escherichia coli	5-methyltetrahydrofolate-homocysteine transferase (AA 1-1200)	673	96
2245	U00039	Escherichia coli	CG Site No. 18190	356	92
2248	U18997	Escherichia coli	ORF_o388	182	94
2249	D90704	Escherichia coli	Hypothetical protein SPAC24B11.10c	183	100
2250	M23550	Escherichia coli	inorganic pyrophosphatase	160	100
2252	M64675	Escherichia coli	tgs	171	100
2255	AJ237695	Escherichia coli	putative aliphatic sulfonate transport membrane component	162	96
2258	U18997	Escherichia coli	ORF_o622; reading frame open far upstream of start; possible frameshift, linking to previous ORF	199	87
2259	AF228498	Escherichia coli	AgdD	183	100
2261	D90855	Escherichia coli	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) chain A, anaerobic	157	100
2263	D83536	Escherichia coli	D-serine deaminase activator.	270	100
2264	U73857	Escherichia coli	hypothetical protein	355	94
2265	U28375	Escherichia coli	ORF_o292	151	100
2272	AE000432	Escherichia coli K12	putative dehydrogenase	192	100
2275	U18997	Escherichia coli	ORF_o783	264	96
2276	D83536	Escherichia coli	Lipid-a-disaccharide synthase (EC 2.4.1.182).	179	100
2281	AE000413	Escherichia coli K12	putative transport system permease protein	150	100
2283	X04581	Escherichia coli	exonuclease V (AA 1-1180)	302	92
2284	X04619	Escherichia coli	A protein (AA 1-388)	211	95

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2285	D83536	Escherichia coli	DNA polymerase III, alpha chain (EC 2.7.7.7).	164	96
2287	U29581	Escherichia coli	ORF_f447	193	100
2288	AE004123	Vibrio cholerae	iron-sulfur cluster-binding protein	389	69
2291	AE000273	Escherichia coli K12	orf, hypothetical protein	183	100
2293	AE000246	Escherichia coli K12	putative ATP-binding component of a transport system	254	96
2294	X13065	Bacteriophage phi-80	gene 14 (AA 1 - 229)	402	98
2295	V00361	Escherichia coli	thrA gene	173	100
2296	X69160	Escherichia coli	trehalose-6-phosphate synthase	166	100
2297	J05260	Escherichia coli	phnF protein	419	91
2299	D90733	Escherichia coli	Lon protease (lon) homolog	215	97
2302	M38304	Escherichia coli	RNA polymerase (rpoB)	403	91
2303	U93405	Escherichia coli	2,4-dienoyl-CoA reductase	156	100
2304	D90727	Escherichia coli	Dimethylsulfoxide reductase chain a	165	96
2306	L19201	Escherichia coli	formate dehydrogenase-O alpha subunit	239	100
2307	U00006	Escherichia coli	thiG	194	100
2309	X66836	Escherichia coli	inhibitor of chromosome initiation	150	100
2311	Y09439	Escherichia coli	UUP protein	166	96
2312	U14003	Escherichia coli	ORF_o761	207	100
2313	AF176620	Escherichia coli	RecC1001	161	100
2314	X04516	Escherichia coli	penicillin-binding protein 2 (PBP2)	156	100
2315	M92358	Escherichia coli	UDP-N-acetylglucosamine enolpyruvyl transferase	188	100
2316	AF053073	Shigella flexneri	YrbB	196	97
2317	M76411	Escherichia coli	cadA	213	97
2319	D90820	Escherichia coli	Selenide, water dikinase (EC 2.7.9.3) (Selenophosphate synthetase) (Selenium donor protein).	196	100
2321	D90745	Escherichia coli	ORF_ID:o237#7	204	100
2322	M93239	Escherichia coli	transmembrane protein	168	100
2323	M38319	Pseudomonas putida	RNA polymerase (rpoB) (EC 2.7.7.6)	172	91
2325	D90766	Escherichia coli	ORF_ID:o255#12; similar to	170	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2327	D90757	Escherichia coli	Respiratory nitrate reductase I alpha chain (EC 1.7.99.4).	238	95
2332	J05492	Escherichia coli	cytochrome o ubiquinol oxidase subunit II	152	100
2334	AE000258	Escherichia coli K12	orf, hypothetical protein	253	80
2335	U00039	Escherichia coli	nikB	182	100
2337	M58000	Escherichia coli	permease	269	98
2338	M92358	Escherichia coli	UDP-N-acetylglucosamine enolpyruvyl transferase	188	100
2339	L29397	Escherichia coli	phosphoglycerate dehydrogenase	183	100
2341	X54151	Escherichia coli	mprA	266	100
2342	M74072	Escherichia coli	tehB	150	100
2343	D90864	Escherichia coli	CHAPERONE PROTEIN PMFD PRECURSOR.	266	98
2344	L25055	Escherichia coli	NADH dehydrogenase	319	98
2345	X04619	Escherichia coli	A protein (AA 1-388)	213	75
2347	M12987	Plasmid F	Protein E	162	76
2349	AF119817	Homo sapiens	discs, large (Drosophila) homolog-associated protein 2	214	93
2350	U18997	Escherichia coli	ORF_f147; gtg start	209	100
2352	U28377	Escherichia coli	ORF_f390	164	96
2353	D90727	Escherichia coli	Dimethylsulfoxide reductase chain a	166	97
2355	V01498	Escherichia coli	aceF	159	100
2357	D90829	Escherichia coli	Flagellar biosynthesis protein FlhA.	208	100
2358	AE000474	Escherichia coli K12	regulator of acetyl CoA synthetase	184	85
2360	AB035920	Escherichia coli O157:H7	molybdopterin-guanine dinucleotide biosynthesis protein B	288	94
2361	X04619	Escherichia coli	A protein (AA 1-388)	251	97
2362	D90875	Escherichia coli	PUTATIVE MALATE OXIDOREDUCTASE (NAD) (EC 1.1.1.38) (MALIC ENZYME).	170	100
2363	AB016764	Escherichia coli	potB	162	100
2366	AE000114	Escherichia coli K12	possible synthesis of cofactor for carnitine racemase and dehydratase	174	96
2367	D90741	Escherichia coli	MdoG protein.	196	100
2368	AF119818	Homo sapiens	discs, large (Drosophila) homolog-associated protein 2	41	33
2369	U29579	Escherichia coli	alternate gene name ygbA; ORF_f117	229	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2370	D31701	<i>Escherichia coli</i>	MukB	288	96
2371	J04039	<i>Escherichia coli</i>	homologous to a Streptomyces cacaoi beta-lactamase regulatory protein	536	94
2372	D90778	<i>Escherichia coli</i>	RtoA protein.	200	100
2375	U73857	<i>Escherichia coli</i>	hypothetical protein	212	100
2380	J01652	<i>Escherichia coli</i>	motB protein for chemotaxis	163	100
2381	U18997	<i>Escherichia coli</i>	ORF_f646	215	83
2383	AE000411	<i>Escherichia coli</i> K12	probable phosphoribulokinase	203	97
2385	D90721	<i>Escherichia coli</i>	Hypothetical 51.7 kd protein in dnaJ-rpsU intergenic region.	579	99
2386	D90855	<i>Escherichia coli</i>	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) chain A, anaerobic	161	100
2389	U28377	<i>Escherichia coli</i>	ORF_o386; alternate name ygiC; orfA of M77129	152	100
2390	D90737	<i>Escherichia coli</i>	Sensor protein torS (EC 2.7.3.-)	154	100
2392	U14003	<i>Escherichia coli</i>	cycZ gene product	158	100
2394	U00009	<i>Escherichia coli</i>	yeeF	152	100
2395	AB000275	<i>Homo sapiens</i>	DAP-2	160	53
2396	D83536	<i>Escherichia coli</i>	Hypothetical protein 1	153	100
2397	D83536	<i>Escherichia coli</i>	Hypothetical 49.1 kd protein in odsA-hlpA intergenic region.	174	100
2400	AF039916	<i>Homo sapiens</i>	CD39L2	120	92
2401	AL035252	<i>Homo sapiens</i>	dJ738P15.2 (CD39-like 2 (a nucleoside phosphatase))	348	97
2402	AF039916	<i>Homo sapiens</i>	CD39L2	495	90
2403	AF176707	<i>Homo sapiens</i>	F-box protein FBX29	732	98
2404	M82977	<i>Bos taurus</i>	alpha-collagen	949	96
2405	U90313	<i>Homo sapiens</i>	glutathione-S-transferase homolog	147	96
2406	AJ006701	<i>Homo sapiens</i>	putative serine/threonine protein kinase	642	93
2407	AF147709	<i>Homo sapiens</i>	MYB-binding protein 1A	671	97
2408	AF177941	<i>Homo sapiens</i>	collagen type V alpha 3 chain	544	83
2409	Y99418	<i>Homo sapiens</i>	Human PRO1317 (UNQ783) amino acid sequence SEQ ID NO:277.	629	96
2412	J04569	<i>Homo sapiens</i>	glial fibrillary acidic protein	501	79
2413	X86691	<i>Homo sapiens</i>	Mt-2 protein	176	97
2414	U21734	<i>Caenorhabditis elegans</i>	UNC-44	162	32
2416	AJ223828	<i>Homo sapiens</i>	small glutamine-rich tetratricopeptide (SGT)	186	64
2417	AF179867	<i>Homo sapiens</i>	STE20-like kinase	654	95
2418	AF077818	<i>Mus musculus</i>	syntrophin-associated serine-threonine protein kinase	467	69
2419	AJ011372	<i>Homo sapiens</i>	sugar transporter	742	98
2421	M13577	<i>Homo sapiens</i>	myelin basic protein	563	92

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2422	G01395	Homo sapiens	Human secreted protein, SEQ ID NO: 5476.	267	80
2423	U37673	Homo sapiens	beta-NAP	685	95
2428	AF151843	Homo sapiens	CGI-85 protein	131	61
2429	U14972	Homo sapiens	ribosomal protein S10	264	83
2430	D50857	Homo sapiens	DOCK180 protein	467	73
2431	X56932	Homo sapiens	23 kD highly basic protein	529	78
2434	AC003682	Homo sapiens	ZNF134	420	71
2435	AF005043	Homo sapiens	poly(ADP-ribose) glycohydrolase	334	98
2436	M25013	Ctenopharyngodon idella	beta-actin	667	92
2438	L19704	Homo sapiens	alternative first exon	186	94
2439	X01703	Homo sapiens	alpha-tubulin	468	92
2440	D86966	Homo sapiens	similar to human ZFY protein.	412	55
2441	AE003444	Drosophila melanogaster	CG12125 gene product	154	65
2443	U22394	Mus musculus	mSin3A	702	98
2444	AF095150	Homo sapiens	protein O-mannosyl-transferase 1	552	100
2446	L32162	Homo sapiens	transcription factor	598	79
2447	X65157	Mus musculus	desmoyokin	235	36
2448	AC005498	Homo sapiens	R31665_1	366	62
2449	X87832	Homo sapiens	NOV/plexin-A1 protein	612	100
2451	AB020684	Homo sapiens	KIAA0877 protein	357	54
2452	AY010111	Homo sapiens	cadherin-23	621	98
2453	M22967	Bos taurus	synaptophysin	192	87
2454	AF288403	Mus musculus	putative transcription factor Zfp319	734	95
2455	U36918	Mesocricetus auratus	mucin	152	49
2456	Y17833	Human endogenous retrovirus K	env protein	73	39
2457	G03678	Homo sapiens	Human secreted protein, SEQ ID NO: 7759.	293	96
2459	AL121891	Homo sapiens	dJ1187M17.2 (KIAA0552 protein)	170	35
2460	X58199	Homo sapiens	beta adducin	590	89
2461	X76132	Homo sapiens	tumour suppressor	3929	100
2462	AL109804	Homo sapiens	dJ1009E24.1.1 (A novel protein similar to the mouse sialoadhesin, a macrophage sialic acid binding receptor, isoform 1)	717	100
2463	M22960	Homo sapiens	protective protein precursor	426	98
2464	AF130079	Homo sapiens	PRO2852	155	78
2465	AL333715	Homo sapiens	bK3184A7.3.1 (helicase-like protein NHL)	682	98
2466	AK023130	Homo sapiens	unnamed protein product	660	97
2467	AJ242523	Chlamydomonas reinhardtii	1 beta dynein heavy chain	469	63
2468	AB014516	Homo sapiens	KIAA0616 protein	702	96
2469	Y15067	Homo sapiens	ZNF232	213	37
2471	AL031588	Homo sapiens	dJ1163J1.1 (mostly supported by GENSCAN, FGENES and GENEWISE)	40	47
2472	W40412	Homo sapiens	Human NOS flavodoxin protein fragment.	211	95

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2473	AF248953	Homo sapiens	golgi matrix protein GM130	659	99
2474	AF263742	Homo sapiens	golgin-like protein	605	92
2475	D50925	Homo sapiens	The KIAA0135 gene is related to pim-1 oncogene.	192	100
2477	AB027251	Homo sapiens	zinc finger protein (ZFD25)	543	61
2478	W48848	Homo sapiens	Human receptor tyrosine kinase LMR3 h N-terminal polypeptide.	730	98
2479	AJ269499	Homo sapiens	lipoxigenase-3	642	96
2480	AF263742	Homo sapiens	golgin-like protein	453	77
2481	AF152097	Homo sapiens	CGI-05 protein	167	100
2483	AB037728	Homo sapiens	KIAA1307 protein	655	96
2484	AC005578	Homo sapiens	F20887_1, partial CDS	624	98
2485	AL117233	Homo sapiens	hypothetical protein	248	94
2486	AF308601	Homo sapiens	NOTCH 2	586	92
2487	AB023151	Homo sapiens	KIAA0934 protein	249	97
2489	AF031841	Caenorhabditis elegans	GLY7	341	50
2490	AJ225124	Mus musculus	hyperpolarization-activated cation channel, HAC3	253	94
2491	U47856	Araneus diadematus	fibroin-4	149	40
2492	AB011127	Homo sapiens	KIAA0555 protein	330	57
2493	G02402	Homo sapiens	Human secreted protein, SEQ ID NO: 6483.	305	93
2494	M27877	Homo sapiens	HPF1 protein	491	68
2495	AL390114	Leishmania major	probable proteophosphoglycan	195	47
2496	AL161502	Arabidopsis thaliana	putative WD-repeat membrane protein	299	42
2497	AF274058	Rattus norvegicus	GRIP-associated protein 1 short form	552	90
2498	AF044774	Homo sapiens	breakpoint cluster region protein 2	604	92
2499	AF313464	Rattus norvegicus	ankyrin repeat-rich membrane-spanning protein	661	98
2500	AF161544	Homo sapiens	HSPC059	503	66
2501	Y44453	Homo sapiens	Human carbamoyl phosphate synthase homologue.	624	88
2502	AF277374	Homo sapiens	enhancer of polycomb	670	92
2503	AF205935	Mus musculus	MGA protein	513	72
2504	AF234532	Homo sapiens	myosin X	758	100
2505	AF155132	Homo sapiens	FOXJ2 forkhead factor	1118	100
2507	AC007954	Homo sapiens	unknown	646	97
2508	AB037808	Homo sapiens	KIAA1387 protein	623	97
2509	AC004076	Homo sapiens	R30217_1	499	66
2510	Y79220	Homo sapiens	Human transferase TRNSFS-12.	594	94
2511	AK024186	Homo sapiens	unnamed protein product	365	78
2512	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	225	89
2514	AB029826	Homo sapiens	3-methylcrotonyl-CoA carboxylase biotin-containing subunit	292	94
2515	AF191337	Homo sapiens	anaphase-promoting complex subunit 2	651	98
2516	AF255326	Drosophila yakuba	unknown	119	29
2517	AK022708	Homo sapiens	unnamed protein product	245	48

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SEQ ID NO.	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2518	AK026410	Homo sapiens	unnamed protein product	609	98
2520	Y41716	Homo sapiens	Human PRO860 protein sequence.	602	87
2521	Y41716	Homo sapiens	Human PRO860 protein sequence.	631	90
2522	AF280816	Rattus norvegicus	nuclear GTPase PIKE	239	39
2523	AF231022	Homo sapiens	protocadherin Fat 2	337	85
2525	AJ293573	Homo sapiens	zinc finger protein Cezanne	342	78
2526	AJ293573	Homo sapiens	zinc finger protein Cezanne	326	76
2527	AB032261	Homo sapiens	stearoyl-CoA desaturase	739	100
2528	AF044414	Homo sapiens	alpha mannosidase 6A8B	700	97
2529	AJ271669	Homo sapiens	putative sialoglycoprotease	211	97
2531	AP002521	Oryza sativa	Similar to Drosophila melanogaster shuttle craft protein (U09306)	305	40
2532	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	76	60
2533	AB023656	Mus musculus	KIF1B-beta	662	93
2534	AX022162	unidentified	TPC2	574	86
2535	L31881	Homo sapiens	nuclear factor I-X	564	86
2536	Y27658	Homo sapiens	Human secreted protein encoded by gene No. 92.	349	95
2537	AF071172	Homo sapiens	HERC2	477	89
2538	G00988	Homo sapiens	Human secreted protein, SEQ ID NO: 5069.	610	90
2539	AB033026	Homo sapiens	KIAA1200 protein	657	100
2540	D42138	Homo sapiens	PIG-B	213	95
2541	AL121929	Homo sapiens	bA416N2.2 (similar to murine FISH (an SH3 and PX domain-containing protein, and Src substrate))	336	57
2542	AF102527	Mus musculus	olfactory receptor E3	363	53
2543	AF071172	Homo sapiens	HERC2	588	92
2544	AF076167	Rattus norvegicus	UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T6	408	81
2545	AJ272269	Homo sapiens	zinc-binding protein	610	96
2547	AL096711	Homo sapiens	dJ403A15.3 (novel protein)	270	50
2548	AF228058	Mus musculus	oracle 2 protein	37	37
2549	X60549	Saccharomyces cerevisiae	non-essential protein kinase	176	32
2550	L11370	Homo sapiens	protocadherin 42	599	88
2551	AF215896	Mus musculus	striated muscle-specific serine/threonine protein kinase	632	92
2552	AC004021	Homo sapiens	kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079096)	2590	100
2553	Y79220	Homo sapiens	Human transferase TRNSFS-12.	473	98
2554	AC002086	Homo sapiens	similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185)	588	90
2555	AF132021	Homo sapiens	myosin X	655	96
2556	AJ012824	Homo sapiens	huntingtin-associated protein 1	30	35
2557	AB016488	Homo sapiens	This gene includes jumping translocation breakpoint	654	98

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2605	AB002317	Homo sapiens	KIAA0319	480	76
2606	AB042199	Homo sapiens	APC-stimulated guanine nucleotide exchange factor	397	60
2607	AC003682	Homo sapiens	R27945.1	664	60
2608	U02313	Mus musculus	protein kinase	481	81
2609	U09413	Homo sapiens	zinc finger protein ZNF135	581	72
2610	U00001	Homo sapiens	Human homologue of S. pombe nuc2+ and A. nidulans bimA	414	67
2612	AB010071	Arabidopsis thaliana	gene_id:MCO15.7-	246	29
2613	AL035106	Homo sapiens	dJ998C11.1 (continues in Em:AL445192 as bA269H4.1)	538	75
2614	AL035106	Homo sapiens	dJ998C11.1 (continues in Em:AL445192 as bA269H4.1)	519	73
2616	AF217522	Homo sapiens	uncharacterized bone marrow protein BM046	230	46
2617	L05186	Homo sapiens	focal adhesion kinase	212	81
2618	D80011	Homo sapiens	similar to rat rhoGAP.	510	85
2619	AB001601	Homo sapiens	ATP-dependent RNA helicase #3	199	95
2620	AF081155	Rattus norvegicus	CL3AB	690	100
2621	AL137554	Homo sapiens	hypothetical protein	317	95
2622	AB046783	Homo sapiens	KIAA1563 protein	335	45
2623	AF188700	Homo sapiens	actin filament associated protein	689	97
2625	AF263913	Mus musculus	fidgetin	761	96
2626	AK000126	Homo sapiens	unnamed protein product	55	84
2627	AF026169	Homo sapiens	SALF	289	44
2628	AB046632	Macaca fascicularis	unnamed protein product	685	92
2629	AF217411	Homo sapiens	neuroigin 3 isoform HNL3	708	99
2630	U42580	Paramecium bursaria Chlorella virus 1	contains 10 ankryrin-like repeats; similar to human ankryrin, corresponds to Swiss-Prot Accession Number P16157	189	37
2631	AB015046	Homo sapiens	xylokinase	341	71
2632	AF175292	Mus musculus	neuronal IL-16	485	74
2633	AE004683	Pseudomonas aeruginosa	probable acyl-CoA dehydrogenase	206	53
2635	Y95436	Homo sapiens	Human calcium channel SOC-3/CRAC-2.	667	97
2636	AJ293624	Homo sapiens	type XIII collagen	374	52
2637	B06334	Homo sapiens	Human subtilisin-kexin isoenzyme 1.	585	88
2638	X59244	Homo sapiens	ZNF43	436	63
2639	AL080239	Homo sapiens	bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))	636	98
2641	AB022158	Mus musculus	chaperonin containing TCP-1 epsilon subunit	340	88
2642	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	154	64
2643	X68684	Homo sapiens	ZNF11B	267	54
2644	Y99355	Homo sapiens	Human PRO1295 (UNQ664) amino acid sequence SEQ ID NO:54.	605	96
2645	M12130	Mus musculus	RNA polymerase II	201	97

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2646	AJ278348	Homo sapiens	pregnancy-associated plasma protein-E	653	100
2647	AB046632	Macaca fascicularis	unnamed protein product	674	92
2648	AF182317	Homo sapiens	myoferlin	704	100
2650	AB011110	Homo sapiens	KIAA0538 protein	165	88
2651	AF152514	Homo sapiens	protocadherin gamma A7 short form protein	758	95
2654	AL031118	Homo sapiens	dJ153G14.3 (novel C2H2 type Zinc Finger protein)	223	39
2655	AC004770	Homo sapiens	BC269730_4	441	68
2657	X56597	Homo sapiens	fibrillarin	389	89
2658	AB023658	Rattus norvegicus	Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha	280	98
2660	Y94903	Homo sapiens	Human secreted protein clone pG32_1 protein sequence SEQ ID NO:12.	351	56
2663	AB011370	Mus musculus	Ankh3	412	76
2665	B20997	Homo sapiens	Human nucleic acid-binding protein, NuABP-1.	355	98
2666	R56494	Homo sapiens	TATA-binding protein-associated factor hTAFII130.	155	72
2667	AF105987	Homo sapiens	methylene tetrahydrofolate reductase	217	70
2670	D87076	Homo sapiens	similar to human bromodomain protein BR140(JC2069)	301	45
2671	AF228527	Homo sapiens	TRIAD3	55	100
2672	AB025259	Mus musculus	granuphilin-b	262	44
2674	U40714	Homo sapiens	tyrosyl-tRNA synthetase	635	91
2675	L20450	Mus musculus	DNA-binding protein	564	59
2677	X52142	Homo sapiens	CTP synthetase (AA 1-591)	274	96
2678	X53827	Bos taurus	79KDa heat shock cognate protein	636	94
2680	AJ131112	Sus scrofa	swine leucocyte antigen 2/2(SLA-2/2)	111	87
2681	AE003840	Drosophila melanogaster	CG1399 gene product	92	56
2682	AF013214	Bos taurus	acidic ribosomal phosphoprotein PO	548	88
2683	M29273	Homo sapiens	myelin-associated glycoprotein precursor	388	72
2684	AF082871	Homo sapiens	arsenate resistance protein ARS2	299	100
2686	M36676	Homo sapiens	apolipoprotein B100	518	77
2687	A00279	synthetic construct	Human serum albumin	648	96
2688	X15729	Homo sapiens	protein p68 (AA 1-614)	546	85
2689	U25634	Agrobacterium vitis	putative hydroxypyruvate reductase; inducible by tartrate; Method: conceptual translation supplied by author	194	37
2690	M33375	Homo sapiens	chlorocone reductase	38	100
2691	Y10816	Homo sapiens	Amino acid sequence of a human secreted protein.	315	96
2692	Z23064	Homo sapiens	hnRNP G protein	731	97
2693	X80754	Homo sapiens	GTP-binding protein	645	94
2694	AB024435	Homo sapiens	beta-1,4-galactosyltransferase III	656	95

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2695	AF073994	Drosophila melanogaster	gamma-tubulin	144	75
2696	Z98046	Homo sapiens	dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE)	677	91
2697	J04209	Cricetulus griseus	inosine-5'-monophosphate dehydrogenase	379	92
2698	AJ245820	Homo sapiens	type I transmembrane receptor	770	96
2699	X06956	Homo sapiens	alpha-tubulin	654	89
2700	M62843	Homo sapiens	brain protein	602	92
2701	AL117435	Homo sapiens	hypothetical protein	154	39
2702	AF010404	Homo sapiens	ALR	586	89
2703	B10545	Homo sapiens	Human aspartate protease psn-like4 protein.	734	96
2704	Y08685	Homo sapiens	serine palmitoyltransferase, subunit I	663	96
2705	AF081484	Homo sapiens	alpha-tubulin isoform 1	643	96
2706	AB014515	Homo sapiens	KIAA0615 protein	156	93
2707	AB036836	Homo sapiens	Carbonic anhydrase-related protein 10	717	99
2709	U03268	Homo sapiens	acyl-CoA oxidase	283	89
2710	W48978	Homo sapiens	Mature human chordin protein.	58	83
2712	Y12781	Homo sapiens	transducin (beta) like 1 protein	591	80
2713	AF077226	Homo sapiens	copine III	281	42
2714	U38810	Homo sapiens	CAGR1	574	90
2715	AB016485	Homo sapiens	LIM homeobox protein cofactor (CLIM-2)	534	88
2716	W95629	Homo sapiens	Homo sapiens secreted protein gene clone gm196_4.	221	87
2717	D86962	Homo sapiens	similar to mouse growth factor receptor-binding protein Grb10.	570	79
2718	Y13357	Homo sapiens	Amino acid sequence of protein PRO227.	493	74
2719	AJ001340	Homo sapiens	U3 snoRNP associated 55 kDa protein	299	94
2720	W62040	Homo sapiens	Protein isolated from leukocytes of IgA nephropathy patients.	677	92
2721	AF263539	Homo sapiens	arginine N-methyltransferase	582	95
2722	L02897	Canis familiaris	beta-spectrin	259	98
2723	AF123320	Homo sapiens	lymphocyte activation-associated protein	155	31
2724	D84296	Homo sapiens	TPRDIII	627	90
2725	AF071172	Homo sapiens	HERC2	642	92
2726	Y66688	Homo sapiens	Membrane-bound protein PRO1152.	542	84
2727	X03663	Homo sapiens	put. c-fms precursor	605	94
2728	AE004683	Pseudomonas aeruginosa	probable acyl-CoA dehydrogenase	484	68
2729	X71810	Homo sapiens	IEF SSP 9306	680	96
2730	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)	652	90
2732	AD000864	Homo sapiens	amyloid precursor-like protein 1	666	95
2733	Y08100	Homo sapiens	Human PRO331 protein.	665	97
2734	AK022517	Homo sapiens	unnamed protein product	634	87
2735	AB018345	Homo sapiens	KIAA0802 protein	193	41
2736	AF215896	Mus musculus	striated muscle-specific serine/threonine protein kinase	173	35

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2737	Y66678	Homo sapiens	Membrane-bound protein PRO1009.	188	62
2738	X76184	Homo sapiens	ets-related protein	761	99
2740	Y23330	Homo sapiens	Human tumour suppressor (kismet) protein.	208	33
2741	AF208227	Homo sapiens	transcriptional coactivator AIB3	634	94
2743	X72781	Homo sapiens	trypsinogen IV a-form	777	98
2744	AL031259	Homo sapiens	dJ191N21.1 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG)	754	92
2745	AF226045	Homo sapiens	GK002	55	64
2746	AC007136	Homo sapiens	Putative map kinase interacting kinase	729	97
2747	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	103	72
2748	AF090942	Homo sapiens	PRO0657	63	62
2749	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	206	72
2750	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	130	59
2751	AF130079	Homo sapiens	PRO2852	126	63
2752	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	127	74
2753	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	185	53
2754	AF309553	Homo sapiens	meiotic recombination protein REC14	191	97
2756	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	82	52
2759	R95913	Homo sapiens	Neural thread protein.	188	56
2760	AF118082	Homo sapiens	PRO1902	267	62
2761	R95913	Homo sapiens	Neural thread protein.	202	53
2762	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	310	66
2764	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	281	67
2765	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	194	57
2767	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	137	51
2769	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	238	81
2771	G00531	Homo sapiens	Human secreted protein, SEQ ID NO: 4612.	274	96
2773	Y73373	Homo sapiens	HTRM clone 921803 protein sequence.	232	93
2774	AF130089	Homo sapiens	PRO2550	176	67
2775	AK022814	Homo sapiens	unnamed protein product	160	73
2777	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	50	83
2778	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	85	52
2779	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	142	62
2781	AF237586	Homo sapiens	recombinant IgG4 heavy chain	245	48
2782	AF119851	Homo sapiens	PRO1722	198	69
2783	M36501	Homo sapiens	alpha-2-macroglobulin	215	46
2784	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone	144	51

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			HTDAD22		
2785	Y36203	Homo sapiens	Human secreted protein #75.	179	66
2786	AF119851	Homo sapiens	PRO1722	223	64
2787	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	183	80
2788	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	58	73
2789	X03145	Homo sapiens	pot. ORF V	67	40
2790	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	49	80
2792	Y19742	Homo sapiens	SEQ ID NO 460 from WO922243.	254	79
2793	AF119851	Homo sapiens	PRO1722	152	76
2794	AF130089	Homo sapiens	PRO2550	208	63
2795	AF130079	Homo sapiens	PRO2852	51	71
2796	AF161356	Homo sapiens	HSPC093	126	56
2797	AF119851	Homo sapiens	PRO1722	88	56
2798	AF173868	Homo sapiens	DNA binding protein p96PIF	251	77
2799	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	76	59
2801	AF130089	Homo sapiens	PRO2550	158	55
2803	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	200	71
2807	G00641	Homo sapiens	Human secreted protein, SEQ ID NO: 4722.	128	46
2808	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	112	45
2812	AF116712	Homo sapiens	PRO2738	187	51
2814	AK000385	Homo sapiens	unnamed protein product	112	47
2815	AF130089	Homo sapiens	PRO2550	158	79
2818	R95913	Homo sapiens	Neural thread protein.	119	74
2819	AK025047	Homo sapiens	unnamed protein product	82	68
2820	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	126	58
2821	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	205	69
2822	AF130079	Homo sapiens	PRO2852	288	67
2823	AF130089	Homo sapiens	PRO2550	158	70
2825	AF119855	Homo sapiens	PRO1847	81	76
2826	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	307	64
2828	AF119851	Homo sapiens	PRO1722	249	58
2829	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	168	66
2830	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	186	59
2831	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	74	87
2832	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	376	76
2833	AF119851	Homo sapiens	PRO1722	73	57
2835	AB046048	Macaca fascicularis	unnamed protein product	332	66
2836	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	97	65
2837	AF130079	Homo sapiens	PRO2852	271	74
2838	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	197	49
2843	G03786	Homo sapiens	Human secreted protein, SEQ	134	76

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 7867.		
2844	AF130089	Homo sapiens	PRO2550	160	59
2845	Y36156	Homo sapiens	Human secreted protein #28.	71	57
2846	AF130079	Homo sapiens	PRO2852	190	56
2847	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	140	64
2848	U28739	Caenorhabditis elegans	similar to alcohol dehydrogenase/ribitol dehydrogenase	59	50
2850	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	47	81
2851	AF130089	Homo sapiens	PRO2550	226	62
2852	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	133	57
2853	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	212	50
2854	X92485	Plasmodium vivax	pva1	130	54
2859	X72781	Homo sapiens	trypsinogen IV a-form	240	40
2860	U55376	Homo sapiens	repressor transcriptional factor	171	38
2861	AF130051	Homo sapiens	PRO0898	281	71
2862	AB046048	Macaca fascicularis	unnamed portein product	52	64
2863	AF119851	Homo sapiens	PRO1722	175	70
2864	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	71	46
2865	AF130089	Homo sapiens	PRO2550	43	39
2866	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	131	55
2867	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	236	80
2868	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	212	64
2870	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	46	80
2871	U93568	Homo sapiens	putative p150	306	36
2872	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	159	66
2873	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	186	50
2874	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	108	62
2876	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	38	53
2877	AF119851	Homo sapiens	PRO1722	165	53
2878	U51167	Mus musculus	isocitrate dehydrogenase	374	87
2879	G03628	Homo sapiens	Human secreted protein, SEQ ID NO: 7709.	70	59
2880	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	237	59
2881	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	87	51
2882	AF130089	Homo sapiens	PRO2550	158	64
2883	AF161356	Homo sapiens	HSPC093	92	56
2884	AF119851	Homo sapiens	PRO1722	131	66
2885	AF130089	Homo sapiens	PRO2550	162	59
2886	R95913	Homo sapiens	Neural thread protein.	107	59

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
2887	G02386	Homo sapiens	Human secreted protein, SEQ ID NO: 6467.	172	79
2888	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	72	31
2890	X92485	Plasmodium vivax	pva1	161	43
2891	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	71	60
2892	Y36156	Homo sapiens	Human secreted protein #28.	144	60
2893	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	245	55
2894	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	294	61
2896	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	222	65
2897	S80119	Rattus sp.	reverse transcriptase homolog	61	59
2898	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	66
2899	B24548	Homo sapiens	Human secreted protein sequence encoded by gene 30 SEQ ID NO:174.	799	75
2900	U93569	Homo sapiens	p40	173	54
2902	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	162	46
2903	AF130079	Homo sapiens	PRO2852	156	68
2904	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	222	54
2906	AF119851	Homo sapiens	PRO1722	188	70
2907	AF130079	Homo sapiens	PRO2852	304	63
2908	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	66
2909	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	211	66
2910	AF119851	Homo sapiens	PRO1722	80	62
2911	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	269	66
2912	AF285758	Homo sapiens	lysyl-tRNA synthetase	724	51
2913	AF116661	Homo sapiens	PRO1438	94	90
2914	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	209	73
2916	U93563	Homo sapiens	putative p150	72	50
2919	AF130089	Homo sapiens	PRO2550	122	71
2920	R95913	Homo sapiens	Neural thread protein.	148	60
2921	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	149	75
2922	AF130089	Homo sapiens	PRO2550	166	79
2923	X92485	Plasmodium vivax	pva1	140	72
2924	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	54	62
2925	M11942	Rattus norvegicus	70 kDa heat-shock-like protein	168	40
2928	AF130079	Homo sapiens	PRO2852	223	61
2932	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	119	57
2933	G03798	Homo sapiens	Human secreted protein, SEQ	168	64

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 7879.		
2934	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	45	50
2938	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	110	60
2939	AF119851	Homo sapiens	PRO1722	154	65
2940	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	162	72
2942	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	124	70
2943	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	66	61
2945	AF130079	Homo sapiens	PRO2852	262	78
2946	AF130089	Homo sapiens	PRO2550	178	75
2947	U49974	Homo sapiens	mariner transposase	243	52
2948	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	98	51
2949	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	76	64
2950	AF119884	Homo sapiens	PRO2521	1952	97
2952	AB033016	Homo sapiens	KIAA1190 protein	214	97
2954	AF130079	Homo sapiens	PRO2852	218	70
2955	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	332	73
2956	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	101	65
2958	AF229067	Homo sapiens	PADI-H protein	197	75
2959	AF119900	Homo sapiens	PRO2822	73	68
2960	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	179	69
2961	AF130089	Homo sapiens	PRO2550	304	63
2962	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	82	54
2965	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	169	76
2966	AB000216	Rattus norvegicus	CCA3	110	74
2967	X81206	Drosophila hydei	histone H3.3	60	45
2969	R95913	Homo sapiens	Neural thread protein.	206	47
2970	AF130089	Homo sapiens	PRO2550	160	75
2973	AF130089	Homo sapiens	PRO2550	121	62
2975	S80119	Rattus sp.	reverse transcriptase homolog	149	50
2976	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	111	74
2977	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	97	67
2978	X03475	Rattus norvegicus	ribosomal protein L35a (aa 1-110)	277	98
2979	U22376	Homo sapiens	alternatively spliced product using exon 13A	137	70
2980	X76013	Homo sapiens	glutamyl-tRNA synthetase	310	72
2982	AF090894	Homo sapiens	PRO0113	39	52
2983	S80119	Rattus sp.	reverse transcriptase homolog	151	50
2984	G00541	Homo sapiens	Human secreted protein, SEQ ID NO: 4622.	92	100
2985	X03145	Homo sapiens	pot. ORF III	42	66
2986	G02872	Homo sapiens	Human secreted protein, SEQ	154	64

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 6953.		
2988	AK002011	Homo sapiens	unnamed protein product	33	100
2989	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	165	55
2990	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	138	72
2992	AF118078	Homo sapiens	PRO1848	115	63
2994	AF130079	Homo sapiens	PRO2852	88	81
2995	AF130089	Homo sapiens	PRO2550	177	81
2996	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	217	66
2997	AL137798	Homo sapiens	dJ1182A14.3 (similar to MST1 (macrophage stimulating 1 (hepatocyte growth factor-like)))	168	91
2998	Y12627	Homo sapiens	Human 5' EST secreted protein SEQ ID NO: 292 from WO 9906553.	145	93
2999	S80119	Rattus sp.	reverse transcriptase homolog	103	55
3003	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	45	57
3005	Y36203	Homo sapiens	Human secreted protein #75.	78	44
3007	AF130089	Homo sapiens	PRO2550	64	56
3009	AF113685	Homo sapiens	PRO0974	169	51
3010	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	48	38
3012	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	82	51
3013	AF264014	Homo sapiens	scavenger receptor cysteine-rich type 1 protein M160 precursor	950	72
3014	D12621	Homo sapiens	cytochrome P-450LTBV	114	50
3015	U70935	Peromyscus maniculatus	reverse transcriptase	215	55
3016	Y52399	Homo sapiens	Human keratin KERT-3.	831	62
3018	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	314	70
3019	AF132912	Drosophila melanogaster	ARP-like protein	52	52
3020	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	111	64
3021	AF229067	Homo sapiens	PADI-H protein	140	61
3022	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	68	93
3023	AL390173	Homo sapiens	hypothetical protein	78	45
3025	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	77	53
3026	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	52
3027	AF047472	Homo sapiens	spleen mitotic checkpoint BUB3	489	87
3028	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	51	57
3031	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	54	61
3033	AF130089	Homo sapiens	PRO2550	207	54
3035	Y00918	Homo sapiens	Human Rab protein, RABP-1.	78	93

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			protein sequence.		
3037	X06747	Homo sapiens	protein A1-alpha (AA 1-320)	190	61
3042	AC002394	Homo sapiens	Gene product with similarity to dynein beta subunit	156	36
3043	AB046048	Macaca fascicularis	unnamed porlein product	60	68
3044	AB015332	Homo sapiens	HRIHFB2018	347	87
3045	X92485	Plasmodium vivax	pva1	169	56
3047	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	45	88
3048	U89337	Homo sapiens	NG7	461	76
3049	B10550	Homo sapiens	Human aspartate protease psl 4 protein.	849	59
3050	AF130079	Homo sapiens	PRO2852	186	75
3052	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	52	54
3054	X92485	Plasmodium vivax	pva1	76	60
3055	Y36203	Homo sapiens	Human secreted protein #75.	239	56
3057	X92485	Plasmodium vivax	pva1	177	48
3058	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	273	61
3059	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	215	54
3060	AF090930	Homo sapiens	PRO0478	108	75
3061	R95913	Homo sapiens	Neural thread protein.	91	57
3063	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	160	59
3064	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2 Antigen)	217	37
3065	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	199	53
3066	AB047600	Macaca fascicularis	hypothetical protein	77	62
3067	AJ404326	Homo sapiens	SR+89	209	92
3068	Y36203	Homo sapiens	Human secreted protein #75.	50	75
3069	AK023140	Homo sapiens	unnamed protein product	149	43
3070	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	244	55
3071	AF090120	Takifugu rubripes	splicing factor U2AF35	319	92
3072	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	150	56
3075	A59874_cd1	Homo sapiens	07-NOV-1997 cDNA encoding human vesicle trafficking protein-2 (VTP-2).	200	100
3076	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	247	75
3077	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	180	54
3078	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	176	52
3079	W85461	Homo sapiens	Secreted protein encoded by clone dn809_5.	625	100
3080	AF119855	Homo sapiens	PRO1847	194	64
3081	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	183	55

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3082	AF118082	Homo sapiens	PRO1902	60	64
3083	AF098297	Homo sapiens	CBF1 interacting corepressor CIR	101	74
3084	AF229067	Homo sapiens	PADI-H protein	236	70
3085	X92485	Plasmodium vivax	pva1	154	58
3086	AF130089	Homo sapiens	PRO2550	112	56
3088	AF043628	Homo sapiens	DNA polymerase eta	405	96
3092	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	61	48
3094	AJ001562	Myoxus glis	cytochrome oxidase II	189	54
3097	M12987	Plasmid F	Protein D	99	80
3098	L27428	Homo sapiens	reverse transcriptase	44	50
3100	D90819	Escherichia coli	DNA topoisomerase III (EC 5.99.1.-)	320	67
3101	U62577	Amblysomus hottentotus	cytochrome c oxidase subunit II	166	61
3102	U62577	Amblysomus hottentotus	cytochrome c oxidase subunit II	204	63
3105	X61296	Rattus norvegicus	open reading frame 2	76	44
3107	S80119	Rattus sp.	reverse transcriptase homolog	110	31
3108	X52031	Escherichia coli	ebgR product, repressor (AA 1-126)	479	95
3115	G03866	Homo sapiens	Human secreted protein, SEQ ID NO: 7947.	177	94
3116	AF130109	Homo sapiens	PRO1512	253	44
3117	Y36203	Homo sapiens	Human secreted protein #75.	229	77
3121	AE003740	Drosophila melanogaster	CG17141 gene product	58	47
3122	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	60	81
3124	B12307	Homo sapiens	Human secreted protein encoded by gene 7 clone HAMFE82.	283	61
3127	AJ233591	Mus musculus	reverse transcriptase	60	48
3129	AF131766	Homo sapiens	Similar to Ena-VASP like protein	172	62
3131	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	125	71
3132	U87607	Rattus norvegicus	putative RNA binding protein 1	35	41
3133	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	211	72
3134	U80746	Homo sapiens	CAGH4	123	47
3135	AK024481	Homo sapiens	FLJ00075 protein	93	46
3136	X61046	Hydra sp.	mini-collagen	121	50
3137	AB037839	Homo sapiens	KIAA1418 protein	644	93
3138	AL390114	Leishmania major	extremely cysteine/valine rich protein	314	47
3139	Y99367	Homo sapiens	Human PRO1377 (UNQ714) amino acid sequence SEQ ID NO-95.	620	99
3140	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	200	81
3141	AF153906	Mus musculus	erythroid membrane-associated protein ERMAP	236	81
3143	AJ001981	Homo sapiens	OXA1L	614	50
3144	Y02693	Homo sapiens	Human secreted protein	66	66

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			encoded by gene 44 clone HTDAD22.		
3145	Y27133	Homo sapiens	Human glioblastoma-derived polypeptide (clone OA004LD).	234	42
3147	U70935	Peromyscus maniculatus	reverse transcriptase	43	83
3148	Y95849	Homo sapiens	Autoantigen diagnostic of endometriosis.	652	96
3149	AF151046	Homo sapiens	HSPC212	387	59
3150	Z36243_cd1	Homo sapiens	30-DEC-1997 cDNA encoding a bone marrow secreted protein designated BMS199.	539	77
3153	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	196	71
3156	AF161356	Homo sapiens	HSPC093	278	58
3157	AF009668	multiple sclerosis associated retrovirus	polyprotein	158	40
3158	AF009668	multiple sclerosis associated retrovirus	polyprotein	156	34
3160	X56603	Mus musculus	mouse 57-KD Calcium-binding protein (MCaBP)	138	59
3161	AC005258	Homo sapiens	R30783_1	313	100
3162	X96783	Homo sapiens	synaptotagmin V	718	83
3163	G03873	Homo sapiens	Human secreted protein, SEQ ID NO: 7954.	225	50
3164	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	42	64
3165	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	341	70
3166	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	75	58
3167	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	192	75
3168	AF023451	Bos taurus	guanine nucleotide-exchange protein	119	81
3171	Y36203	Homo sapiens	Human secreted protein #75.	65	72
3172	Z98204	Hordeum vulgare	extensin	114	34
3173	AK000385	Homo sapiens	unnamed protein product	75	69
3174	AK026709	Homo sapiens	unnamed protein product	220	100
3175	AF034633	Homo sapiens	GPR39	168	47
3176	AL137478	Homo sapiens	hypothetical protein	504	66
3177	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	116	75
3178	AF130089	Homo sapiens	PRO2550	62	66
3179	R95913	Homo sapiens	Neural thread protein.	225	53
3180	D83004	Homo sapiens	ubiquitin-conjugating enzyme E2 Ubch-ben	160	54
3181	AF130079	Homo sapiens	PRO2852	66	75
3183	Y35994	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 379.	179	87
3184	AF130089	Homo sapiens	PRO2550	194	66
3185	AF130089	Homo sapiens	PRO2550	102	72

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3186	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	72	66
3188	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	318	73
3190	AK001762	Homo sapiens	unnamed protein product	614	48
3191	AF090930	Homo sapiens	PRO0478	66	64
3192	AE004213	Vibrio cholerae	prpE protein	335	50
3194	AF130089	Homo sapiens	PRO2550	83	70
3195	AK000665	Homo sapiens	unnamed protein product	607	66
3196	R56282	Homo sapiens	Human tissue plasminogen-activator 39 kDa protein.	118	79
3197	W77290	Homo sapiens	Human differentiation enhancing factor 2 gene.	48	55
3198	X53778	Homo sapiens	uracil DNA glycosylase	259	97
3199	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	85	59
3201	AK025947	Homo sapiens	unnamed protein product	158	86
3202	Y11983	Homo sapiens	Human 5' EST secreted protein SEQ ID No: 583.	122	100
3205	X61047	Hydra sp.	mini-collagen	93	41
3207	X92485	Plasmodium vivax	pval	110	50
3208	AF162767	Homo sapiens	17beta-hydroxysteroid dehydrogenase type 7	324	84
3209	M32295	Homo sapiens	melanocyte-specific secreted glycoprotein	582	89
3211	AF161356	Homo sapiens	HSPC093	183	47
3212	AF130089	Homo sapiens	PRO2550	55	47
3213	AF130089	Homo sapiens	PRO2550	265	80
3214	Y13143	Homo sapiens	Human secreted protein encoded by 5' EST SEQ ID NO: 157.	146	70
3215	AF130089	Homo sapiens	PRO2550	190	68
3216	X12876	Homo sapiens	cytokeratin 18 (232 AA)	105	80
3217	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	317	67
3218	M26361	Mus musculus	LINE/Ig H-chain fusion protein	134	50
3219	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	121	72
3220	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	207	75
3221	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	70	60
3222	AF130089	Homo sapiens	PRO2550	95	73
3223	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	68	93
3224	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	40	52
3228	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	45	45
3229	AF130089	Homo sapiens	PRO2550	176	73
3231	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	133	46
3232	U93568	Homo sapiens	p40	158	56
3233	T72662_cd1	Homo sapiens	28-NOV-1995 Human smooth muscle cell-derived migration factor cDNA.	127	100
3234	AF182215	Tilapia mossambica	chloride channel CLC-3	176	66

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3235	U22376	Homo sapiens	alternatively spliced product using exon 13A	180	71
3240	AF130089	Homo sapiens	PRO2550	239	61
3241	X92485	Plasmodium vivax	pva1	76	62
3242	AF130079	Homo sapiens	PRO2852	279	78
3244	X55656	Homo sapiens	gamma-G globin	132	82
3245	AF119851	Homo sapiens	PRO1722	92	81
3246	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	53	66
3247	M25113	Homo sapiens	sickle beta-hemoglobin	588	97
3248	AF090894	Homo sapiens	PRO0113	129	64
3250	X06821	Homo sapiens	rhoC coding region (AA 1-193)	361	79
3251	AF130089	Homo sapiens	PRO2550	179	81
3252	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	159	65
3253	Y36007	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 392.	469	87
3254	AF130089	Homo sapiens	PRO2550	140	75
3255	AL136125	Homo sapiens	dj304B14.2.1 (novel protein isoform 1)	952	86
3256	AF130089	Homo sapiens	PRO2550	197	71
3257	Z94055	Homo sapiens	tenascin-R (restrictin)	207	93
3258	AL031115	Homo sapiens	ZXDA, ZXDB (zinc finger X-linked protein)	765	70
3259	X92485	Plasmodium vivax	pva1	115	72
3260	AF118082	Homo sapiens	PRO1902	82	66
3261	AF161356	Homo sapiens	HSPC093	170	41
3262	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	185	92
3263	AK000385	Homo sapiens	unnamed protein product	168	80
3264	AF042107	Eimeria tenella	ribosomal protein S3a	261	96
3265	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	145	50
3267	U49974	Homo sapiens	mariner transposase	248	78
3268	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	225	67
3269	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	142	58
3270	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	138	82
3271	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	163	55
3272	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	94	76
3275	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	198	76
3276	AB020236	Homo sapiens	ribosomal protein L27A	215	84
3277	U93565	Homo sapiens	putative p150	699	76
3278	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	251	58
3281	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	105	84
3282	AF130089	Homo sapiens	PRO2550	196	69
3284	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	129	65

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3286	AF155740	Homo sapiens	vacuolar sorting protein 4	97	94
3287	AF130089	Homo sapiens	PRO2550	136	75
3288	Y36203	Homo sapiens	Human secreted protein #75.	98	66
3290	S54641	Homo sapiens	HZF-16.2= zinc finger {alternatively spliced}	188	70
3292	X60661	Rattus rattus	potential ligand-binding protein	237	81
3293	AF119851	Homo sapiens	PRO1722	66	63
3294	AF090942	Homo sapiens	PRO0657	192	70
3295	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	192	69
3296	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	46	45
3298	U49974	Homo sapiens	mariner transposase	137	62
3299	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	43	72
3300	AF130089	Homo sapiens	PRO2550	216	69
3301	Y36156	Homo sapiens	Human secreted protein #28.	205	72
3303	U09414	Homo sapiens	zinc finger protein ZNF137	257	74
3305	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	145	53
3306	X62447	Homo sapiens	PR 264	231	50
3307	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	151	72
3309	U70932	Peromyscus leucopus	reverse transcriptase	106	63
3311	AF119851	Homo sapiens	PRO1722	81	75
3312	X96395	Homo sapiens	canalicular multidrug resistance protein	59	68
3313	L29217	Homo sapiens	clk3-490; putative	261	67
3314	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	153	68
3315	AC004770	Homo sapiens	BC269730 2	392	93
3317	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	162	62
3318	M20372	Homo sapiens	ornithine decarboxylase (EC 4.1.1.17)	153	86
3320	AK025116	Homo sapiens	unnamed protein product	132	57
3321	AL121896	Homo sapiens	bA287B20.1 (KIAA1272 (similar to tuberins and rat Tulp1))	39	100
3322	X92485	Plasmodium vivax	pva1	82	48
3323	AF110103	Tupaia belangeri	beta-actin	132	39
3324	AF153127	Gallus gallus	SAPK interacting protein	140	93
3326	AF158370	Gallus gallus	DEAD-box RNA helicase	228	79
3327	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	91	66
3328	AF118082	Homo sapiens	PRO1902	83	51
3330	AF130079	Homo sapiens	PRO2852	134	67
3331	AF116614	Homo sapiens	PRO0989	86	100
3332	AK021627	Homo sapiens	unnamed protein product	809	80
3333	AJ005821	Homo sapiens	X-like 1 protein	5032	97
3334	U70932	Peromyscus leucopus	reverse transcriptase	103	60
3336	AF119855	Homo sapiens	PRO1847	182	65
3337	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	52	56
3338	X53800	Homo sapiens	macrophage inflammatory	199	97

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			protein-2beta precursor		
3339	AL133057	Homo sapiens	hypothetical protein	209	70
3340	W96225	Homo sapiens	Smad5 protein C-terminal fragment.	42	58
3341	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	172	51
3342	X52174	Homo sapiens	precursor protein (AA -32 to 354)	518	100
3343	AK021848	Homo sapiens	unnamed protein product	54	61
3346	D90719	Escherichia coli	Hypothetical protein 1	663	81
3348	M96268	Escherichia coli	chorismate lyase	407	94
3349	X04619	Escherichia coli	A protein (AA 1-388)	210	50
3351	D90868	Escherichia coli	BILE ACID-INDUCIBLE OPERON PROTEIN F.	249	89
3355	U00039	Escherichia coli	trf	245	95
3356	AI.035252	Homo sapiens	dJ738P15.3 (IL-6SAG this overlaps dJ738P15.2)	219	93
3357	AB005624	Sus scrofa	rig-analog DNA-binding protein	71	92
3359	X70326	Homo sapiens	MacMARCKS	259	65
3360	AF151889	Homo sapiens	CGI-131 protein	411	51
3361	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	128	60
3362	Y57908	Homo sapiens	Human transmembrane protein HTPMPN-32.	338	98
3363	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	245	52
3364	AF188700	Homo sapiens	actin filament associated protein	300	98
3365	Z68907	Homo sapiens	NAD (H)-specific isocitrate dehydrogenase gamma subunit precursor	375	76
3366	AF060503	Homo sapiens	zinc finger protein	392	86
3367	U14972	Homo sapiens	ribosomal protein S10	506	94
3368	B00073	Homo sapiens	Human lysyl oxidase related protein (Lor)-2.	359	84
3370	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	224	75
3371	Z27113	Homo sapiens	RNA Polymerase II subunit 14.4 kD	159	84
3372	AF171030	Homo sapiens	succinate dehydrogenase flavoprotein subunit	136	96
3373	Y10929	Homo sapiens	kruppel-type zinc finger protein	1014	82
3374	AF288813	Mus musculus	synembryn	206	50
3375	AF123653	Homo sapiens	FEZ1	2271	84
3376	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	82	51
3377	AF071317	Mus musculus	COP9 complex subunit 7b	335	90
3378	AF217411	Homo sapiens	neuroigin 3 isoform HNL3	1335	91
3379	Z83760	Ciona intestinalis	COS41.4	123	52
3386	Y41256	Homo sapiens	Amino acid sequence of short human FAIM.	664	97
3387	X12966	Homo sapiens	3-oxoacyl-CoA thiolase	397	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			propeptide (424 AA)		
3388	AB016089	Homo sapiens	RNA binding protein	161	42
3389	AK001441	Homo sapiens	unnamed protein product	256	63
3391	U73941	Mus musculus	Rap2 interacting protein 8	299	68
3392	Y36156	Homo sapiens	Human secreted protein #28.	59	70
3395	AB035966	Homo sapiens	testis-specific adriamycin sensitivity protein	153	71
3396	AF151843	Homo sapiens	CGI-85 protein	1525	99
3397	W61624	Homo sapiens	Clone HHFEK40 of TM4SF superfamily.	61	75
3398	AK022609	Homo sapiens	unnamed protein product	150	39
3399	W88758	Homo sapiens	Polypeptide fragment encoded by gene 15.	590	83
3400	Z98882	Homo sapiens	c356B8.1 (K1AA0665)	63	50
3401	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	316	84
3402	D87666	Homo sapiens	heat shock protein 90	160	84
3403	Y59871	Homo sapiens	Human normal uterus tissue derived protein 34.	178	52
3404	AF151839	Homo sapiens	CGI-81 protein	256	65
3408	AF261093	Homo sapiens	Thy-1 co-transcribed protein	175	43
3409	AL035587	Homo sapiens	dJ475N16.1 (CTG4A)	39	100
3410	AC004976	Homo sapiens	glycyl tRNA synthetase	156	88
3412	L07758	Homo sapiens	IEF SSP 9502	224	95
3413	U88324	Rattus norvegicus	G protein beta1 subunit	133	90
3414	AF130089	Homo sapiens	PRO2550	89	90
3415	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein 3	217	88
3416	Y00281	Homo sapiens	precursor	430	90
3417	D28540	Homo sapiens	Human Diff6,H5,CDC10 homologue	188	82
3419	W71748	Homo sapiens	Human ubiquitin conjugation system protein 1.	676	94
3420	AF132205	Homo sapiens	PRO2292	96	100
3421	W82841	Homo sapiens	Human cerebral protein-1.	116	91
3422	D28540	Homo sapiens	Human Diff6,H5,CDC10 homologue	225	93
3423	AC005258	Homo sapiens	R30783.1	155	85
3424	AF194537	Homo sapiens	NAG13	188	60
3425	U09367	Homo sapiens	zinc finger protein ZNF136	632	87
3428	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	171	61
3429	AK022900	Homo sapiens	unnamed protein product	371	79
3431	AF119851	Homo sapiens	PRO1722	268	59
3433	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	60	68
3435	U09087	Homo sapiens	thymopoietin beta	509	82
3438	AF130089	Homo sapiens	PRO2550	201	65
3439	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	298	63
3440	AF119851	Homo sapiens	PRO1722	149	62
3443	AB046048	Macaca fascicularis	unnamed portein product	134	45
3446	X07373	Homo sapiens	ventricular myosin light chain 1 (AA 1 - 195)	164	80
3447	X56932	Homo sapiens	23 kD highly basic protein	539	85

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3448	M80254	Homo sapiens	cyclophilin 3 protein	227	74
3451	Y19643	Homo sapiens	SEQ ID NO 361 from WO922243.	370	97
3453	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	149	54
3454	AY009951	Homo sapiens	hedgehog-interacting protein	237	85
3455	U47621	Homo sapiens	nucleolar autoantigen No55	229	97
3456	U38904	Homo sapiens	zinc finger protein C2H2-25	198	55
3457	AB030238	Rattus norvegicus	hepatocarcinogenesis-related transcription factor (HTF)	201	87
3458	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	123	81
3460	Y76509	Homo sapiens	Human ovarian tumor EST fragment encoded protein 5.	288	75
3461	AF119851	Homo sapiens	PRO1722	315	63
3462	U93569	Homo sapiens	p40	378	62
3463	X69654	Homo sapiens	ribosomal protein S26	305	72
3468	AF119900	Homo sapiens	PRO2822	157	82
3469	AF130089	Homo sapiens	PRO2550	283	63
3470	X92485	Plasmodium vivax	pva1	176	62
3471	AF119851	Homo sapiens	PRO1722	200	63
3474	X83617	Homo sapiens	RanBP1	150	82
3475	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	84	72
3478	Y08890	Homo sapiens	Ran GTP binding protein 5	410	100
3481	AF220530	Homo sapiens	myo-inositol 1-phosphate synthase A1	529	97
3482	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	222	63
3483	AF130089	Homo sapiens	PRO2550	282	61
3487	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	156	54
3489	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	120	58
3493	AF130089	Homo sapiens	PRO2550	310	73
3494	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	155	68
3495	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	65
3496	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	149	75
3498	AK025047	Homo sapiens	unnamed protein product	267	66
3500	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	110	50
3501	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	115	43
3504	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	86	75
3506	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	257	69
3508	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	201	60
3509	X92485	Plasmodium vivax	pva1	161	37
3511	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	182	80
3514	AF217973	Homo sapiens	unknown	218	68
3515	G03482	Homo sapiens	Human secreted protein, SEQ	115	66

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 7563.		
3517	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	37	57
3518	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	99	67
3520	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	130	87
3521	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	98	90
3522	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	253	61
3524	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	225	51
3526	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	37	77
3527	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	42	80
3528	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	260	64
3531	AF119851	Homo sapiens	PRO1722	105	76
3533	M63819	Plasmodium falciparum	malaria antigen	151	43
3537	AL137266	Homo sapiens	hypothetical protein	220	72
3538	AF118082	Homo sapiens	PRO1902	181	56
3540	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	63	41
3541	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	40	47
3543	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	277	63
3544	AF090894	Homo sapiens	PRO0113	62	66
3545	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	151	56
3546	AK025116	Homo sapiens	unnamed protein product	261	72
3548	AF130079	Homo sapiens	PRO2852	196	45
3549	Y36303	Homo sapiens	Human secreted protein encoded by gene 80.	509	100
3550	AF161356	Homo sapiens	HSPC093	99	47
3557	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	143	62
3558	AF014008	Bos taurus	myocardial vascular inhibition factor	182	76
3559	AF119855	Homo sapiens	PRO1847	36	75
3561	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	148	66
3562	U14966	Homo sapiens	ribosomal protein L5	337	85
3563	D17654	Sus scrofa	HBp15/L22	332	79
3564	X80199	Homo sapiens	MLN 51	912	99
3566	AF235100	Homo sapiens	matrix protein for thyroid hormone synthesis	386	88
3570	X56390	Canis familiaris	rac2	356	83
3571	AK023452	Homo sapiens	unnamed protein product	270	95
3573	AF130079	Homo sapiens	PRO2852	163	72
3575	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	234	71
3576	AF130089	Homo sapiens	PRO2550	210	84
3578	Y36455	Homo sapiens	Fragment of human secreted	255	80

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			protein encoded by gene 14.		
3579	AK025116	Homo sapiens	unnamed protein product	42	54
3582	AF118082	Homo sapiens	PRO1902	180	51
3584	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	70	63
3585	AK025269	Homo sapiens	unnamed protein product	395	98
3591	D38037	Homo sapiens	hFKBP12-like protein	468	83
3592	X69910	Homo sapiens	P63 protein	2042	97
3594	R60520	Homo sapiens	Human alpha-2-MRBDv.	148	90
3595	M31211	Homo sapiens	myosin light chain 1 slow	159	66
3597	AB028449	Homo sapiens	Helicase-MOI	305	82
3599	AL390738	Homo sapiens	bA438F9.2 (novel protein similar to heterogeneous nuclear ribonucleoprotein A1 (HNRP1))	161	60
3602	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	43	63
3606	Y06432	Homo sapiens	Human protease HUPM-1.	342	100
3608	M15530	Homo sapiens	B-cell growth factor	131	66
3610	AB037847	Homo sapiens	KIAA1426 protein	79	48
3611	G01479	Homo sapiens	Human secreted protein, SEQ ID NO: 5560.	248	100
3613	U17032	Homo sapiens	p190-B	536	91
3615	AF090930	Homo sapiens	PRO0478	138	77
3616	L20686	Homo sapiens	guanine nucleotide releasing factor	196	80
3617	AF161356	Homo sapiens	HSPC093	76	50
3619	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	133	57
3620	AF119851	Homo sapiens	PRO1722	177	64
3621	AF130079	Homo sapiens	PRO2852	258	66
3625	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	151	72
3627	AF006065	Fowlpox virus	gag	158	39
3628	X68249	Xenopus laevis	Proline rich protein	273	75
3630	AF130089	Homo sapiens	PRO2550	317	65
3632	X60128	Cavia porcellus	p21 protein	244	88
3633	AF119851	Homo sapiens	PRO1722	59	43
3634	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	177	63
3636	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	153	59
3637	X85373	Homo sapiens	Sm protein G	264	94
3639	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	256	68
3640	U83303	Homo sapiens	line-1 reverse transcriptase	109	57
3641	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	155	61
3642	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	94	55
3644	AF159615	Homo sapiens	PGF receptor activating protein 1	253	68
3645	AL080065	Homo sapiens	hypothetical protein	476	84
3646	M76543	Bos taurus	casein kinase I-alpha	342	89
3648	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	185	66
3654	AF009205	Homo sapiens	unknown	163	84

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3655	J04030	Escherichia coli	prepriming protein I	504	96
3657	U00006	Escherichia coli	similar to Desulfurolobus ambivalens hypoth. 28.3 kDa protein in sor 3' region	432	81
3658	L19201	Escherichia coli	CG Site No. 702	492	96
3659	U03101	Salmonella typhimurium	Fis	373	94
3660	D90704	Escherichia coli	ORF_ID:o170#3	479	90
3661	L22858	Autographa californica nucleopolyhedr ovirus	AcOrf-91 peptide	156	40
3663	L10328	Escherichia coli	similar to E. coli ORF adjacent to suc operon; similar to gntR class of regulatory proteins	330	79
3665	D90781	Escherichia coli	pca operon transcriptional activator.	673	90
3670	AL035252	Homo sapiens	dJ738P15.3 (IL-6SAG this overlaps dJ738P15.2)	267	78
3671	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	333	60
3673	T44317_cd1	Homo sapiens	03-APR-1995 Human cytokine HCC-1 (cDNA).	155	68
3675	AF177377	Homo sapiens	cytoplasmic protein	939	98
3678	AF219990	Homo sapiens	corneal N-acetylglucosamine-6-O-sulfotransferase	647	98
3679	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	316	70
3680	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	294	77
3682	AL390114	Leishmania major	extremely cysteine/valine rich protein	169	49
3685	G01877	Homo sapiens	Human secreted protein, SEQ ID NO: 5958.	304	92
3686	AB032997	Homo sapiens	KIAA1171 protein	511	87
3688	M21190	Homo sapiens	fructose 1,6-diphosphate aldolase A (EC 4.1.2.13)	159	100
3689	U73167	Homo sapiens	similar to hyaluronoglycosaminidase; 40% Similarity to U96078 (PID:g2314820)	325	79
3690	K00557	Homo sapiens	alpha-tubulin	362	86
3691	AF132944	Homo sapiens	CGI-10 protein	247	90
3693	U44731	Mus musculus	purine nucleotide binding protein	522	58
3694	AF130089	Homo sapiens	PRO2550	256	69
3696	AF156530	Mus musculus	ETS-domain transcriptional repressor PE1	458	75
3697	L28010	Homo sapiens	HnRNP F protein	494	87
3699	AF016430	Caenorhabditis elegans	contains similarity to a BR-C/TTK domain	207	44
3700	AF119851	Homo sapiens	PRO1722	327	74
3702	AF243140	Canis familiaris	cyclophilin A	351	81
3704	AF246221	Homo sapiens	transmembrane protein BRI	380	89
3706	U52701	Homo sapiens	adrenal Creb-rp homolog	131	96
3707	U30826	Homo sapiens	SRp40-1	538	87

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3710	Y83089	Homo sapiens	F-box protein FBP-21.	636	87
3711	AF141968	Homo sapiens	trabeculin-alpha	626	89
3712	Q51475_cd1	Homo sapiens	24-APR-1992 MK gene.	180	90
3713	AF267986	Homo sapiens	15 kDa selenoprotein	576	91
3720	AJ225022	Homo sapiens	membrane glycoprotein gp36	209	93
3721	W78208	Homo sapiens	Human secreted protein encoded by gene 83 clone HSAWD74.	280	51
3722	X77452_cd1	Homo sapiens	11-JUN-1997 Human PxTE cDNA.	204	95
3723	X75935	Bos taurus	coatomer	352	80
3725	L19713	Homo sapiens	dematin	753	98
3726	U07223	Homo sapiens	beta2-chimaerin	594	97
3728	AC005021	Homo sapiens	paraoxonase/arylesterase	711	100
3729	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	293	72
3730	Y00339	Homo sapiens	carbonic anhydrase II (AA 1-260)	236	80
3731	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	143	70
3732	G03617	Homo sapiens	Human secreted protein, SEQ ID NO: 7698.	73	100
3733	AF130089	Homo sapiens	PRO2550	359	73
3735	U30884	Homo sapiens	SRP40-2	222	95
3737	X02515	Homo sapiens	T-cell receptor beta 1 chain	177	92
3738	U95726	Homo sapiens	thyroid hormone sulfotransferase	809	99
3741	AF078856	Homo sapiens	p47	519	100
3742	Q55625_cd1	Homo sapiens	22-JUN-1992 Human beta globin 5'-UTR-CDS-3'-UTR.	540	93
3743	Z83247	Homo sapiens	human leukocyte antigen-Cw*1205	1181	98
3744	Q86126_cd1	Homo sapiens	16-SEP-1993 H4-1BB receptor protein cDNA.	218	97
3745	L16558	Homo sapiens	ribosomal protein L7	367	100
3748	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	44	61
3749	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	75
3751	U82469	Homo sapiens	tubby related protein 2 TULP2	204	97
3752	X52138	Homo sapiens	L7a protein	159	57
3753	AL096766	Homo sapiens	dA59H18.1 (K1AA0767 protein)	191	97
3755	AJ012463	Homo sapiens	transcription factor	1129	99
3756	M26095	Homo sapiens	calcinonin precursor	579	91
3757	D38595	Homo sapiens	inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP)	3776	100
3758	AK000452	Homo sapiens	unnamed protein product	1075	87
3760	U60805	Homo sapiens	oncostatin-M specific receptor beta subunit	394	100
3761	M77693	Homo sapiens	spermidine/spermine N1-acetyltransferase	208	94
3762	AF000574	Homo sapiens	immunoglobulin-like transcript 4; ILT4	2068	94
3763	AC005175	Homo sapiens	TA2R HUMAN, BETA ISOFORM; TXA2-R;	420	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			PROSTANOID TP RECEPTOR		
3764	AF201333	Homo sapiens	delta-tubulin	651	99
3765	AL163280	Homo sapiens	IGSF5	307	100
3766	AK025116	Homo sapiens	unnamed protein product	346	71
3767	D87073	Homo sapiens	similar to Human zinc finger protein(ZNF142)	198	100
3768	Q44800_cd1	Homo sapiens	28-AUG-1992 Encodes single-stranded DNA binding (PUR) protein.	191	92
3769	AY009951	Homo sapiens	hedgehog-interacting protein	161	97
3771	Z94941_cd1	Homo sapiens	01-OCT-1998 Human carbohydrate-associated protein CRBAP-1 cDNA.	302	100
3772	M25246	Homo sapiens	vimentin	195	100
3773	X15187	Homo sapiens	precursor polypeptide (AA -21 to 782)	356	95
3774	M88370	Homo sapiens	DNA-binding protein	166	61
3775	AF208499	Rattus norvegicus	replication factor C subunit 2	179	94
3776	Y25917	Homo sapiens	Human GPC3 protein fragment.	229	97
3778	AF118086	Homo sapiens	PRO1992	144	60
3779	R95913	Homo sapiens	Neural thread protein.	49	55
3781	Y15224	Homo sapiens	Human receptor protein (HURP) 3 amino acid sequence.	88	37
3782	B09885	Homo sapiens	Hsp70 C-terminal 92 amino acid polypeptide sequence.	154	90
3783	AF035268	Homo sapiens	phosphatidylserine-specific phospholipase A1	379	98
3784	AB001429	Mus musculus	motor domain of KIF13A	205	100
3785	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	75	92
3788	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	160	57
3789	AF004133	Sus scrofa	adipocyte membrane protein	913	95
3790	M29580	Homo sapiens	zinc finger protein 7 (ZFP7)	157	96
3791	AJ011915	Homo sapiens	synaptosome associated protein of 23 kilodaltons, isoform A	353	100
3792	AF311913	Homo sapiens	Eag-related gene member 2	549	100
3793	X00063	Homo sapiens	renin (aa 105 to 401)	205	97
3794	X00737	Homo sapiens	PNP	210	97
3795	AF077954	Homo sapiens	protein inhibitor of activated STAT protein PIASx-beta	287	96
3797	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICE1) protein sequence.	265	90
3798	AB007146	Homo sapiens	ribosomal protein Sa	238	97
3799	AB037824	Homo sapiens	KIAA1403 protein	353	97
3800	X64707	Homo sapiens	BBC1	211	100
3802	U95301	Homo sapiens	calcium-dependent group X phospholipase A2	147	100
3803	G03554	Homo sapiens	Human secreted protein, SEQ ID NO: 7635.	183	96
3805	AF311388	Homo sapiens	livin inhibitor-of-apoptosis	155	40
3806	Z95331	Homo sapiens	bK941F9.2 (Fibulin 1 (isoform C))	284	100
3808	X92841	Homo sapiens	MHC class I chain-related protein A	302	100
3809	AB016768	Mus musculus	thrombospondin type 1 domain	184	73

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3810	J03075	Homo sapiens	80K-H protein	242	93
3811	AB033768	Homo sapiens	peptidylarginine deiminase type I	679	99
3813	M95936	Homo sapiens	protein serine/threonine kinase	173	100
3814	AF130089	Homo sapiens	PRO2550	374	78
3815	D13891	Homo sapiens	Id-2H	188	95
3817	AB033586	potamotrygon motoro	ryPTPR2Ac	152	100
3818	M25746	Homo sapiens	osteonectin	152	93
3820	AJ249900	Homo sapiens	secreted modular calcium-binding protein	218	100
3822	M13520	Homo sapiens	N-acetyl-alpha-glucosaminidase prepro-polypeptide	153	100
3829	AF118090	Homo sapiens	PRO2044	375	92
3832	AF145122	Homo sapiens	lipopolysaccharide specific response-7 protein	819	92
3836	AB026674	Mus musculus	Arx homeodomain protein	193	100
3838	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	99	65
3844	AF130089	Homo sapiens	PRO2550	434	84
3848	AF229067	Homo sapiens	PADI-H protein	164	70
3850	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	172	59
3852	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	93	47
3853	AF130089	Homo sapiens	PRO2550	52	84
3854	AF130089	Homo sapiens	PRO2550	125	56
3855	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	196	58
3857	D10884	Bos taurus	neurocalcin	144	96
3860	AF130089	Homo sapiens	PRO2550	267	71
3861	AF097994	Homo sapiens	L-kynurenine/alpha-aminoadipate aminotransferase	325	98
3862	A16768	synthetic construct	kunitz type protease inhibitor	163	44
3863	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	167	47
3867	AB024930	Rattus norvegicus	nuclear receptor binding factor-2	1337	90
3868	AF220264	Homo sapiens	MOST-1	153	78
3876	Z95114	Homo sapiens	bK212A2.2 (apolipoprotein L ₂)	339	98
3877	Y28815	Homo sapiens	PL776 6 secreted protein.	945	83
3880	S69339	Homo sapiens	surface antigen CD70, ligand for CD27-type II transmembrane protein	264	100
3881	AF130089	Homo sapiens	PRO2550	325	67
3882	X03077	Homo sapiens	lactate dehydrogenase-A	171	62
3883	Y68769	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-1.	208	88
3884	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	196	83
3885	X71480	Homo sapiens	cytochrome P450	189	91
3886	D49387	Homo sapiens	NADP dependent leukotriene b4 12-hydroxydehydrogenase	603	100
3887	T77304_cd1	Homo sapiens	19-JAN-1995 DNA encoding methenyltetrahydrofolate synthetase.	349	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3888	Q11701_cd1	Homo sapiens	20-OCT-1989 Human alpha-interferon receptor protein encoding sequence.	174	97
3889	M58509	Homo sapiens	adrenodoxin reductase	234	80
3890	Z83819	Homo sapiens	CSTF2 (CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT)	194	100
3891	Q89840_cd1	Homo sapiens	12-OCT-1993 Human death associated protein DAP-3.	292	98
3892	W75248	Homo sapiens	Fragment of human secreted protein encoded by gene 16.	227	95
3894	AL031228	Homo sapiens	dJ1033B10.9 (Short-chain alcohol dehydrogenase family member (HKE6, RING2))	490	96
3895	AF064484	Homo sapiens	natural resistance-associated macrophage protein 2 non-IRE form	283	100
3896	AL050343	Homo sapiens	dJ657D16.1 (nardilysin (N-arginine diabolic convertase))	893	100
3898	Y48312	Homo sapiens	Human prostate cancer-associated protein 9.	1139	82
3899	AL080253	Arabidopsis thaliana	putative snRNP protein	144	41
3900	M24895	Homo sapiens	alpha-amylase	378	85
3903	U34819	Homo sapiens	JNK3 alpha2 protein kinase	1170	100
3905	AF090894	Homo sapiens	PRO0113	128	66
3906	AF151850	Homo sapiens	CGI-92 protein	646	99
3908	D10884	Bos taurus	neurocalcin	150	100
3909	Z86040	Bos taurus	hypothetical protein	192	88
3910	AK000385	Homo sapiens	unnamed protein product	107	51
3912	X95826	Homo sapiens	mono-ADP-ribosyltransferase	396	100
3913	AF169796	Homo sapiens	zinc finger DNA binding protein	83	100
3914	AB000220	Homo sapiens	semaphorin E	715	100
3916	AF226667	Homo sapiens	CTP synthetase isoform	501	96
3917	AF187318	Homo sapiens	F-box protein Fbx2	441	84
3919	M35074	Homo sapiens	met oncogene	149	100
3920	M77663	Homo sapiens	keratin 10	288	78
3921	L08187	Homo sapiens	cytokine receptor	368	100
3923	D78011	Homo sapiens	dihydropyrimidinase	201	97
3924	AE003963	Xylella fastidiosa	DNA repair system specific for alkylated DNA	297	45
3925	U09088	Homo sapiens	thymopoietin gamma	635	99
3926	AF090942	Homo sapiens	PRO0657	136	49
3927	Y22236	Homo sapiens	Human KDR signal transduction inducer protein sequence.	485	59
3928	L05568	Homo sapiens	Na ⁺ /Cl ⁻ dependent serotonin transporter	269	100
3930	D83032	Homo sapiens	nuclear protein, NP220	168	100
3931	AF175279	Mus musculus	neurotensin receptor 3	174	97
3932	AB033548	Homo sapiens	hBAT1	679	100
3933	AF134726	Homo sapiens	NG23	398	82
3934	AF104359	Mus musculus	Ezh2 protein	266	86
3935	J04122	Mesocricetus auratus	nuclear factor 1-like protein	226	100
3936	AF131748	Homo sapiens	GTP-specific succinyl-CoA synthetase beta subunit	163	87
3937	AK021815	Homo sapiens	unnamed protein product	744	93

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3938	X22400_cd1	Homo sapiens	15-JUL-1997 Human live cytosolic beta-glucosidase cDNA.	341	98
3939	U95113	Rattus norvegicus	Histone H2a	398	94
3941	X79440	Homo sapiens	NADP+-dependent malic enzyme	1515	99
3942	Z29093	Homo sapiens	receptor tyrosine kinase	2753	100
3943	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	175	71
3945	AF006621	Homo sapiens	embryonic lung protein	1652	99
3946	M86752	Homo sapiens	transformation-sensitive protein	152	100
3950	U10990	Homo sapiens	hTAK1	295	92
3953	AF270937	Plutella xylostella	PxORF73 peptide	112	51
3954	AF191744	Homo sapiens	NFY-C variant DS2.8	834	100
3955	Y94951	Homo sapiens	Human secreted protein clone dw78_1 protein sequence SEQ ID NO: 108.	465	97
3956	X74818	Homo sapiens	AHNAK-related protein	547	79
3957	Y76136	Homo sapiens	Human secreted protein encoded by gene 13.	167	53
3958	AF177144	Mus musculus	mammalian inositol hexakisphosphate kinase 1	637	59
3959	AB020714	Homo sapiens	KIAA0907 protein	256	97
3961	AF117382	Mus musculus	hypermethylated in cancer 2 protein; HIC2	1333	91
3962	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	168	72
3963	AF151892	Homo sapiens	CGI-134 protein	194	76
3964	AB023172	Homo sapiens	KIAA0955 protein	186	83
3965	Y66718	Homo sapiens	Membrane-bound protein PRO1106.	226	81
3967	X78282	Homo sapiens	aryl sulfotransferase	510	98
3968	AF110645	Homo sapiens	candidate tumor suppressor p33 ING1 homolog	533	93
3969	AF090930	Homo sapiens	PRO0478	149	82
3970	AF208852	Homo sapiens	BM-010	109	54
3971	M12329	Cricetulus griseus	alpha-tubulin III	644	98
3972	Y76136	Homo sapiens	Human secreted protein encoded by gene 13.	167	53
3973	M80613	Homo sapiens	putative	167	82
3974	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	220	57
3976	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	173	53
3980	AF006621	Homo sapiens	embryonic lung protein	598	100
3981	L05568	Homo sapiens	Na+/Cl- dependent serotonin transporter	253	97
3982	X01410	Homo sapiens	T-cell receptor beta chain	181	90
3985	U61843	Homo sapiens	discs large protein P-dlg	166	88
3986	Z82022	Homo sapiens	GlcNAc-1-P transferase	252	90
3987	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	177	76
3988	AK026098	Homo sapiens	unnamed protein product	658	63
3989	Y36270	Homo sapiens	Human secreted protein encoded by gene 47.	359	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
3991	AF028789	Homo sapiens	UNC-119b	283	100
3994	AF190625	Coturnix coturnix	qdg1-1	205	100
3995	AF056966	Homo sapiens	mutant membrane protein RhCe	154	100
3996	L08850	Homo sapiens	AD amyloid	349	95
3999	AF079359	Setaria digitata	actin	397	85
4000	AK022945	Homo sapiens	unnamed protein product	261	84
4001	Y60268	Homo sapiens	Human endometrium tumour EST encoded protein 328.	135	53
4008	AL121969	Homo sapiens	dJ1214M20.1 (glutathione S-transferase A3)	493	98
4009	Y12781	Homo sapiens	transducin (beta) like 1 protein	326	92
4010	AF047695	Homo sapiens	cap-binding protein 4EHP	299	86
4011	U50825	Homo sapiens	SRp30c	259	97
4012	K02920	Homo sapiens	lysosomal glucocerebrosidase precursor, EC 3.2.1.45	598	94
4014	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	209	70
4016	Z22968	Homo sapiens	M130 antigen	179	97
4017	AF151042	Homo sapiens	HSPC208	740	100
4018	AK024372	Homo sapiens	unnamed protein product	142	79
4019	X61296	Rattus norvegicus	open reading frame 2	170	38
4021	AL133572	Homo sapiens	hypothetical protein	328	81
4023	AL122036	Homo sapiens	hypothetical protein	150	100
4024	AK002136	Homo sapiens	unnamed protein product	322	98
4030	AL121896	Homo sapiens	bA287B20.1 (KIAA1272 (similar to tuberins and rat Tulip))	500	98
4032	U33882	Homo sapiens	beta 1 integrin isoform D	138	100
4034	AB020335	Homo sapiens	Pancreas-specific gene	1587	99
4035	M92449	Homo sapiens	putative	1256	98
4037	U43368	Homo sapiens	VEGF related factor isoform VRF186 precursor	437	82
4038	L24038	Homo sapiens	ARAF1	2630	99
4039	AF033565	Mus musculus	cdc2/CDC28-like protein kinase 3	1974	99
4041	AJ289241	Mus musculus	calpain 12	774	81
4042	AB017335	Homo sapiens	kinesin-like DNA binding protein	542	99
4043	U00978	Mus musculus	type I inosine monophosphate dehydrogenase	415	97
4045	AF130079	Homo sapiens	PRO2852	146	82
4046	AB018283	Homo sapiens	KIAA0740 protein	207	88
4047	U11732	Homo sapiens	t(5;12) translocation breakpoint occurs after nucleotide 487	1552	100
4048	U20979	Homo sapiens	chromatin assembly factor-I p150 subunit	167	100
4050	AL109658	Homo sapiens	dJ776F14.1 (ortholog of mouse P47)	534	100
4051	X52174	Homo sapiens	precursor protein (AA -32 to 354)	273	88
4054	AL121891	Homo sapiens	dJ1187M17.1.2 (Novel protein, isoform 2)	415	83
4055	AF078749	Homo sapiens	organic cation transporter 3	232	100
4058	AF111858	Homo sapiens	dimethylglycine dehydrogenase precursor	926	99
4059	Z75330	Homo sapiens	nuclear protein SA-1	354	97
4060	AB017507	Homo sapiens	App12	251	98

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
4061	AK024426	Homo sapiens	FLJ00015 protein	485	100
4063	AJ271735	Homo sapiens	sprouty (Drosophila) homolog 3	328	100
4064	AF021031	Mus musculus	Dgcr6 protein	157	83
4065	AB007891	Homo sapiens	KIAA0431	1341	99
4073	X68301	Escherichia coli	NADH dehydrogenase I, subunit nuoB	147	96
4076	M87049	Escherichia coli	o261	228	86
4077	U00007	Escherichia coli	yohK	145	96
4079	D90819	Escherichia coli	DNA topoisomerase III (EC 5.99.1.-)	579	98
4080	L02312	Escherichia coli	quinone oxidoreductase	515	94
4081	M12987	Plasmid F	Protein D	394	93
4082	M17102	Escherichia coli	hexose phosphate transport protein UlpT	417	89
4083	M13549	Escherichia coli	threonine-tRNA ligase (EC 6.1.1.3)	155	100
4084	J01594	Escherichia coli	ATP synthase alpha subunit (atp-6)	157	83
4086	M12987	Plasmid F	Protein D	376	89
4087	U28375	Escherichia coli	ORF_f163	211	93
4088	U14003	Escherichia coli	ORF_f224	517	94
4089	L18867	Escherichia coli	ATP-dependent protease ATPase subunit	194	100
4090	U00008	Escherichia coli	yejD	268	94
4091	D90704	Escherichia coli	ORF_ID:o170#3	344	86
4094	U18997	Escherichia coli	ORF_f408	255	100
4096	X03416	Escherichia coli	hisB protein	307	98
4098	AE000357	Escherichia coli K12	putative dehydrogenase	262	98
4100	J04216	Escherichia coli	enterochelin esterase	526	76
4101	AF009204	Homo sapiens	PSD-95/SAP90-associated protein-2	4944	99
4102	D90812	Escherichia coli	msm operon regulatory protein.	182	82
4103	X67326	Escherichia coli	alcohol dehydrogenase	180	97
4109	U28375	Escherichia coli	ORF_f163	218	97
4110	M12987	Plasmid F	Protein D	382	95
4112	AL035252	Homo sapiens	dJ738P15.3 (IL-6SAG this overlaps dJ738P15.2)	353	90
4113	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	183	46
4114	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	484	88
4115	AF134726	Homo sapiens	NG35	2395	100
4117	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in	629	91

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			pSSI.		
4118	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	174	67
4119	Z44123_cd1	Homo sapiens	04-DEC-1998 Human EGR-1 DNA.	464	89
4120	D86198	Homo sapiens	dolichol-phosphate-mannose synthase	207	97
4122	W05402	Homo sapiens	Human clone 53 protein.	162	75
4123	D43633	Oryzias latipes	G protein-coupled seven-transmembrane receptor	192	46
4124	AL359782	Trypanosoma brucei	possible (hlyv-6) u1102, variant a dna, complete virion genome.	172	63
4126	Y58167	Homo sapiens	Human hydrolase homologue HHH-3.	336	81
4127	G01623	Homo sapiens	Human secreted protein, SEQ ID NO: 5704.	292	88
4128	Y73346	Homo sapiens	HTRM clone 619699 protein sequence.	321	54
4130	AL031118	Homo sapiens	dJ153G14.3 (novel C2H2 type Zinc Finger protein)	1793	99
4131	W78193	Homo sapiens	Human secreted protein encoded by gene 68 clone H2CBJ08.	300	57
4133	R04883	Homo sapiens	Human prolidase.	304	91
4134	Z27113	Homo sapiens	RNA Polymerase II subunit 14.4 kD	477	93
4135	AB025413	Mus musculus	Ten-m4	1520	95
4136	D16593	Homo sapiens	hippocalcin	152	100
4137	V04070_cd1	Homo sapiens	05-JUN-1996 Human DNA encoding DP.75, putative GDP dissociation stimulator.	239	100
4138	U09825	Homo sapiens	acid finger protein	174	100
4139	U69133	Mus musculus	Zik1	546	67
4141	Y56882	Homo sapiens	Human apoptotic inhibitor protein 6 (AIP-6).	585	94
4142	AF288480	Homo sapiens	tubby super-family protein	659	97
4144	U29156	Mus musculus	involved in signaling by the epidermal growth factor receptor; Method: conceptual translation supplied by author	459	92
4146	A00137	synthetic construct	tissue plasminogen activator	281	98
4147	AF069765	Homo sapiens	signal recognition particle 72	535	99
4148	D49547	Homo sapiens	HSP40	379	100
4150	Y15067	Homo sapiens	ZNF232	280	65
4151	X84907	Homo sapiens	carbonate dehydratase	351	85
4153	AK000755	Homo sapiens	unnamed protein product	192	40
4155	AF286598	Homo sapiens	angiostatin binding protein 1	611	96
4156	X75346	Homo sapiens	MAP kinase activated protein kinase-2	613	100
4157	Y36119	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 504.	170	75
4158	Y00339	Homo sapiens	carbonic anhydrase II (AA 1-260)	238	93
4159	AF106682	Homo sapiens	spindlin	647	91
4160	U33761	Homo sapiens	cyclin A/CDK2-associated p45	567	93
4162	L10414	Homo sapiens	farnesyl-protein transferase beta-subunit	150	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
4163	AK026944	Homo sapiens	unnamed protein product	483	97
4164	U41831	Macaca mulatta	MHC class I antigen Mamu A*05	144	90
4165	AB028893	Homo sapiens	ribosomal protein S11	257	86
4166	U38896	Homo sapiens	zinc finger protein C2H2-171	198	64
4167	AF176329	Homo sapiens	alphaCP-3	344	100
4168	AF131839	Homo sapiens	Human neuronal olfactomedin related ER localized protein	568	76
4169	AB018247	Homo sapiens	Fe65L2	338	85
4171	AF236056	Homo sapiens	golgi membrane protein GP73	602	93
4172	AF157321	Homo sapiens	30 kDa protein	594	86
4177	X87142	Mus musculus	alpha-KAP	305	88
4179	X87142	Mus musculus	alpha-KAP	296	73
4180	AB037750	Homo sapiens	KIAA1329 protein	437	97
4181	Y76351	Homo sapiens	Fragment of human secreted protein encoded by gene 48.	188	39
4182	U18300	Homo sapiens	DDBb p48	272	75
4183	X76538	Homo sapiens	hMpv17	206	95
4185	M83679	Rattus norvegicus	RAB15	150	90
4188	Y60167	Homo sapiens	Human endometrium tumour EST encoded protein 227.	488	94
4189	Z34289	Homo sapiens	nucleolar phosphoprotein p130	296	90
4191	AF272043	Homo sapiens	BRI3	284	94
4192	L12760	Homo sapiens	phosphoenolpyruvate carboxykinase	580	97
4193	AB051901	Homo sapiens	VDUP1	125	100
4194	AB051901	Homo sapiens	VDUP1	129	100
4195	M11306	Oryctolagus cuniculus	creatine kinase B	230	95
4196	M11306	Oryctolagus cuniculus	creatine kinase B	244	100
4199	L39068	Homo sapiens	deoxyhypusine synthase	518	100
4200	W19348	Homo sapiens	Filamin C-terminal polypeptide.	217	97
4201	D87914	Homo sapiens	ornithine decarboxylase antizyme	477	85
4202	V00518	Homo sapiens	chorionic gonadotropin	325	98
4203	J04440	Homo sapiens	semenogelin	159	73
4204	X79537	Homo sapiens	glycogenin	274	100
4205	M19169	Homo sapiens	cysteine-proteinase inhibitor	230	95
4206	W19348	Homo sapiens	Filamin C-terminal polypeptide.	574	98
4207	V43605_cd1	Homo sapiens	11-DEC-1996 Human secreted protein 5 encoding DNA.	338	96
4208	AK000494	Homo sapiens	unnamed protein product	350	100
4209	AF259078	Bos taurus	serine-threonine kinase PIM-1	156	100
4210	U50929	Homo sapiens	betaine:homocysteine methyltransferase	262	98
4211	AJ243663	Homo sapiens	NICE-3 protein	494	95
4212	AF087433	Rattus norvegicus	leprecan	180	67
4213	AB006191	Mus musculus	cornichon-like protein	347	94
4214	U25147	Homo sapiens	citrate transporter protein	171	94
4215	AL050158	Homo sapiens	hypothetical protein	236	85
4216	Y53054	Homo sapiens	Human secreted protein clone mj301_1 protein sequence SEQ ID NO:114.	147	100
4217	W50922	Homo sapiens	Amino acid sequence of a heterogenous ribonucleotide	144	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			protein.		
4218	D88035	Rattus norvegicus	glycoprotein specific UDP-glucuronyltransferase	498	100
4219	AB007891	Homo sapiens	KIAA0431	434	96
4222	AF107620	Homo sapiens	regulator of G-protein signaling-6 short isoform	490	82
4223	D49958	Homo sapiens	membrane glycoprotein M6	267	82
4224	S81083	Homo sapiens	adducin beta subunit 63 kDa isoform/membrane skeleton protein	292	87
4225	U51000	Mus musculus	DLX-1	248	75
4226	Z11700_cd1	Homo sapiens	11-JUN-1998 Human CEPR (hCEPR) receptor polypeptide encoding cDNA.	265	100
4227	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	154	62
4228	X05323	Homo sapiens	MRC OX-2	308	95
4229	AL110158	Homo sapiens	hypothetical protein	219	74
4231	AF205888	Homo sapiens	AXIN2	221	97
4232	R22403	Homo sapiens	Partial sequence of N-lipocortin encoded by lambda-NLip6-1X.	209	82
4233	Y10498	Homo sapiens	thymidine kinase	501	90
4235	L07758	Homo sapiens	IEF SSP 9502	263	98
4236	AF039916	Homo sapiens	CD39L2	415	93
4237	U49082	Homo sapiens	transporter protein	162	54
4238	AF119851	Homo sapiens	PRO1722	95	79
4239	M97676	Homo sapiens	homeobox protein	199	95
4240	U49719	Homo sapiens	hydroxymethylglutaryl-CoA lyase	226	95
4241	AF264765	Homo sapiens	actopaxin	260	100
4242	AF242524	Homo sapiens	hypothetical nuclear factor SBB122	418	100
4243	X15187	Homo sapiens	precursor polypeptide (AA -21 to 782)	512	99
4244	D32050	Homo sapiens	alanyl-tRNA synthetase	191	90
4245	AF043611	Homo sapiens	zinc-finger protein MCG4	219	93
4246	M34665	Cricetulus griseus	T-complex protein 1	652	96
4248	AC005546	Homo sapiens	R29425_1	146	96
4252	AF194537	Homo sapiens	NAG13	53	57
4255	L27428	Homo sapiens	reverse transcriptase	237	44
4256	L27428	Homo sapiens	reverse transcriptase	68	30
4257	AF182293	Homo sapiens	U6 snRNA-associated Sm-like protein LSm7	159	100
4258	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	44	57
4259	M13100	Rattus norvegicus	unknown protein	48	43
4261	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	276	70
4262	G00808	Homo sapiens	Human secreted protein, SEQ ID NO: 4889.	302	83
4266	U13991	Homo sapiens	TATA-binding protein associated factor 30 kDa subunit	157	74
4267	AF118082	Homo sapiens	PRO1902	47	60
4270	R95913	Homo sapiens	Neural thread protein.	67	70
4275	U83303	Homo sapiens	line-1 reverse transcriptase	65	53
4276	U70932	Peromyscus	reverse transcriptase	76	55

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		leucopus			
4279	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	82	55
4280	AF017368	Mus musculus	faciogenital dysplasia protein 2	187	66
4281	L24521	Homo sapiens	transformation-related protein	166	50
4282	U93570	Homo sapiens	putative p150	158	30
4283	X15311	Woolly monkey sarcoma virus	reverse transcriptase (476 AA)	49	83
4284	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	87	69
4285	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	115	70
4286	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	126	82
4287	AF194537	Homo sapiens	NAG13	57	45
4289	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	177	70
4290	L22480	Anas platyrhynchos	cytochrome oxidase subunit I	56	52
4292	AF118082	Homo sapiens	PRO1902	193	73
4293	AF130079	Homo sapiens	PRO2852	126	75
4295	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	103	67
4296	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	270	62
4297	AB047600	Macaca fascicularis	hypothetical protein	99	75
4298	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	150	46
4300	Y52386	Homo sapiens	Human transmembrane protein HP02000.	82	50
4301	W08602	Homo sapiens	Human apolipoprotein A-1 variant "Paris" protein sequence.	131	63
4302	AF130051	Homo sapiens	PRO0898	65	43
4305	M22332	Homo sapiens	unknown protein	49	52
4307	M13953	Homo sapiens	purine nucleoside phosphorylase	344	45
4308	AF083897	Equus caballus	glyceraldehyde-3-phosphate dehydrogenase	55	57
4309	M15386	Homo sapiens	gamma-globin	170	70
4310	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	85	43
4311	L27428	Homo sapiens	reverse transcriptase	107	54
4312	AF108841	Homo sapiens	pol protein	110	85
4315	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	224	56
4316	AK025751	Homo sapiens	unnamed protein product	306	100
4317	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	271	57
4319	AF119851	Homo sapiens	PRO1722	92	67
4322	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	187	46
4324	S58722	Homo sapiens	X-linked retinopathy protein	102	75

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			[C-terminal, clone XEH.8c]		
4325	AF130079	Homo sapiens	PRO2852	66	73
4326	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	245	56
4327	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	73	46
4328	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	177	73
4329	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	99	64
4331	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	204	60
4332	AF161356	Homo sapiens	HSPC093	182	59
4333	AF119851	Homo sapiens	PRO1722	83	77
4334	Z21513	Rattus norvegicus	integral membrane glycoprotein	731	56
4338	AF194537	Homo sapiens	NAG13	106	46
4341	L24521	Homo sapiens	transformation-related protein	235	58
4342	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	182	64
4344	L24521	Homo sapiens	transformation-related protein	45	100
4345	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	64	40
4346	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	61	40
4347	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	158	49
4348	AL121787	Homo sapiens	dJ512E2.1 (novel protein (ortholog of mouse transcription regulator BACH2 (BTB and CNC homolog 2)))	53	100
4349	R13556	Homo sapiens	Protein encoded downstream of hhc M oncoprotein.	153	69
4350	D84649	Felis catus	p27/Kip1	326	72
4354	X03725	Mus musculus	ORF 2 (466 aa)	104	62
4355	AF123880	multiple sclerosis associated retrovirus element	gag polyprotein	184	53
4357	R95913	Homo sapiens	Neural thread protein.	216	53
4359	AF116695	Homo sapiens	PRO2221	144	43
4362	L24521	Homo sapiens	transformation-related protein	181	58
4363	AK000496	Homo sapiens	unnamed protein product	148	88
4364	AB046048	Macaca fascicularis	unnamed protein product	102	63
4366	AF130089	Homo sapiens	PRO2550	215	53
4367	L06498	Homo sapiens	ribosomal protein S20	114	88
4368	AF130089	Homo sapiens	PRO2550	90	55
4369	Y70024	Homo sapiens	Human Protease and associated protein-18 (PPRG-18).	251	83
4370	AF161459	Homo sapiens	HSPC109	265	49
4372	L27428	Homo sapiens	reverse transcriptase	181	55
4373	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	115	51
4376	AK026226	Homo sapiens	unnamed protein product	1272	93
4383	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	142	69
4384	G02872	Homo sapiens	Human secreted protein, SEQ	270	53

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 6953.		
4385	G03490	Homo sapiens	Human secreted protein, SEQ ID NO: 7571.	450	96
4391	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	52	76
4394	Y73344	Homo sapiens	HTRM clone 0258181 protein sequence.	145	46
4395	AF128806	Oryzias latipes	cap binding protein cIF-4E	81	57
4396	AB037816	Homo sapiens	KIAA1395 protein	407	43
4397	M16959	Homo sapiens	MHC HLA-DR2 (non-Dw2/non-Dw12)b glycoprotein beta-chain	345	61
4399	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	148	53
4400	AF057170	Homo sapiens	bestrophin	415	97
4401	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	72	55
4402	AF305687	Homo sapiens	transcription factor ATFx	156	62
4403	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	73
4404	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	150	64
4406	Y87290	Homo sapiens	Human signal peptide containing protein HSPP-67 SEQ ID NO:67.	252	75
4408	AJ271448	Homo sapiens	protein phosphatase 4 regulatory subunit 2	240	73
4409	D38100	Rattus norvegicus	Rat kidney AGT2 precursor	950	59
4410	AF118082	Homo sapiens	PRO1902	131	57
4411	AF130052	Homo sapiens	PRO0956	67	56
4412	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	108	52
4413	M33014	Drosophila melanogaster	ubiquitin	150	62
4414	AL121845	Homo sapiens	dJ583P15.5.1 (novel protein (isoform 1))	349	92
4416	AF130089	Homo sapiens	PRO2550	224	56
4417	L06505	Homo sapiens	ribosomal protein L12	152	40
4419	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	60	66
4420	M13230	Homo sapiens	lysosomal proteinase cathepsin B	155	44
4422	AF119851	Homo sapiens	PRO1722	178	71
4424	AB047630	Macaca fascicularis	hypothetical protein	117	69
4425	R13556	Homo sapiens	Protein encoded downstream of hbc M oncprotein.	47	46
4426	AF130089	Homo sapiens	PRO2550	224	56
4428	M26361	Mus musculus	LINE/ig H-chain fusion protein	40	58
4429	U22231	Felis catus	ribosomal protein S3a	275	53
4430	AB046048	Macaca fascicularis	unnamed portein product	68	59
4431	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	68	68
4434	AB015856	Homo sapiens	ATF6	1091	81
4435	L15309	Homo sapiens	zinc finger protein	361	65
4437	AF118082	Homo sapiens	PRO1902	142	60

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
4438	G01479	Homo sapiens	Human secreted protein, SEQ ID NO: 5560.	488	100
4439	X82782	Drosophila melanogaster	ribosomal protein L7a	205	63
4443	AK022281	Homo sapiens	unnamed protein product	49	50
4446	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	197	66
4448	W88400	Homo sapiens	Human foetal brain secreted protein ck390_4.	1068	95
4449	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	134	44
4450	U14134	Homo sapiens	transcription factor IIIA	97	65
4457	AF003535	Homo sapiens	ORF2-like protein	50	66
4458	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	67	70
4466	M12987	Plasmid F	Protein A	246	43
4478	AL035587	Homo sapiens	dJ475N16.1 (CTG4A)	411	73
4479	AF038554	Homo sapiens	density regulated protein drp1	411	76
4480	AF118078	Homo sapiens	PRO1848	40	47
4481	AC005099	Homo sapiens	match to AJ222572 (NID:g3804775)	416	97
4483	U16800	Xenopus laevis	ribonucleoprotein	231	95
4484	W82397	Homo sapiens	Human UBP protein #3.	48	100
4487	M22538	Homo sapiens	NADH-ubiquinone reductase	397	66
4488	AB029309	Homo sapiens	Npw38-binding protein NpwBP	193	69
4489	AB027137	Homo sapiens	RAB-26	163	62
4492	X03145	Homo sapiens	pot. ORF III	148	54
4493	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	187	53
4494	S66427	Homo sapiens	retinoblastoma binding protein 1, RBP1	139	42
4496	AJ238969	Drosophila melanogaster	cap binding protein 20	149	43
4499	Y73350	Homo sapiens	HTRM clone 1425691 protein sequence.	258	47
4500	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	263	59
4505	AB046048	Macaca fascicularis	unnamed protein product	138	63
4507	AK026968	Homo sapiens	unnamed protein product	2690	99
4508	AF119900	Homo sapiens	PRO2822	162	86
4509	AC006283	Arabidopsis thaliana	En/Spm-like transposon protein	156	31
4511	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	55	51
4512	Y33297	Homo sapiens	Human membrane spanning protein MSP-4.	264	100
4513	AB037839	Homo sapiens	KIAA1418 protein	535	80
4514	AF130079	Homo sapiens	PRO2852	76	66
4519	AB040895	Homo sapiens	KIAA1462 protein	701	95
4522	X12881	Homo sapiens	cytokeratin 18	217	73
4524	Y11628	Homo sapiens	Human 5' EST secreted protein SEQ ID NO:280.	161	100
4526	AF057297	Homo sapiens	ornithine decarboxylase antizyme 2	155	63
4528	AE003462	Drosophila melanogaster	CG3173 gene product	200	43
4529	X56597	Homo sapiens	fibrillarin	277	70
4530	M81757	Homo sapiens	S19 ribosomal protein	163	59

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
4531	Z48810	Homo sapiens	TX protease precursor	104	55
4532	D17554	Homo sapiens	TAXREB107	154	40
4533	AF119851	Homo sapiens	PRO1722	170	64
4534	D00137	Homo sapiens	alcohol dehydrogenase beta 1	420	83
4535	Y36156	Homo sapiens	Human secreted protein #28.	83	84
4536	AF113685	Homo sapiens	PRO0974	54	62
4537	AK000826	Homo sapiens	unnamed protein product	279	40
4538	Y13204	Homo sapiens	Human secreted protein encoded by 5' EST SEQ ID NO: 218.	228	100
4539	X01703	Homo sapiens	alpha-tubulin	555	97
4540	L14788	Homo sapiens	DNA-binding protein	563	73
4544	U09202	Homo sapiens	ornithine decarboxylase antizyme	103	90
4545	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	231	60
4547	M86442	Drosophila melanogaster	protein phosphatase 2A 65 kDa regulatory subunit	566	45
4548	Y99346	Homo sapiens	Human PRO831 (UNQ471) amino acid sequence SEQ ID NO:22.	356	98
4550	G04074	Homo sapiens	Human secreted protein, SEQ ID NO: 8155.	161	87
4551	U73167	Homo sapiens	similar to hyaluronoglucosaminidase; 40% Similarity to U96078 (PID:g2314820)	642	90
4552	M13934	Homo sapiens	ribosomal protein S14	461	92
4553	M19285	Homo sapiens	glucocerebrosidase	220	97
4555	D88894	Homo sapiens	brain acyl-CoA hydrolase	90	84
4557	AB047846	Homo sapiens	gamma1-COP	429	93
4558	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	51	71
4559	AF020591	Homo sapiens	zinc finger protein	274	100
4560	M34059	Homo sapiens	beta-globin	110	90
4561	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	71	81
4563	AF236061	Oryctolagus cuniculus	RING-finger binding protein	259	51
4567	Y36156	Homo sapiens	Human secreted protein #28.	295	67
4568	AF071172	Homo sapiens	HERC2	114	84
4569	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	47	48
4571	U73200	Mus musculus	p116Rip	342	98
4572	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	207	62
4574	AF151084	Homo sapiens	HSPC250	385	64
4575	V00488	Homo sapiens	alpha globin	384	87
4579	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	160	62
4582	AF130079	Homo sapiens	PRO2852	178	64
4584	AB046048	Macaca fascicularis	unnamed portein product	272	57
4586	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	216	57
4587	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	72	68
4591	Z14019	Nicotiana tabacum	pistil extensin like protein	176	29

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
4592	X05472	Rattus norvegicus	ORF 2	125	47
4597	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	288	68
4599	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	388	76
4602	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	120	64
4603	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	104	67
4604	AK024465	Homo sapiens	FLJ00058 protein	883	98
4607	AL049569	Homo sapiens	dj37C10.5 (K1AA0445)	440	87
4608	L13802	Homo sapiens	ribosomal protein small subunit	695	96
4610	AF130051	Homo sapiens	PRO0898	57	54
4611	AF092130	Homo sapiens	GTP-binding protein Sara	374	51
4612	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	65	77
4614	R65760	Homo sapiens	Human hepatic parenchymal cell growth factor.	209	78
4616	AJ296290	Homo sapiens	putative protein kinase	267	81
4617	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	51	64
4619	L13391	Homo sapiens	helix-loop-helix phosphoprotein	307	90
4620	AF074924	Homo sapiens	heparan sulfate N-deacetylase/N-sulfotransferase 3	2418	86
4622	AF130089	Homo sapiens	PRO2550	375	72
4623	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	134	71
4624	Y94933	Homo sapiens	Human secreted protein clone rb789_14 protein sequence SEQ ID NO:72.	471	96
4626	AB008164	Homo sapiens	ST1C2	496	88
4627	M12681	Homo sapiens	apolipoprotein B-100 precursor	206	87
4628	Y11484	Homo sapiens	Human 5' EST secreted protein SEQ ID No 306.	194	88
4629	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	203	65
4631	AL049482	Arabidopsis thaliana	putative protein	174	40
4633	X69089	Homo sapiens	165kD protein	43	87
4634	M13751	Escherichia coli	branching enzyme (EC 2.4.1.18)	274	77
4636	X04051	Bacteriophage phi-80	pot. int-polypeptide (aa 1-416) (longest form, no atg)	324	100
4637	L19046	Plasmodium falciparum	MSA-2	145	55
4639	AF064539	Bacteriophage N15	gp7	221	97
4644	AF000377	Escherichia coli K12	galactose-proton symport of transport system	73	87
4646	AC006538	Homo sapiens	BC41195_1	60	66
4647	AF006621	Homo sapiens	embryonic lung protein	302	43
4650	U63289	Homo sapiens	CUG-BP/hNab50	459	92
4653	AJ278475	Homo sapiens	transport-secretion protein 2.1 (TTS-2.1)	533	48
4655	W74884	Homo sapiens	Human secreted protein encoded by gene 157 clone HLTED27.	157	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
4656	AF188700	Homo sapiens	actin filament associated protein	228	73
4657	B01398	Homo sapiens	Neuron-associated protein.	143	86
4659	M11902	Mus musculus	proline-rich salivary protein	149	43
4660	AB033050	Homo sapiens	KIAA1224 protein	259	52
4662	K01626	Rattus norvegicus	cytochrome P-450e	87	39
4665	AL353715	Homo sapiens	bK3184A7.3.2 (KIAA1088)	127	62
4666	L32164	Homo sapiens	Zinc finger	64	62
4667	M29472	Rattus norvegicus	mevalonate kinase (EC 2.7.1.36)	139	74
4668	X01703	Homo sapiens	alpha-tubulin	130	96
4669	S46006	Homo sapiens	calbindin D28K	176	91
4670	W85470	Homo sapiens	ATG-1120 (allograft inflammatory factor-1-delta) protein.	252	96
4671	L12711	Homo sapiens	transketolase	121	68
4672	X60036	Homo sapiens	phosphate carrier protein	173	82
4673	X04898	Homo sapiens	apolipoprotein	169	97
4674	J03275	Bos taurus	ADP-ribosylation factor	410	90
4675	V00488	Homo sapiens	alpha globin	459	89
4676	AF002210	Homo sapiens	copper chaperone for superoxide dismutase	515	89
4677	Y92175	Homo sapiens	Human cardiovascular system associated protein tyrosine phosphatase 2.	521	97
4678	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	497	84
4679	M21007	Homo sapiens	argininosuccinate lyase	59	91
4681	AF130089	Homo sapiens	PRO2550	40	76
4682	AF263277	Chionodraco rostrispinosus	alpha tubulin	314	74
4683	AF151850	Homo sapiens	CGI-92 protein	208	95
4685	AK024442	Homo sapiens	FLJ00032 protein	526	77
4686	AL049759	Homo sapiens	dJ930L11.1 (similar to KIAA0397)	71	45
4688	G02005	Homo sapiens	Human secreted protein, SEQ ID NO: 6086.	270	70
4689	AF090895	Homo sapiens	PRO0117	40	53
4690	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	211	64
4691	Z81024	Homo sapiens	TCR alpha	562	92
4692	U92698	Rattus norvegicus	ribosomal protein S2	223	73
4696	AF130089	Homo sapiens	PRO2550	176	70
4697	M81321	Macaca fascicularis	proline-rich protein	155	41
4702	AB015610	Chlorocebus aethiops	ribosomal protein S4X	612	92
4704	U08092	Homo sapiens	histamine N-methyltransferase	245	87
4705	Y60563	Homo sapiens	Human normal bladder tissue EST encoded protein 235.	130	100
4706	J03634	Homo sapiens	erythroid differentiation protein precursor	239	86
4708	S85655	Homo sapiens	prohibitin	253	83
4710	W54352	Homo sapiens	Heat shock 27 kD protein and prohibitin (admixture).	245	72
4711	W54352	Homo sapiens	Heat shock 27 kD protein and prohibitin (admixture).	263	73

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
4712	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	38	70
4713	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	175	62
4715	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	150	62
4716	AF119851	Homo sapiens	PRO1722	201	69
4717	S35960	Homo sapiens	laminin receptor homolog	610	89
4721	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	156	96
4723	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	307	64
4724	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	155	61
4725	AK021848	Homo sapiens	unnamed protein product	206	69
4726	U14990	Homo sapiens	ribosomal protein S3	491	86
4727	AF116719	Homo sapiens	PRO2987	617	95
4728	M15386	Homo sapiens	gamma-globin	560	93
4729	AF116719	Homo sapiens	PRO2987	595	89
4730	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	146	59
4733	AF069732	Homo sapiens	ADA2-like protein	278	100
4735	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	38	34
4737	AF118082	Homo sapiens	PRO1902	72	72
4745	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	209	60
4747	X56438	Drosophila melanogaster	protein phosphatase 1	161	51
4752	M27826	Homo sapiens	neutral protease large subunit	143	57
4754	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	218	58
4763	AF130089	Homo sapiens	PRO2550	121	82
4764	D13118	Homo sapiens	ATP synthase subunit c precursor	262	74
4765	AF090931	Homo sapiens	PRO0483	147	67
4767	AF228021	Bos taurus	cyclophilin I	209	73
4769	Y59664	Homo sapiens	Secreted protein 108-004-5-0-E8-FL.	531	93
4770	M62387	Oryctolagus cuniculus	ubiquitin conjugating-protein	227	83
4771	AF036874	Homo sapiens	multiple endocrine neoplasia type 1 candidate protein number 18	277	86
4772	M15661	Homo sapiens	ribosomal protein	123	72
4773	AK026068	Homo sapiens	unnamed protein product	245	100
4776	V00488	Homo sapiens	alpha globin	478	86
4777	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	160	43
4780	AK025047	Homo sapiens	unnamed protein product	284	66
4783	M62387	Oryctolagus cuniculus	ubiquitin conjugating-protein	248	87
4787	AF161467	Homo sapiens	HSPC118	263	98
4789	AC004908	Homo sapiens	similar to ribosomal protein L23a; similar to P29316 (PID:g132848)	359	97
4796	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	216	60
4798	G00238	Homo sapiens	Human secreted protein, SEQ	401	76

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 4319.		
4801	AB028070	Homo sapiens	activator of S phase Kinase	335	86
4804	AF228021	Bos taurus	cyclophilin 1	189	72
4808	X12796	Bos taurus	HMG1 protein (AA 1 - 215)	441	95
4810	AE000186	Escherichia coli K12	putative transferase	188	80
4811	X78412	Serratia marcescens	Deoxyadenosyl-methyltransferase	340	47
4815	M12987	Plasmid F	Protein E	289	95
4820	U83504	Tapirus terrestris	cytochrome c oxidase subunit II	227	67
4821	J04982	Homo sapiens	ATP/ADP translocator	439	75
4822	AF257466	Homo sapiens	N-acetylneuraminic acid phosphate synthase	536	93
4823	B01202	Homo sapiens	Human GTPase associated protein-27.	509	92
4826	D45131	Homo sapiens	basigin	560	86
4827	L08850	Homo sapiens	AD amyloid	252	92
4829	L06498	Homo sapiens	ribosomal protein S20	510	93
4830	J04456	Homo sapiens	lectin precursor	515	87
4831	D16111	Homo sapiens	human homologue of rat phosphatidylethanolamine binding protein	574	87
4833	X82835	Homo sapiens	sodium channel alpha subunit	163	97
4834	G03153	Homo sapiens	Human secreted protein, SEQ ID NO: 7234.	283	67
4835	L25878	Homo sapiens	epoxide hydrolase	678	92
4836	U39904	Mus musculus	citron	438	87
4842	U89715	Homo sapiens	PHR1 isoform 1	474	92
4843	Y19188	Homo sapiens	aczonin	554	99
4845	AK025518	Homo sapiens	unnamed protein product	556	82
4847	AF233523	Homo sapiens	beta V spectrin	547	95
4848	Y85565	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/2) sequence.	561	97
4849	AF047472	Homo sapiens	spleen mitotic checkpoint BUB3	564	92
4850	Y95436	Homo sapiens	Human calcium channel SOC-3/CRC-2.	309	90
4853	AF039918	Homo sapiens	CD39L4	299	81
4855	AC007263	Homo sapiens	checkpoint suppressor 1	236	90
4858	W96153	Homo sapiens	Human FADD-interacting protein (FIP).	223	71
4860	AF044955	Homo sapiens	NADH:ubiquinone oxidoreductase B9 subunit	143	55
4861	U74667	Homo sapiens	tat interactive protein	611	90
4862	G02368	Homo sapiens	Human secreted protein, SEQ ID NO: 6449.	178	100
4864	AF182293	Homo sapiens	U6 snRNA-associated Sm-like protein LSm7	173	84
4866	U18759	Homo sapiens	nuclear factor I	603	88
4867	D00654	Homo sapiens	enteric smooth muscle gamma-actin	591	91
4868	M17655	Homo sapiens	T-cell receptor alpha-chain V-region (V-J-C) precursor	207	63
4870	AF039029	Homo sapiens	snurportin 1	511	93
4871	AL133353	Homo sapiens	ba483F11.2.2 (COX15 (yeast) homolog, cytochrome c oxidase assembly protein (isoform 2))	552	88
4872	X01703	Homo sapiens	alpha-tubulin	585	95

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
4873	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	165	56
4876	AC004382	Homo sapiens	Unknown gene product	428	77
4878	X91911	Homo sapiens	rtvp-1	228	39
4879	AF076776	Drosophila melanogaster	helicase DOMINO A	53	40
4880	AF150734	Homo sapiens	PC326 protein	582	91
4881	Y00486	Homo sapiens	adenine phosphoribosyltransferase (aprt)	616	91
4882	Y66634	Homo sapiens	Membrane-bound protein PRO190.	1141	97
4883	AB000911	Sus scrofa	ribosomal protein	627	92
4884	L32558	Homo sapiens	sequence is expressed in human Tera-2 clone 13 (embryonal carcinoma) cells. The sequence may contain mismatches (one strand sequenced only once). 97% identical in 320 bp overlap with human 54 kDa prot; ORF	266	94
4886	R04883	Homo sapiens	Human prolidase.	525	86
4887	X69819	Homo sapiens	ICAM-3	1117	99
4890	AJ233670	Mus saxicola	reverse transcriptase	277	64
4891	AF055470	Homo sapiens	ZNF258	169	59
4893	G01581	Homo sapiens	Human secreted protein, SEQ ID NO: 5662.	149	64
4895	AB046100	Macaca fascicularis	unnamed protein product	113	70
4896	AF231706	Oncorhynchus mykiss	vitelline envelope protein alpha	223	41
4897	AF030880	Homo sapiens	pendrin	209	100
4899	Y15163	Mus musculus	mrg1 protein	445	100
4900	AC003110	Homo sapiens	F14150_1	147	36
4903	Y95435	Homo sapiens	Human calcium channel SOC-2/CRAC-1.	371	100
4904	AB046048	Macaca fascicularis	unnamed protein product	297	64
4905	AJ272050	Homo sapiens	transcription initiation factor 1A protein	164	68
4906	AF145613	Drosophila melanogaster	BcdDNA.GH03108	263	50
4907	L14019	Bos taurus	UDP-glucose pyrophosphorylase	215	60
4909	X15940	Homo sapiens	ribosomal protein L31 (AA 1-125)	595	95
4910	AJ388517	Canis familiaris	splicing factor	445	91
4911	W54352	Homo sapiens	Heat shock 27 kD protein and prohibitin (admixture).	216	71
4912	AF125392	Homo sapiens	insulin induced protein 2	304	75
4915	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	159	80
4916	AB004884	Homo sapiens	PKU-alpha	235	94
4917	L03303	Oryctolagus cuniculus	small GTP-binding protein	184	97
4918	U79260	Homo sapiens	unknown	152	70
4919	U31875	Homo sapiens	Hep27 protein	218	95
4920	AB000911	Sus scrofa	ribosomal protein	155	96
4923	U66372	Bos taurus	ribosomal protein S29	208	78
4924	AF114817	Homo sapiens	KRAB-zinc finger protein	177	97

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			SZF1-2		
4925	U23803	Homo sapiens	heterogeneous ribonucleoprotein A0	233	95
4928	Y16794	Homo sapiens	keratin, type I	411	100
4929	Y09862	Homo sapiens	legumain	453	96
4930	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	147	63
4932	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	58	68
4933	AF116719	Homo sapiens	PRO2987	545	86
4934	G01044	Homo sapiens	Human secreted protein, SEQ ID NO: 5125.	347	100
4935	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	548	87
4936	V00488	Homo sapiens	alpha globin	623	92
4937	M26708	Homo sapiens	prothymosin alpha	324	87
4938	AK022519	Homo sapiens	unnamed protein product	46	81
4939	AB042636	Homo sapiens	junctophilin type3	192	36
4941	Y27668	Homo sapiens	Human secreted protein encoded by gene No. 107.	42	41
4943	AB005543	Homo sapiens	MCM3 import factor	161	90
4946	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	164	62
4947	AK025116	Homo sapiens	unnamed protein product	52	61
4948	AB029150	Homo sapiens	KRAB zinc finger protein HFB101L	222	84
4949	AF194537	Homo sapiens	NAG13	283	75
4950	D38122	Homo sapiens	Fas ligand	404	84
4952	AJ132860	Bos taurus	receptor for activated C kinase	428	89
4957	W36173	Homo sapiens	GST-ATM epitope fusion peptide.	295	96
4960	M34709	Saccharomyces cerevisiae	glucose-6-phosphate dehydrogenase (ZWF1) (EC 1.1.1.49)	192	100
4961	AF222802	Mus musculus	taube nuss	1288	95
4962	D38496	Homo sapiens	LZTR-1	396	88
4963	L15441	Macropus eugenii	ATP-dependent RNA-helicase	186	91
4967	AB041399	Homo sapiens	homeodomain protein OPTX2	271	89
4968	U04810	Homo sapiens	tastin	596	85
4972	Z25749	Homo sapiens	ribosomal protein S7	144	81
4974	AF022178	Mus musculus	TAFII250 transcription factor	156	61
4975	M19439	Escherichia coli	FlbB protein (ggg start codon)	170	39
4976	AF126245	Homo sapiens	acyl-Coenzyme A dehydrogenase-8 precursor	180	97
4977	U93563	Homo sapiens	putative p150	176	62
4980	G01852	Homo sapiens	Human secreted protein, SEQ ID NO: 5933.	337	100
4981	AB021642	Homo sapiens	gonadotropin inducible transcription repressor-2	950	98
4982	M10119	Homo sapiens	ferritin light subunit	368	100
4983	U23803	Homo sapiens	heterogeneous ribonucleoprotein A0	415	100
4984	AF090988	Homo sapiens	U5 snRNP-specific 40 kDa protein	1342	98
4987	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	143	57

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
4990	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	52	91
4991	B01203	Homo sapiens	Human GTPase associated protein-28.	436	100
4992	AL121754	Homo sapiens	dJ629F1.1 (novel protein)	373	73
4993	U18271	Homo sapiens	thymopoietin beta	224	100
4995	S61070	Homo sapiens	reverse transcriptase homolog-pol {retroviral element}	238	76
4996	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	160	61
5001	Z30174	Mus musculus domesticus	zinc finger protein 30	270	66
5002	AP001745	Homo sapiens	similar to zinc finger 5 protein	157	62
5005	AF119851	Homo sapiens	PRO1722	157	64
5006	D85777	Homo sapiens	cysteine dioxygenase	224	97
5007	Y56511	Homo sapiens	Human Jurkat cell clone P2-2 AIM6 longest ORF protein sequence.	246	93
5008	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	93	72
5011	L25337	Mus musculus	RNA helicase	169	97
5012	AF070655	Homo sapiens	F1F0-type ATP synthase subunit g	376	91
5015	G03089	Homo sapiens	Human secreted protein, SEQ ID NO: 7170.	514	89
5016	U35451	Homo sapiens	heterochromatin protein p25	228	95
5017	AK000959	Homo sapiens	unnamed protein product	132	39
5018	AJ243460	Leishmania major	proteophosphoglycan	162	28
5019	W39264	Homo sapiens	Human cathepsin K exon 2 encoded polypeptide.	179	96
5021	AF295773	Homo sapiens	ral guanine nucleotide dissociation stimulator	308	100
5024	M11154	Mus musculus	myosin heavy chain	320	96
5025	AF072506	Homo sapiens	envelope protein precursor	274	76
5026	AF116719	Homo sapiens	PRO2987	347	97
5027	R65760	Homo sapiens	Human hepatic parenchymal cell growth factor.	274	92
5029	M16594	Homo sapiens	glutathione S-transferase Ha subunit 2 (EC 2.5.1.18)	460	98
5031	G01471	Homo sapiens	Human secreted protein, SEQ ID NO: 5552.	200	97
5032	AL035419	Homo sapiens	dJ1100H13.1 (KJAA1219 (similar to Drosophila GH09358 and C. elegans D2085.5))	168	100
5035	L11244	Homo sapiens	C4b-binding protein beta-chain	187	96
5037	M77232	Homo sapiens	ribosomal protein S6	544	92
5039	M13100	Rattus norvegicus	unknown protein	144	71
5040	AF309553	Homo sapiens	meiotic recombination protein REC14	201	100
5041	V00488	Homo sapiens	alpha globin	530	94
5042	AF226056	Homo sapiens	HHGP	608	100
5045	AL021917	Homo sapiens	dJ45P21.2 (novel Butyrophilin)	441	93
5046	D17512	Rattus norvegicus	CRP2 (cysteine-rich protein 2)	341	55
5047	X05972	Homo sapiens	beta-1-D4 exon	168	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5050	U93563	Homo sapiens	putative p150	202	50
5051	U93563	Homo sapiens	putative p150	202	50
5052	AF041248	Homo sapiens	cyclin-dependent kinase inhibitor	187	100
5053	M16973	Homo sapiens	complement protein C8 beta subunit precursor	169	100
5054	D43951	Homo sapiens	KIAA0099 protein	525	98
5055	AF112886	Bos taurus	differentiation enhancing factor 1	993	100
5056	R99141	Homo sapiens	Ligand binding cytokine-receptor-complementary region G-CSF receptor.	151	96
5058	AK024334	Homo sapiens	unnamed protein product	328	64
5059	Y31742	Homo sapiens	Human protease HPRM-1.	395	100
5060	AC006530	Homo sapiens	EIF-2B	473	90
5061	G03862	Homo sapiens	Human secreted protein, SEQ ID NO: 7943.	568	91
5063	Y48591	Homo sapiens	Human breast tumour-associated protein 52.	202	100
5064	Z69028	Homo sapiens	beta 2 isoform of 61kDa regulatory subunit of PP2A	344	98
5065	AF132959	Homo sapiens	CGI-25 protein	1553	100
5066	AF063308	Homo sapiens	coiled-coil related protein DEEPEST	675	98
5067	G03153	Homo sapiens	Human secreted protein, SEQ ID NO: 7234.	403	87
5068	AF183428	Homo sapiens	28.4 kDa protein	536	93
5073	D87905	Homo sapiens	mitogen-activated protein 6	410	98
5077	AB042827	Rattus norvegicus	Nadrin	527	86
5078	W82841	Homo sapiens	Human cerebral protein-1.	1112	98
5082	AE000136	Escherichia coli K12	putative transcriptional regulator LYSR-type	144	77
5084	M12987	Plasmid F	Protein E	207	97
5086	AF034975	Bacteriophage H-19B	nin orf-204	205	50
5087	U82664	Escherichia coli	ATP-dependent protease LA	265	87
5088	U66040	Salmonella typhimurium	DNA polymerase III gamma subunit	339	97
5090	U14003	Escherichia coli	ORF_o417a	199	91
5091	D83536	Escherichia coli	Ribonuclease H (EC 3.1.26.4) II.	189	95
5092	U28377	Escherichia coli	ORF_f130	476	89
5093	M12987	Plasmid F	Protein E	207	95
5095	U28377	Escherichia coli	agmatine ureohydrolase	247	79
5096	M10123	Escherichia coli	bifunctional protein	276	96
5097	L19046	Plasmodium falciparum	MSA-2	150	60
5098	AP001918	Plasmid F	96 pct identical to gp:AB021078_30	261	92
5100	M12987	Plasmid F	Protein E	157	100
5101	M12987	Plasmid F	Protein E	157	100
5102	M12987	Plasmid F	Protein E	212	97
5103	U36840	Escherichia	ORF_o357	410	97

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		coli			
5104	M68935	Escherichia coli	dedA	296	76
5105	M12987	Plasmid F	Protein E	206	95
5106	M12987	Plasmid F	Protein E	283	96
5107	X13065	Bacteriophage phi-80	cl gene (AA 1 - 236)	348	97
5108	M12987	Plasmid F	Protein E	149	96
5109	M12987	Plasmid F	Protein E	150	96
5112	M12987	Plasmid F	Protein E	157	100
5113	M12987	Plasmid F	Protein E	157	100
5114	X04051	Bacteriophage phi-80	pot. int.-polypeptide (aa 1-416) (longest form, no atg)	427	87
5115	M12987	Plasmid F	Protein E	157	100
5116	M12987	Plasmid F	Protein E	150	96
5117	M12987	Plasmid F	Protein E	157	100
5118	M12987	Plasmid F	Protein E	157	100
5119	AE000185	Escherichia coli K12	putative transport system permease protein	164	100
5122	AE000362	Escherichia coli K12	putative glucarate dehydratase	512	90
5123	M99354	Simian virus 40	major structural protein VP1	235	95
5124	M12987	Plasmid F	Protein E	157	100
5125	D90736	Escherichia coli	Hypothetical 11.5 protein in torD-cbpA intergenic region (orf2).	179	97
5127	D10483	Escherichia coli	UDP-MurNac-tripeptide synthetase (MurE)	627	94
5128	X06091	Escherichia coli	L-arabinose binding preprotein (AA -23 to 306)	334	92
5130	AF039916	Homo sapiens	CD39L2	460	88
5131	AF039916	Homo sapiens	CD39L2	462	89
5132	D13146	Homo sapiens	2',3'-cyclic-nucleotide 3'-phosphodiesterase (CNP11)	290	100
5133	Z99109	Bacillus subtilis	similar to glycerophosphodiester phosphodiesterase	161	50
5136	G00715	Homo sapiens	Human secreted protein, SEQ ID NO: 4796.	443	92
5138	AF095136	Homo sapiens	protein O-mannosyl-transferase 1	526	100
5139	AF017079	Sus scrofa	glyceraldehyde 3-phosphate dehydrogenase	342	95
5140	U96721	Homo sapiens	alternative Hermansky-Pudlak syndrome associated protein	256	92
5141	AF196972	Homo sapiens	JM24 protein	223	68
5142	AF145648	Drosophila melanogaster	BcdNA.GH08385	161	32
5143	U60987	Mus musculus	FAD-linked glycerol-3-phosphate dehydrogenase	176	100
5144	M17614	Homo sapiens	transferrin precursor (AA at 8)	264	88
5145	AF209712	Homo sapiens	membrane cofactor protein CD46 variant	452	83
5146	U96722	Bos taurus	Cdc42-associated tyrosine kinase ACK-2	153	91
5147	AB019408	Homo sapiens	unique gene expressed in fibroblasts of periodontal ligament	431	77
5148	U96722	Bos taurus	Cdc42-associated tyrosine	175	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			kinase ACK-2		
5149	X03638	Rattus norvegicus	sodium channel protein I (aa 1-2009)	471	96
5150	AF038007	Homo sapiens	FICI	190	49
5151	AF105715	Gallus gallus	ubiquitous nuclear protein	228	46
5152	AB025217	Mus musculus	Sid470p	418	75
5154	X67056	Mus musculus	glycine transporter	427	96
5156	Y76753	Homo sapiens	Human protein kinase homologue, PKH-6.	325	90
5157	R15222	Homo sapiens	Chronic myelogenous leukaemia-derived myeloid-related protein.	472	97
5158	AF228021	Bos taurus	cyclophilin I	73	88
5160	AF269255	Homo sapiens	lysosomal apyrase-like protein 1	652	100
5161	AB001517	Homo sapiens	TMEM1 protein	142	100
5162	U28495	Mus musculus	Ifc	525	83
5163	U18300	Homo sapiens	DDBb p48	469	96
5164	AF161381	Homo sapiens	HSPC263	571	95
5165	Y99672	Homo sapiens	Human GTPase associated protein-23.	563	99
5166	AF009368	Homo sapiens	Luman	467	97
5167	M55654	Homo sapiens	TATA-box binding protein	311	98
5168	D63391	Homo sapiens	platelet activating factor acetylhydrolase IB gamma-subunit	339	72
5169	AF312719	Xenopus laevis	nuclear domain-10 protein NDP52	307	59
5170	D63391	Homo sapiens	platelet activating factor acetylhydrolase IB gamma-subunit	445	94
5171	AF161362	Homo sapiens	HSPC099	858	99
5172	AL135939	Homo sapiens	dJ481F12.3 (RAE (RNA export 1, S.pombe) homolog, (mRNA export protein))	493	93
5173	D13892	Homo sapiens	carboxyl methyltransferase	401	93
5174	AC018908	Arabidopsis thaliana	putative phosphatidylinositol-4-phosphate 5-kinase; I1335-7537	167	39
5175	AF087697	Rattus norvegicus	dlg 3	305	96
5176	D85730	Homo sapiens	Heat shock protein 70 testis variant	224	100
5177	X56976	Homo sapiens	ubiquitin activating enzyme E1	369	97
5178	W82404	Homo sapiens	Human SRE-ZBP analogue GEN 506G10-a protein.	405	100
5179	X79353	Homo sapiens	GDP-dissociation inhibitor	543	96
5181	AF098477	Gallus gallus	cadherin	350	90
5182	AC004460	Homo sapiens	similar to golgi antigen; similar to U50078 (PID:g1477565)	318	100
5184	L22030	Glycine max	hydroxyproline-rich glycoprotein	158	44
5187	U75969	Homo sapiens	CHL1 protein	169	74
5188	AF155913	Mus musculus	putative E1-E2 ATPase	720	92
5190	G01877	Homo sapiens	Human secreted protein, SEQ ID NO: 5958.	304	92
5191	Y85565	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/2) sequence.	190	39
5192	U80739	Homo sapiens	CAGH26	447	92

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5193	AL031295	Homo sapiens	dJ886K2.4 (acyl-protein thioesterase)	188	97
5194	U58754	Caenorhabditis elegans	Similar to casein kinase	211	41
5195	L49431	Homo sapiens	TNFR2-TRAF signalling complex protein	300	93
5199	AB046822	Homo sapiens	KIAA1602 protein	683	97
5200	AB013139	Homo sapiens	NBS1	156	81
5201	AF174604	Homo sapiens	F-box protein Fbx24	710	88
5205	G02757	Homo sapiens	Human secreted protein, SEQ ID NO: 6838.	257	90
5206	Y32153	Homo sapiens	Human secreted protein px129.1.	283	32
5207	AF300649	Homo sapiens	regulator of G-protein signaling	213	95
5208	U03886	Homo sapiens	a gene isolated from a CpG island between STS and KAL	163	100
5209	AB040956	Homo sapiens	KIAA1523 protein	576	94
5212	M13934	Homo sapiens	ribosomal protein S14	524	98
5213	Y29816	Homo sapiens	Human synapse related glycoprotein 1.	574	88
5214	U86782	Homo sapiens	26S proteasome-associated pad1 homolog	234	85
5215	AB051901	Homo sapiens	VDUP1	200	91
5216	AF151850	Homo sapiens	CGI-92 protein	260	94
5217	U01317	Homo sapiens	beta-globin	364	93
5218	M25897	Homo sapiens	platelet factor 4	373	93
5219	Z97653	Homo sapiens	c380A1.1b (novel protein)	527	100
5220	Y53008	Homo sapiens	Human secreted protein clone er311.20 protein sequence SEQ ID NO:22.	482	68
5221	AB046649	Macaca fascicularis	TTYH1	271	42
5222	AF105715	Gallus gallus	ubiquitous nuclear protein	214	45
5223	U03698	Homo sapiens	HLA B-40011	596	98
5224	X04588	Homo sapiens	cytoskeletal tropomyosin (AA 1-248)	150	96
5225	W76215	Homo sapiens	Human FLIP protein.	189	84
5226	M81650	Homo sapiens	SEMGI	644	84
5227	X54667	Homo sapiens	cystatin S	569	98
5228	R63783	Homo sapiens	TG0847 protein.	607	92
5229	X01677	Homo sapiens	glyceraldehyde-3-phosphate dehydrogenase	604	95
5230	X64707	Homo sapiens	BBC1	531	86
5231	J03275	Bos taurus	ADP-ribosylation factor	498	91
5232	U08024	Homo sapiens	dehydroepiandrosterone sulfotransferase	563	92
5233	AF117230	Homo sapiens	protein x 0001	684	99
5234	AB000634	Homo sapiens	protein phosphatase 2A delta (B') regulatory subunit, delta 1 isoform	293	61
5235	M36341	Homo sapiens	ADP-ribosylation factor 4	365	93
5236	L25899	Homo sapiens	ribosomal protein L10	602	93
5237	X01703	Homo sapiens	alpha-tubulin	520	93
5238	Y07442	Homo sapiens	Human guanylate kinase protein.	562	83
5240	U47924	Homo sapiens	A-1	180	97
5241	AF145615	Drosophila melanogaster	BcDNA.GH03377	187	63
5242	AK024011	Homo sapiens	unnamed protein product	526	96

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5243	AK000675	Homo sapiens	unnamed protein product	162	90
5244	Y74025	Homo sapiens	Human prostate tumor EST fragment derived protein #212.	622	89
5245	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	659	98
5246	AL035462	Homo sapiens	dj995j12.1 (similar to ganglioside-induced differentiation associated protein 1)	485	98
5247	AK024966	Homo sapiens	unnamed protein product	604	100
5248	Y30812	Homo sapiens	Human secreted protein encoded from gene 2.	638	86
5249	AC004382	Homo sapiens	Unknown gene product	476	92
5250	AF151823	Homo sapiens	CGI-65 protein	470	97
5251	AF193758	Homo sapiens	synaptotagmin interacting protein STIP2	532	99
5252	AF151827	Homo sapiens	CGI-69 protein	568	94
5253	X73460	Homo sapiens	ribosomal protein L3	645	91
5254	Z23102	Homo sapiens	RNA Polymerase II subunit 14.5 kD	536	89
5255	AL031295	Homo sapiens	dJ886K2.3(GALE (UDP-galactose-4-epimerase))	505	80
5256	W76215	Homo sapiens	Human FLIP protein.	249	96
5257	L13385	Homo sapiens	Miller-Dieker lissencephaly protein	421	93
5258	AJ276894	Homo sapiens	RNA 3'-terminal phosphate cyclase-like protein	446	100
5259	AY007135	Homo sapiens	similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1	529	93
5260	D14696	Homo sapiens	K1AA0108	150	90
5261	G03827	Homo sapiens	Human secreted protein, SEQ ID NO: 7908.	548	94
5262	Y28285	Homo sapiens	Amino acid sequence for the ANTS1 human antigen.	534	91
5263	AJ006291	Homo sapiens	leucine rich protein	730	94
5264	AF161386	Homo sapiens	HSPC268	387	98
5265	D38585	Homo sapiens	TSC-22	183	45
5267	AJ133813	Plasmodium falciparum	Polyubiquitin	490	84
5269	M90696	Homo sapiens	cathepsin S	525	98
5271	G02226	Homo sapiens	Human secreted protein, SEQ ID NO: 6307.	114	91
5272	W69240	Homo sapiens	Clone A Q73_3 protein sequence.	477	82
5275	AF119851	Homo sapiens	PRO1722	93	78
5276	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	259	81
5278	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	233	69
5279	P60657	Homo sapiens	Sequence of human lipocortin.	437	58
5280	AF146191	Homo sapiens	FRG1	528	92
5281	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	280	57
5284	X98263	Homo sapiens	M-phase phosphoprotein 6	527	98
5285	A17786	unidentified	MCP-1	82	67
5286	G03787	Homo sapiens	Human secreted protein, SEQ	48	34

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 7868.		
5287	M24154	Harvey murine sarcoma virus	transforming protein p21 has	313	93
5289	AF132956	Homo sapiens	CGI-22 protein	510	68
5290	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	110	43
5291	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	228	56
5292	X03145	Homo sapiens	pot. ORF II	146	32
5294	AF130089	Homo sapiens	PRO2550	98	86
5295	L25665	Homo sapiens	GTP-binding protein	479	39
5296	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	159	57
5298	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	51	62
5299	AF123880	multiple sclerosis associated retrovirus element	gag polyprotein	154	40
5300	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	239	73
5301	AF130079	Homo sapiens	PRO2852	106	57
5304	D14048	Rattus norvegicus	SP120	1058	54
5306	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	136	71
5307	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	51	61
5308	AF130079	Homo sapiens	PRO2852	160	47
5309	AF151808	Homo sapiens	CGI-50 protein	529	38
5311	AF141923	Macaca mulatta	alpha-tubulin	313	37
5314	AF116719	Homo sapiens	PRO2987	398	74
5315	V01514	Homo sapiens	reading frame AFP	614	43
5316	M64983	Homo sapiens	fibrinogen beta chain	442	54
5317	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	52	47
5318	AF072935	Rattus norvegicus	small GTP-binding protein rab5	235	60
5319	AF130079	Homo sapiens	PRO2852	148	58
5320	AF031548	Homo sapiens	erythrocyte membrane glycoprotein Rh50	933	93
5321	X03234	Pan troglodytes	zeta-1-globin	174	50
5322	M16279	Homo sapiens	antigen	372	52
5324	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	180	57
5325	X52554	Bos taurus	protein phosphatase 2A alpha catalytic subunit (AA 1-309)	544	60
5326	AF020261	Santalum album	proline rich protein	145	31
5327	AF000381	Homo sapiens	non-functional folate binding protein	372	47
5329	AF081192	Homo sapiens	histone H2A.F1/Z variant	209	49
5330	R95913	Homo sapiens	Neural thread protein.	273	61
5332	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	136	66
5333	Y94920	Homo sapiens	Human secreted protein clone pm412_12 protein sequence	375	38

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			SEQ ID NO:46.		
5334	W68004	Homo sapiens	Fragment of human secreted protein encoded by gene 62.	164	100
5336	AF116712	Homo sapiens	PRO2738	66	76
5338	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	152	70
5340	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	116	80
5341	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	173	77
5344	AK023532	Homo sapiens	unnamed protein product	199	90
5345	AK025402	Homo sapiens	unnamed protein product	194	70
5346	AK002129	Homo sapiens	unnamed protein product	144	83
5347	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	281	70
5348	M15530	Homo sapiens	B-cell growth factor	66	66
5352	X05472	Rattus norvegicus	ORF 3	64	46
5353	U49089	Homo sapiens	neuroendocrine-dlg	3540	87
5354	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	199	63
5355	AF078860	Homo sapiens	PTD007	45	72
5361	M27826	Homo sapiens	neutral protease large subunit	522	69
5362	S46006	Homo sapiens	calbindin D28K	45	76
5363	AL021816	Schizosaccharomyces pombe	60s ribosomal protein	189	52
5364	R92114	Homo sapiens	Human ApoE4L1.	53	39
5366	Y74071	Homo sapiens	Human prostate tumor EST fragment derived protein #258.	1615	100
5369	M16247	Homo sapiens	gamma-actin	178	67
5370	AF100761	Homo sapiens	PTD017	199	41
5371	G03981	Homo sapiens	Human secreted protein, SEQ ID NO: 8062.	529	83
5372	AF130079	Homo sapiens	PRO2852	195	59
5373	AF151809	Homo sapiens	CGI-51 protein	273	42
5374	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	195	70
5375	AK025047	Homo sapiens	unnamed protein product	149	39
5376	W61161	Homo sapiens	Human squalene epoxidase (HSQEP) polypeptide.	675	43
5378	U79260	Homo sapiens	unknown	140	33
5380	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	55	66
5382	AB031292	Mus musculus	proteolipid protein 2	127	57
5383	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	177	60
5384	AK025116	Homo sapiens	unnamed protein product	45	48
5387	B07702	Homo sapiens	Protein encoded by the endogenous fragment of HERV-W.	73	30
5389	U54999	Homo sapiens	LGN protein	780	68
5390	AF130079	Homo sapiens	PRO2852	154	66
5392	AB035302	Homo sapiens	cadherin-9	146	49
5393	AF216381	Homo sapiens	enhancer of invasion 10	401	45
5394	M31211	Homo sapiens	myosin light chain 1 slow	306	49
5395	AK000619	Homo sapiens	unnamed protein product	362	57
5396	Y59720	Homo sapiens	Secreted protein 33-77-4-E2-FL1.	305	43

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5397	V40859_cd1	Homo sapiens	11-DEC-1996 Human PYK-2 protein coding sequence.	3154	99
5398	AB010282	Mus musculus	Ku70	311	33
5399	AF078844	Homo sapiens	hqp0376 protein	288	69
5400	AK023443	Homo sapiens	unnamed protein product	159	62
5401	M14221	Homo sapiens	preprocathepsin B	326	40
5403	U93574	Homo sapiens	putative p150	95	39
5404	W18211	Homo sapiens	Human integrin-linked kinase (ILK).	470	44
5406	AB016091	Homo sapiens	RNA binding protein	2757	89
5407	W63114	Homo sapiens	A human apoptosis regulator protein.	133	41
5408	U84720	Homo sapiens	mRNA export protein	483	41
5409	AF130089	Homo sapiens	PRO2550	261	56
5410	Y73469	Homo sapiens	Human secreted protein clone yd109_1 protein sequence SEQ ID NO:160.	288	60
5412	X83544	Homo sapiens	DAP-3	317	38
5413	M10942	Homo sapiens	human metallothionein-1e	66	91
5414	AJ223782	Mus musculus	CDC10	511	51
5416	AF026126	Homo sapiens	heterogeneous nuclear ribonucleoprotein D	586	59
5417	AF113685	Homo sapiens	PRO0974	160	48
5418	AK025033	Homo sapiens	unnamed protein product	404	59
5419	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	228	68
5420	AF005038	Homo sapiens	secretory carrier membrane protein	718	52
5421	U38184	Trypanosoma cruzi	ATPase subunit 6	93	34
5422	M22332	Homo sapiens	unknown protein	57	61
5423	AF130079	Homo sapiens	PRO2852	152	51
5424	AB047600	Macaca fascicularis	hypothetical protein	103	80
5425	Z35093	Homo sapiens	SURF-1	523	48
5427	G04068	Homo sapiens	Human secreted protein, SEQ ID NO: 8149.	171	93
5428	S70290	Homo sapiens	glutamine synthetase, GS [EC 6.3.1.2]	291	33
5429	X17058	Sus scrofa	glucose transport protein	413	50
5430	Y91952	Homo sapiens	Human cytoskeleton associated protein 7 (CYSKP-7).	887	68
5431	Y35969	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 218.	343	40
5432	X90857	Homo sapiens	-14	340	64
5433	AF044958	Homo sapiens	NADH:ubiquinone oxidoreductase ASH1 subunit	274	44
5435	A07588	synthetic construct	placenta protein 9	261	40
5436	D14697	Homo sapiens	The sequence from bp313 to bp1374 is almost identical to human farnesyl pyrophosphate synthetase mRNA.	334	51
5437	AJ132258	Homo sapiens	staufen protein	860	53
5438	U37518	Homo sapiens	TNF-related apoptosis inducing ligand TRAIL	456	46
5439	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	60	68

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5440	AB046100	Macaca fascicularis	unnamed protein product	37	70
5441	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	97	80
5442	AF164791	Homo sapiens	putative 38.3kDa protein	236	41
5444	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	91	50
5445	AF118081	Homo sapiens	PRO1900	213	94
5446	AC004522	Homo sapiens	Zn-alpha2-glycoprotein	326	45
5447	D49677	Homo sapiens	U2AF1-RS2	1001	89
5448	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	129	51
5449	AF010312	Homo sapiens	Pig7	762	70
5451	Y66149	Homo sapiens	Human bladder tumour EST encoded protein 7.	41	35
5452	AC011560	Arabidopsis thaliana	hypothetical protein; 114721-113936	147	30
5453	X04412	Homo sapiens	plasma gelsolin	1137	56
5455	AF130089	Homo sapiens	PRO2550	54	46
5457	L24521	Homo sapiens	transformation-related protein	229	69
5461	U74324	Homo sapiens	guanine nucleotide exchange factor mss4	208	51
5462	Y99428	Homo sapiens	Human PRO1431 (UNQ737) amino acid sequence SEQ ID NO:315.	230	100
5464	AK021798	Homo sapiens	unnamed protein product	241	78
5467	M12987	Plasmid F	Protein E	209	40
5471	M12987	Plasmid F	Protein B	126	89
5473	M12784	Escherichia coli	FlaA1 protein	101	69
5474	X13065	Bacteriophage phi-80	cII gene (AA 1 - 132)	399	68
5477	AK021798	Homo sapiens	unnamed protein product	216	49
5479	AF039916	Homo sapiens	CD39L2	1406	65
5480	AF092084	Mus musculus	P100 polymyositis-scleroderma overlap syndrome associated autoantigen homolog	3316	78
5481	U49857	Homo sapiens	transcriptional activator	130	56
5482	Y08999	Homo sapiens	Sop2p-like protein	121	95
5483	X74402	Rattus norvegicus	rab GDI alpha	428	40
5484	AF078856	Homo sapiens	p47	563	57
5485	M20752	Mus musculus	myelin proteolipid	546	59
5486	U74621	Rattus norvegicus	vesicle-associated membrane protein-1b	390	70
5488	U27315	Mus musculus	adenine nucleotide translocase-1	205	34
5489	L19761	Homo sapiens	nerve terminal protein	169	36
5490	AF312873	Mus musculus	tubulin beta-3	578	45
5491	Y42382	Homo sapiens	Amino acid sequence of fx317 11.	1102	64
5493	W57899	Homo sapiens	Protein of clone C1480 9.	406	42
5494	M63959	Homo sapiens	alpha-2-macroglobulin receptor-associated protein	393	41
5495	M63446	Xenopus laevis	gamma-tubulin	183	38
5496	AF070657	Homo sapiens	glutathione S-transferase subunit 13 homolog	136	96
5497	AF160973	Homo sapiens	p53 inducible protein	2872	86
5498	D00022	Homo sapiens	F1 beta subunit	544	43

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5499	X66503	Homo sapiens	adenylosuccinate synthetase	486	43
5500	D00759	Homo sapiens	proteasome subunit C2	66	66
5503	J04205	Homo sapiens	La protein	675	46
5505	M35266	Rattus norvegicus	cysteine dioxygenase (EC 1.13.11.20)	222	64
5506	U54807	Rattus norvegicus	GTP-binding protein	145	68
5507	AJ238095	Homo sapiens	Lsm3 protein	423	89
5509	S52930	Gallus gallus	beta B2-crystallin	124	71
5510	J04123	Mesocricetus auratus	nuclear factor 1-like protein	373	41
5511	AF209726	Oryctolagus cuniculus	voltage-dependent anion channel 2	197	37
5512	M11717	Homo sapiens	heat shock protein	812	64
5514	M76489	Sagunius oedipus	DRB*02	242	41
5515	U32376	Homo sapiens	channel associated protein of synapse	189	100
5516	U12402	Rattus norvegicus	rARL1	132	38
5518	M12530	Homo sapiens	transferrin precursor	456	45
5519	AK023719	Homo sapiens	unnamed protein product	281	88
5520	Z97029	Homo sapiens	ribonuclease HI large subunit	567	49
5522	U78190	Homo sapiens	GTP cyclohydrolase I feedback regulatory protein	192	60
5523	X55448	Homo sapiens	glucose-6-phosphate dehydrogenase	436	98
5524	AF041483	Homo sapiens	histone macroH2A1.2	371	40
5525	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	142	44
5526	W75855	Homo sapiens	Human secretory protein of clone CN729-3.	1376	81
5527	AB031069	Homo sapiens	protein containing CXXC domain 1	1204	74
5529	D85181	Homo sapiens	fungal sterol-C5-desaturase homolog	901	76
5531	D63475	Homo sapiens	product is related to clathrin-associated protein.	408	40
5533	M87503	Homo sapiens	IFN-alpha responsive transcription factor	793	53
5534	AL035494	Homo sapiens	dJ635G19.2.3 (novel protein (PUTATIVE PARTIAL isoform 3))	331	89
5535	AC003058	Arabidopsis thaliana	unknown protein	137	54
5536	U28963	Homo sapiens	Gps2	134	38
5538	U06698	Homo sapiens	neuronal kinesin heavy chain	2703	93
5539	U73167	Homo sapiens	weakly similar to furin-like proteases; 35% Similarity to U23177 (PID:g726412)	325	40
5540	AJ294707	Gallus gallus	eukaryote initiation factor 2 beta	434	50
5541	D42073	Homo sapiens	reticulocalbin	393	43
5542	AF151823	Homo sapiens	CGI-65 protein	135	48
5543	G03931	Homo sapiens	Human secreted protein, SEQ ID NO: 8012.	167	51
5546	AP001752	Homo sapiens	pyridoxal kinase	801	62
5548	AK023742	Homo sapiens	unnamed protein product	281	41
5549	D55716	Homo sapiens	P1cd47	442	50

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5550	Y76556	Homo sapiens	Human ovarian tumor EST fragment encoded protein 52.	260	64
5552	J05497	Rattus norvegicus	snRNP-associated polypeptide N	203	37
5553	AF082569	Homo sapiens	D-type cyclin-interacting protein 1	387	54
5554	AF112227	Homo sapiens	TDE homolog	66	100
5555	L42451	Homo sapiens	pyruvate dehydrogenase kinase	614	54
5556	U83246	Homo sapiens	copine 1	498	52
5558	Y94848	Homo sapiens	Human protein clone HP01550.	172	58
5559	AF058955	Mus musculus	ATP-specific succinyl-CoA synthetase beta subunit	183	82
5560	D86081	Mus musculus	S-II-T1	280	95
5561	AC005336	Homo sapiens	F20191_1, partial CDS	297	93
5562	W74904	Homo sapiens	Human secreted protein encoded by gene 177 clone HE9CM64.	547	63
5563	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	131	40
5565	Y53002	Homo sapiens	Human secreted protein clone pd278_5 protein sequence SEQ ID NO:10.	396	50
5566	AB017019	Homo sapiens	JKTBP2	750	52
5567	U30255	Homo sapiens	phosphogluconate dehydrogenase	958	53
5568	AF041429	Homo sapiens	pRGR1	200	37
5569	D83522	Rattus norvegicus	proteasomal ATPase (rat TBPI)	128	92
5571	M36647	Homo sapiens	mitochondrial hinge protein precursor	180	63
5572	R34934	Homo sapiens	Human glucose regulated protein GRP78.	374	57
5573	L13788	Styela clava	alpha-muscle actin	103	100
5574	L47233	Homo sapiens	cyclin-dependent kinase	426	57
5575	R47503	Homo sapiens	Protein derived from G-CSF stimulated monocyte (Clone GIG1b).	392	55
5576	M96552	Equus caballus	5-lipoxygenase-activating protein	160	50
5577	X69549	Homo sapiens	Human rho GDP-dissociation inhibitor 2(IEF 8120)	201	40
5579	Y44415	Homo sapiens	Mature human beta-2 microglobulin S55V variant.	181	57
5580	D00510	Homo sapiens	calphobindin II	1548	63
5581	AF057297	Homo sapiens	ornithine decarboxylase antizyme 2	146	52
5582	U44839	Homo sapiens	UHX1 protein	361	39
5584	M54788	Homo sapiens	pyruvate dehydrogenase E1-beta subunit	428	42
5585	AL137347	Homo sapiens	hypothetical protein	528	75
5586	M33680	Homo sapiens	26-kDa cell surface protein TAPA-1	504	59
5587	AJ132343	Callithrix jacchus	angiotensinogen	177	45
5588	G00728	Homo sapiens	Human secreted protein, SEQ ID NO: 4809.	168	41
5589	L11244	Homo sapiens	C4b-binding protein beta-chain	277	43
5590	AF132970	Homo sapiens	CGI-36 protein	142	40
5591	M13690	Homo sapiens	plasma protease (CI) inhibitor	284	44

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			precursor		
5592	AB005803	Homo sapiens	histidine-rich glycoprotein	201	46
5593	J03799	Homo sapiens	laminin-binding protein	436	67
5595	M21533	Homo sapiens	MHC HLA-E precursor	305	38
5596	AF130089	Homo sapiens	PRO2550	224	65
5597	U66619	Homo sapiens	SWI/SNF complex 60 KDa subunit	415	37
5599	W88104	Homo sapiens	A Rab protein designated HRAB5-2.	220	46
5600	AF121961	Homo sapiens	dJ104A17.1 (novel protein)	411	100
5601	M81637	Homo sapiens	grancalcin	621	62
5602	X07982	Homo sapiens	ME491 antigen precursor (AA - 1 to 237)	254	41
5604	AF121953	Homo sapiens	dJ493F7.2 (PTD013 similar to CGI-24 protein)	217	38
5605	R95913	Homo sapiens	Neural thread protein.	140	51
5606	AB024597	Homo sapiens	casein kinase I epsilon	783	53
5607	L27428	Homo sapiens	reverse transcriptase	249	40
5608	U63323	Mus musculus	translation initiation factor	805	37
5609	X99717	Homo sapiens	SRcyp protein	676	49
5610	U51205	Homo sapiens	COP9 signalosome subunit 1 CSN1	174	40
5611	Y17169	Homo sapiens	A6 related protein	158	44
5613	W88544	Homo sapiens	Secreted protein encoded by gene 11 clone HOUDL 69.	209	100
5614	Z36243_cdl	Homo sapiens	30-DEC-1997 cDNA encoding a bone marrow secreted protein designated BMS199.	344	48
5615	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	132	62
5617	U00697	Gallus gallus	orphan receptor COUP-TFII	447	58
5618	AF043611	Homo sapiens	zinc-finger protein MCG4	388	47
5619	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899	348	56
5620	U37251	Homo sapiens	Description: KRAB zinc finger protein; this is a splicing variant that contains a stop codon and frame shift between the KRAB box and the zinc finger region; Method: conceptual translation supplied by author	81	35
5621	AJ002305	Homo sapiens	synaptogyrin 1a	74	82
5622	AK000334	Homo sapiens	unnamed protein product	298	71
5623	AF033095	Homo sapiens	testis enhanced gene transcript protein	745	66
5626	X58114	Drosophila hydei	testis-specific RNA	46	85
5629	X00962	Bos taurus	acetylcholine receptor beta-subunit precursor	302	68
5630	AF093135	Mus musculus	PLK interacting protein	1080	82
5632	L19526	Mus musculus	GM2 activator protein	206	70
5634	AF001294	Homo sapiens	IPL	341	70
5635	Z29372	Ovis aries	aldolase B	145	71
5636	Z17227	Homo sapiens	transmembrane receptor precursor	1454	95
5637	T73917_cdl	Homo sapiens	14-NOV-1995 E6-binding protein E6-BPSD22 cDNA.	106	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5638	AF109907	Homo sapiens	S164	153	44
5640	Z12172	Homo sapiens	putative homeotic protein	108	42
5641	AJ001015	Homo sapiens	RAMP2	192	63
5642	U56734	Mus musculus	lectin lambda	6243	81
5644	L05093	Homo sapiens	ribosomal protein L18a	143	48
5645	AL021707	Homo sapiens	dJ508115.2 (KIAA0063)	764	74
5646	V00488	Homo sapiens	alpha globin	627	93
5648	AF097942	Homo sapiens	monocyte antigen CD14 precursor	236	38
5649	M15530	Homo sapiens	B-cell growth factor	92	54
5650	AF069762	Homo sapiens	map kinase phosphatase-like protein MK-STYX	564	53
5651	AB000099	Homo sapiens	DCRB	295	75
5653	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	64	54
5654	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	157	78
5655	U08139	Caenorhabditis elegans	similar to yeast RAD6 DNA repair protein, Swiss-Prot Accession Number P06104	159	88
5656	R92114	Homo sapiens	Human ApoE4L1.	117	78
5657	Z75156	Canis familiaris	rod transducin	345	100
5658	X85545	Homo sapiens	protein kinase	44	32
5659	D25215	Homo sapiens	KIAA0032	3015	95
5663	L20000	Homo sapiens	dehydroepiandrosterone sulfotransferase	594	51
5664	AL024498	Homo sapiens	dJ417M14.1 (novel protein)	43	100
5665	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	105	48
5666	B01372	Homo sapiens	Neuron-associated protein.	146	59
5668	AF112204	Homo sapiens	Vacuolar proton pump subunit SFD alpha isoform	54	91
5670	Z23115	Homo sapiens	bcl-xL	1030	87
5671	AF155655	Homo sapiens	protein x 0009	577	96
5673	AF086837	Homo sapiens	snapi	135	58
5674	AF177862	Homo sapiens	HNI protein	183	44
5675	AF130079	Homo sapiens	PRO2852	164	62
5676	AL049732	Homo sapiens	dA14C6.1 (KIAA1114 (similar to BCG1 and melanoma associated antigen MAGE-D1))	257	85
5678	AF123880	multiple sclerosis associated retrovirus element	unknown protein U5/1	85	80
5680	A61249	unidentified	HUMAN MAT1	540	98
5681	Y48616	Homo sapiens	Human breast tumour-associated protein 77.	144	93
5682	Y59878	Homo sapiens	Human normal uterus tissue derived protein 41.	367	57
5683	AF023476	Homo sapiens	meltrin-L precursor	4212	87
5684	X87212	Homo sapiens	cathepsin C	525	42
5686	U97198	Homo sapiens	unknown	768	72
5687	Z98752	Homo sapiens	dJ138B7.3.1 (lethal (3) malignant brain tumor (l(3)mb) protein (Drosophila) homolog (isoform 1))	826	95
5688	AF161491	Homo sapiens	HSPC142	171	28

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5689	AF130089	Homo sapiens	PRO2550	74	61
5690	X55188	Homo sapiens	lymphocyte antigen	378	48
5691	AF041248	Homo sapiens	cyclin-dependent kinase inhibitor	359	54
5692	L29349	Homo sapiens	granulocyte-macrophage colony-stimulating factor receptor alpha-subunit 3	915	90
5695	AF211943	Homo sapiens	WW domain-containing protein WWOX	1422	99
5697	AF144056	Homo sapiens	apoptosis related protein APR-5	378	69
5698	X69397	Homo sapiens	cell surface antigen	252	79
5699	X91014	Mus musculus	alpha 1 type XI collagen	137	36
5709	L07507	Mus musculus	alternate	315	40
5710	AK022609	Homo sapiens	unnamed protein product	154	61
5711	AL021546	Homo sapiens	predicted protein 15E1.2	98	41
5712	L25270	Homo sapiens	escapes X-chromosome inactivation	5406	82
5714	U36787	Homo sapiens	holocytochrome c-type synthetase	165	36
5715	M63509	Homo sapiens	glutathione transferase	164	52
5716	D87911	Mus musculus	Ki antigen	278	77
5717	M13934	Homo sapiens	ribosomal protein S14	407	65
5718	X12765	Homo sapiens	platelet proteoglycan (125 AA)	225	50
5719	AF090950	Homo sapiens	negative growth-regulatory protein MyD118	79	39
5720	L13391	Homo sapiens	helix-loop-helix phosphoprotein	385	47
5721	G01018	Homo sapiens	Human secreted protein, SEQ ID NO: 5099.	153	50
5722	M25077	Homo sapiens	ribonucleoprotein autoantigen 60 kd subunit	342	68
5723	R65969	Homo sapiens	Glioblastoma-derived T98G polypeptide.	249	44
5725	X52606	Homo sapiens	calmodulin	150	43
5726	W88497	Homo sapiens	Human epidermoid carcinoma clone HP10389-encoded protein.	110	100
5728	AF155654	Homo sapiens	putative ribosomal protein S1	197	52
5731	X83299	Homo sapiens	SMA3	86	94
5733	G00959	Homo sapiens	Human secreted protein, SEQ ID NO: 5040.	208	60
5734	Y86441	Homo sapiens	Human gene 40-encoded protein fragment, SEQ ID NO:356.	94	69
5736	AL133100	Homo sapiens	hypothetical protein	333	55
5737	X06640	Strongylocentrotus purpuratus	histone L1 H2b	172	68
5739	L19761	Homo sapiens	nerve terminal protein	42	55
5740	Z56281	Homo sapiens	interferon regulatory factor 3	846	60
5741	Z47808	Caenorhabditis elegans	D2013.10	51	45
5742	J03553	Homo sapiens	pulmonary surfactant protein (SP5) precursor	611	99
5743	AB001872	Homo sapiens	leucine zipper bearing kinase	688	54
5744	X07973	Ovis aries	MT-1b protein	123	76
5745	AF130051	Homo sapiens	PRO0898	77	61
5746	AF027300	Drosophila melanogaster	positive transcription elongation factor b small subunit	72	53
5747	S77733	Bos taurus	ubiquitin homolog	144	100
5748	AF130089	Homo sapiens	PRO2550	107	51

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5750	AL135791	Homo sapiens	bA162G10.3 (zinc finger protein)	289	82
5751	U30521	Homo sapiens	P311 HUM	172	97
5753	AF161494	Homo sapiens	HSPC145	355	42
5756	J05037	Homo sapiens	serine dehydratase (EC 4.2.1.13)	1066	81
5757	L05187	Homo sapiens	small proline-rich protein 1	253	72
5758	AB012042	Mus musculus	keratin 6 beta	958	72
5759	M23077	Homo sapiens	pepsinogen C	768	59
5760	M55153	Homo sapiens	transglutaminase	2750	98
5761	AB025432	Homo sapiens	GILZ	573	90
5762	AF118394	Homo sapiens	putative nucleotide binding protein	1050	79
5764	AJ249731	Homo sapiens	putative G8.1 protein	185	54
5765	S79048	Homo sapiens	pHL EIF1=secretory proline-rich protein	350	73
5766	U31383	Homo sapiens	G protein gamma-10 subunit	159	96
5767	AF150105	Homo sapiens	small zinc finger-like protein	181	50
5768	U41745	Homo sapiens	PDGF associated protein	263	46
5769	AF183417	Homo sapiens	microtubule-associated proteins 1A/1B light chain 3	394	85
5770	J02761	Homo sapiens	pulmonary surfactant-associated protein SP-B	179	91
5771	AF042166	Homo sapiens	beta-filamin	12452	92
5772	U89505	Homo sapiens	Hlark	843	53
5773	AB016735	Sus scrofa	protein phosphatase-1 delta	243	76
5775	AF002210	Homo sapiens	copper chaperone for superoxide dismutase	382	46
5777	AC004890	Homo sapiens	C2H2-150	452	63
5779	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	143	38
5782	Y48223	Homo sapiens	Human prostate cancer-associated protein 9.	266	98
5784	AB046048	Macaca fascicularis	unnamed protein product	94	61
5786	AF130089	Homo sapiens	PRO2550	169	63
5791	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	146	48
5792	AC006042	Homo sapiens	diabetes mellitus type 1 autoantigen	179	92
5793	Y36156	Homo sapiens	Human secreted protein #28.	191	72
5800	AB047600	Macaca fascicularis	hypothetical protein	143	64
5801	AF200715	Homo sapiens	PTB domain adaptor protein CED-6	223	97
5803	AK000408	Homo sapiens	unnamed protein product	652	100
5804	U30521	Homo sapiens	P311 HUM	162	91
5806	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	50	84
5807	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	318	72
5808	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	170	54
5812	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	59
5814	M15386	Homo sapiens	gamma-globin	602	90
5816	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	148	46
5817	AF090894	Homo sapiens	PRO0113	186	68

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
5818	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	169	60
5819	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	281	62
5821	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	56
5822	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	157	81
5824	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	61	54
5827	AF116712	Homo sapiens	PRO2738	150	55
5829	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	217	60
5833	AF149205	Mus musculus	Su(var)3-9 homolog Suv39h2	203	100
5834	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	296	75
5835	W88598	Homo sapiens	Secreted protein encoded by gene 65 clone HFVHY45.	53	78
5838	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	109	56
5843	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	68
5846	Y40019	Homo sapiens	Peptide sequence derived from a human secreted protein.	546	98
5847	AF130089	Homo sapiens	PRO2550	167	74
5849	AF218028	Homo sapiens	unknown	154	64
5852	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	83	69
5853	D14530	Homo sapiens	ribosomal protein	493	79
5855	AL137301	Homo sapiens	hypothetical protein	190	56
5856	AF090931	Homo sapiens	PRO0483	129	82
5857	Y59777	Homo sapiens	Human normal ovarian tissue derived protein 54.	475	87
5861	AF090928	Homo sapiens	PRO0470	145	53
5869	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	169	74
5870	AB046048	Macaca fascicularis	unnamed portein product	113	51
5872	AF090928	Homo sapiens	PRO0470	42	41
5873	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	194	54
5874	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	171	78
5875	U79260	Homo sapiens	unknown	131	40
5876	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	186	43
5880	AJ278120	Homo sapiens	putative ankryrin-repeat containing protein	42	28
5881	AP001660	Homo sapiens	putative gene, multidrug resistance associated protein like	638	82
5883	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	99	60
5884	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	157	61
5886	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	176	87
5887	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone	150	76

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			HMSJW18.		
5888	M15530	Homo sapiens	B-cell growth factor	48	61
5889	W88692	Homo sapiens	Secreted protein encoded by gene 159 clone HAGDQ47.	332	96
5890	AL137619	Homo sapiens	hypothetical protein	231	100
5892	AK024014	Homo sapiens	unnamed protein product	191	88
5894	AF116715	Homo sapiens	PRO2829	150	76
5896	Y48583	Homo sapiens	Human breast tumour-associated protein 44.	416	77
5899	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	168	65
5928	AE003908	Xylella fastidiosa	hypothetical protein	140	44
5932	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	145	36
5933	AK022952	Homo sapiens	unnamed protein product	877	89
5937	A47414_cd1	Homo sapiens	11-DEC-1998 Sequence encoding human neuron-associated protein.	630	62
5940	AX022029	unidentified	unnamed protein product	248	100
5941	AF182412	Homo sapiens	MDS025	153	91
5942	AK000427	Homo sapiens	unnamed protein product	610	60
5947	AL034548	Homo sapiens	dJ1103G7.2 (novel protein)	186	100
5948	AF151068	Homo sapiens	HSPC234	430	54
5954	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	160	48
5958	AB047631	Macaca fascicularis	hypothetical protein	363	88
5959	U89439	Bos taurus	ubiquitin-like protein	377	76
5960	AL021578	Homo sapiens	dJ453C12.6.1 (uncharacterized hypothalamus protein (isoform 1))	194	83
5961	AK025848	Homo sapiens	unnamed protein product	217	52
5964	AF262988	Homo sapiens	TRF2-interacting telomeric RAP1 protein	363	60
5968	AF054825	Homo sapiens	VAMP5	428	79
5970	Y12388	Homo sapiens	Human 5' EST secreted protein SEQ ID NO:419.	313	80
5971	AF286534	Rattus norvegicus	GTP-binding protein RAB11B	1115	100
5973	AF217963	Homo sapiens	NRAGE	4215	99
5974	Y58167	Homo sapiens	Human hydrolase homologue HHH-3.	1725	99
5978	AF000426	Homo sapiens	cLST1/E splice variant	275	98
5980	Y45264	Homo sapiens	Human secreted protein encoded from gene 8.	229	97
5982	Y65416	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1577.	382	85
5989	L33842	Homo sapiens	inosine monophosphate dehydrogenase type II	2569	98
5991	Y65416	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1577.	478	84
5996	AJ245905	Chlorocebus aethiops	HSBP1-like protein	193	95
5997	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	79	57
5999	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	136	86

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
6000	Y50941	Homo sapiens	Human adult skin cDNA clone vd4_1 derived protein.	793	82
6001	M59250	Homo sapiens	COX5B	651	99
6003	Y08061	Homo sapiens	Human c-myc protein fragment.	153	82
6004	AK000741	Homo sapiens	unnamed protein product	41	37
6007	X66785	Homo sapiens	transacylase	2493	100
6009	Y10874	Homo sapiens	Amino acid sequence of a human secreted protein.	238	63
6010	U10039	Bos taurus	Ac45	337	34
6011	AK024432	Homo sapiens	FLJ00022 protein	105	64
6012	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	64	57
6014	AF090896	Homo sapiens	PRO0131	384	100
6016	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	138	80
6020	AF116715	Homo sapiens	PRO2829	145	67
6021	R59842	Homo sapiens	ApoE4L1 protease.	146	82
6022	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	165	73
6025	M58726	Macaca fascicularis	amyloid b-protein precursor	150	100
6027	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	134	65
6030	AJ001383	Homo sapiens	NK receptor	54	91
6034	M34059	Homo sapiens	beta-globin	51	63
6035	G02691	Homo sapiens	Human secreted protein, SEQ ID NO: 6772.	346	98
6037	AB020623	Homo sapiens	DAM1	1170	100
6038	AF116661	Homo sapiens	PRO1438	145	63
6040	G01129	Homo sapiens	Human secreted protein, SEQ ID NO: 5210.	231	80
6041	W11945	Homo sapiens	p53 binding protein p53UBC.	835	96
6042	AC004832	Homo sapiens	similar to 45 kDa secretory protein ; similar to CAA10644.1 (PID:g4164418)	2147	99
6043	X16978	Bos taurus	epsilon subunit of ATP synthetase	245	84
6046	AJ238097	Homo sapiens	Lsm5 protein	462	100
6048	AF090896	Homo sapiens	PRO0131	384	100
6050	U60882	Rattus norvegicus	protein arginine N-methyltransferase	1232	99
6051	AF006070	Homo sapiens	alpha-catenin related protein	3671	99
6052	M20430	Homo sapiens	MHC HLA-DR-beta chain precursor old gene name 'HLA-DRA1'	1411	100
6054	AJ271448	Homo sapiens	protein phosphatase 4 regulatory subunit 2	248	54
6056	AF170563	Mus musculus	ubiquitin-specific processing protease	269	47
6057	AF125535	Homo sapiens	pp21 homolog	554	100
6060	AB033043	Homo sapiens	KIAA1217 protein	38	39
6063	X00568	Homo sapiens	apoCII protein	506	100
6064	AC006042	Homo sapiens	diabetes mellitus type 1 autoantigen	203	100
6067	Y53024	Homo sapiens	Human secreted protein clone am748_5 protein sequence SEQ ID NO:54.	286	72
6068	AL121586	Homo sapiens	dJ47704.2 (CGL-54)	2027	100
6069	Y65416	Homo sapiens	Human 5' EST related	436	87

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			polypeptide SEQ ID NO:1577.		
6072	R89418	Homo sapiens	Mucin-derived protein MUC1/X.	1401	100
6074	AL137619	Homo sapiens	hypothetical protein	223	100
6076	K01664	Drosophila melanogaster	Bkm-like protein	137	70
6078	AK000540	Homo sapiens	unnamed protein product	159	39
6079	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	135	72
6082	M14170	Homo sapiens	preplacental alkaline phosphatase (EC 3.1.3.1)	2782	100
6086	G01692	Homo sapiens	Human secreted protein, SEQ ID NO: 5773.	472	100
6090	M20030	Homo sapiens	small proline rich protein	434	94
6092	Y94896	Homo sapiens	Human protein clone HP10531.	441	64
6095	AJ001417	Homo sapiens	extraneuronal monoamine transporter	2906	100
6099	M10617	Homo sapiens	L-FABP	155	93
6100	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	137	54
6102	AJ272050	Homo sapiens	transcription initiation factor IA protein	854	97
6104	M13485	Homo sapiens	metallothionein I-B	387	100
6105	X53793	Homo sapiens	5' half of the product is homologues to Bacillus subtilis SAICAR synthetase, 3' half corresponds to the catalytic subunit of AIR carboxylase	2229	99
6106	U82812	Homo sapiens	Sp alpha	1949	100
6107	M36281	Homo sapiens	glycophorin A precursor	219	97
6108	Y16521	Homo sapiens	CDS2 protein	2360	99
6109	AJ388518	Canis familiaris	non-histone chromosomal protein HMG-17	150	100
6110	M13932	Homo sapiens	ribosomal protein S17	687	100
6115	AF123757	Homo sapiens	putative transmembrane protein	78	100
6123	D90892	Escherichia coli	similar to	469	87
6141	AL035422	Homo sapiens	dJ164F3.5 (deafness, X-linked 1, progressive)	228	91
6142	AF303889	Homo sapiens	roporin	619	93
6143	AF119900	Homo sapiens	PRO2822	210	81
6144	M58664	Homo sapiens	signal transducer CD24	370	97
6147	X04626	Ovis aries	metallothionein-Ia	189	71
6148	G01131	Homo sapiens	Human secreted protein, SEQ ID NO: 5212.	265	96
6150	X51707	Rattus rattus	ribosomal protein S19 (AA 1-145)	169	60
6151	AJ277275	Homo sapiens	rapa-1	87	100
6155	AF169825	Rattus norvegicus	beta-catenin binding protein	732	85
6157	AF177377	Homo sapiens	cytoplasmic protein	452	79
6158	AF219141	Mus musculus	nuclear ATP/GTP-binding protein	656	89
6162	Y79211	Homo sapiens	Human transferase TRNSFS-3.	1111	95
6163	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	53
6165	Y60397	Homo sapiens	Human normal bladder tissue EST encoded protein 69.	275	60
6167	X13546	Homo sapiens	put. HMG-17 protein	79	66

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
6168	AK024675	Homo sapiens	unnamed protein product	467	93
6169	M94131	Homo sapiens	mucin	7185	100
6170	M15885	Homo sapiens	seminal plasma protein precursor	628	99
6171	M22865	Homo sapiens	cytochrome b5	323	100
6172	Y50941	Homo sapiens	Human adult skin cDNA clone vd4.1 derived protein.	120	83
6174	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	61	73
6180	G01908	Homo sapiens	Human secreted protein, SEQ ID NO: 5989.	307	100

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TABLE 3

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1	6181	A	1	2	199	LKGVNSPIKKPRVASFFKKKNRPLVFCF*K/T/HLFCCKPPGVQKKGWKGIFP ANWKPKKTGGGLLNFDKTAF*PPKF
2	6182	A	2	1	2321	FKKNFFPPRVWGFSPFSP*KSSSPPKAFIFLGGVGPIPPPKKRFFFKNSQGVFPF/PVFKNRPKCFLLPPPISSSSSPPPVNFPGPRVFFKGPPSSSSSSSSSLRQS
3	6183	A	3	2	515	YAKLGTRILRLVKNPPAATGGCPPAS EAQASSQFALSSALYLPGEQ/GSMVPEKMRSAAGSRT*WRRAA*QPWCSGSRAPPWPWAAASATSSSATA/LPQLSDGH*T/SVPPPTPPHSPPLGDCSQRPGNWQSEA*APGQLPGTSLVPLGGSQPSQPCPLPPLSPFLFFPFA
4	6184	A	4	471	910	KWAGTGAGAPDPLQSGLVTTPTQPGFRPTL/PAPCSGLPCPRAPPWYTPSQGAGDPPRTQAADAQEHRARPCCPSAGVLGPVPTCFCPQPALSP*LHPWPT*KVPSHALQPAKALAHLLHGQGHCPHASHPV*AGSHCSCEFPDT
5	6185	A	5	1	1250	ARTFPLALDEAARGAAAEQPAALLGVPAGFRWAEPGAALRGGLAAVVGRGATWRRRRGRCPAGRIVSPVAPCALLPPSGAAGQGQGRGQLRQRRR*AGRALQPGSGQLRCPA/PPGVRRPQPRGAPGQSAFCSPPAALDKRLCGSATPKARJGEAAQRVGSDDLSSGPRGRLSLPSSVYPSWSVPVPGSPVGPVGGADCS/P*QEGRGQGIDDEVPVPALEQAAPTSWQASFWDRGDIA GKCSGGRGLRKE SASSGLDISTPQHSSG*SDP*LAPGHL*GSQAAGDRWPGRPLLPAGATVAP/SGGNQSPPTMCGAPGD*VANGKPPCFSGARAAS/GSEETPLPSAPHLSLGDTRAPYPGQ*WRGISTGVLLGLHLLPSLHVFPAPPSARARPPGRSFPASGLCPPASRRP GNSGQ
6	6186	A	6	31	318	SIVWTATLFLLEQKGTLMKMDQTSTSQMMTQKVNLLKRAKERQIS*GR*RECKMQRPCRKSVNKMFLVFLVLEFAICWAPFHIDRLFFSFVEEWSE
7	6187	A	7	125	419	GGEPYRRNEDKPVAAACGAANSVFN DTLKKVLIGFDW*PIPMGWKKNGIAWRIDKRVKFNPPGGDNLERFKGT SVPGNWLKPAYMLDSEPNNGFI
8	6188	A	8	2	319	FFLRWSL/DSVAPAKVQWRDLGSGGQAPGFTFSCSLSPSSWDYRHPPPRPA NFVFSVEMGFTMLARMISIS*HWDPP TSVSQNAGITGMASHRASLDILLNLVLS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 99/515,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion
9	6189	A	9	1	729	LAVKMAISRVCWARTAVLGSAVTPG HFVTRRLQLGRSGLAWGAPRSSKLH LSPKADVKNLMSYVVTKTKANGKY HRFLGVVIFPRFLYLYTIFMKGRAD VMGDAKKG*RNKAQQLCEGQL*GFIN FQSRMEHLRQFRQDVPKCLFIGHSIP PFANYLVFLMLYLFPRQLLRHFWTP KQQTDFLDIYHAFRKKQSHFEISYLEK VPLISDAGLRWRLTDLCTKIQRGTHP ACMRPLR
10	6190	A	10	1	283	KSVYCW*INLIQKPFWKA VVHSLVK LNIFPCNLVPLLDI*SKLSCVPGARI KIFTALLFILTLIT/VNKNLEHL*HPAE VEWVNQFWYIYIY
11	6191	A	11	15	344	KRPGRPTRPIVPSVYAGSSSKKSL* ASTHMTPTTGKKLSFFSVRSFLLPSF SSSSPRGSPGPPGSSPKASSPGAG/ EPGPKGTPRPNPPEGK*KPGPPGPIK N
12	6192	A	12	2	465	CSPPKKGFSQRPPRGFYPPSKGKKNFS PPPKGIGPPKGLKRAPP*S*/INPPRG PPLFASSP
13	6193	A	13	2	309	EKIFEDIMAKNFWNLVKGTVCVQISE QSPPSRINTKCTIPRPLILQKLTKSNN KIWKAPREKGPIT*EKK/PIQMTSSCN LWRLEAQKSVITYIYETIYISL
14	6194	A	14	27	433	RTTRPSDSEDEEEDDEEIVDVSVVEKR QAPGKRSESGSPSAGGHSKPPHNLV* VLRLLDLTIM*TDSNWTLGKEHSYA/ SPSSSL*QIRVKELFLKNMTIYVPVFLC QDSH*RQTPLVMR*KRHELSRLVYG P*DQ
15	6195	A	15	1	390	SDSEEEQDEDED*IDVSVVEKRRAPGK RAESGSPSAGGHSKPPHNLV*LRLL DLTLM*TDSNRKLSIKEISYAYNSSSPF NRFVIKNS*KI*TFCT/SVCEYSL*R QTPLLRR*KRNELSRLFFGRG
16	6196	A	16	1	239	LRPKIHELLLENLC/IILDIGLKEFMT VPKTOGRKIKITK*/IILKLSFCTATEQ SE/PDNDQEKIFHNYASNRGLISRIKQ
17	6197	A	17	96	714	FHFSFIFLKKPLNSMASREHQRNVNAI SVHLVKQKLDQPPWPAPQAAPPA RQPPGHPTGEPPASPGPPPGCNIPAG LGRGL*GVLSPA/GLPGVGAERQEP CPRAPRGAEGRAG*HQPVLPPRVPG AGAQPASASRSTRLAAPTRPLPGP GWEETAAAVPAAPELWCSILVGEPA S ATAPPLPSPLVSGRPGARHPWQO
18	6198	A	18	15	430	DPIICL*EIHFNKLDTHSLRVKG*QKI VQPSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS P*TYKAILIDLKDEIDYDITILGELNTP LSTVNRRSSQKIYMEIADLNNTLK

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SEQ ID NO. of nucleotide sequence	SEQ ID NO. of peptide sequence	Method	SEQ ID NO. in USN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, ?-possible nucleotide insertion)
19	6199	A	19	3	408	FTSLFSFNVLVLSVQIMPCSGAWQAQPLLKPSGMYCLPSHPLQCGPPHWAPAGFCAETNLR/TLKFIWKLKRPRIAKP/IWKKNNLGGKLKPLHFKTYNKGKVIKTL*YWPKD/RPSDQWKRTESETDSHIYGGQLF
20	6200	A	20	87	607	QVMGHTVKIRLGTRSALWACRGWGQ/KHMHAGL/TEQPLGVLFPEELYGDFE/DLETGDVHKHKGSGPDTQNEDEVEK/KEIDP/DEESAKKKHLDKRKLKEMFD/VEYDEGESTYFDLKGEMQKQAQLN/HAEFEDQDEARVQYEGFRPGMYVQ/VEIENVCEFFV*NFDPRIYPIILG
21	6201	A	21	3	409	GISEAHL/KDREPSKVIYAFIEKTGGVE/AVKNELRRQAPPPPPPSRGRPPPPPPPHKSGPPPPPDGRGGAAPPPPSRAPTV/ALPPPPPSRPSVAVPPPPPNRMYPVPPIPP/ALPSPAPSGPPPPPP*VLGVVPLFRA
22	6202	A	22	3	584	TOAPLTGW*PRSTRGCGSGP/HIPNG/SPFSFHWI/GRQAVGRDYPDSRA/GS/EPLSCPRQASAPGLQGTGRG/PGALSQ/TPQM/RSEPGPPRGLRGSRTVPGSTGL/LGQGTDPDPRAGQDSSLGSVAGQGTW/TGQRLVPVLSSGGQMLVIGAPLGANS/PLRWAPGSVHSTKAAMDASPSAVGT/LVLSLCILITFPVAS
23	6203	A	23	2	440	LAHCNLAHLPGFKRVSCSLSLNSWDY/RHVL/PHLADFCIFSRDGFHHVG*AGL/ELLIS/PIPTSA/FPKRWDYRREPRAR/PRNLI/*FILSPLTVIPTTFNFPPYMM/NHSAFCSYSTLVGWGRKKKKKRNFY/LRNMSPFTLGSERH
24	6204	A	24	1	218	PTRSPFFISQLGDKFFSRFC*ENWITT/*RKIKLCLYLIPCTKMDPGIKN/LVK/GKTM*LIENIEWYL*SMGEKAFFILK/KFOICKE
25	6205	A	25	4	442	VSFFTIENTIVKFKWSLKQL*II*AIVRKNKARGIILLNFPLYVKVVSXKRV/WHYRKHTYKNQ/WNRIESPETNPCIQ/GQRI/LDKGIMNIQFRNYSLVNTWC*K/NWRAPNKRKIVE
26	6206	A	26	214	422	KRESFVSVP*VGGQ/WA/NIGSLKPLPPR/LRQSLGLTLPRTNWNLGAPPVSVNFGLVRKKRGWVWSPGLEKTP
27	6207	A	27	3	189	LVKLQDNDTSKENYRPSFFIMMGTK/L/LNKISVDKIQQYVKKIHHDQVKFISV/IQCRINIQ*ISVDKIQQYVKKIHHDQ/VKFIISVIQCRINIQ
28	6208	A	28	398	0	PTANITFSSE*KAFNLA*ETRIPPS*SPPLFSIVVEILASAVSQETKWK/GLNKRI/VNEEIK/LALFADDEIYV

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29	6209	A	29	1	226	GGGRYGLALS*N*FYEAHTITLIPKSDRY STGKGNWDYIPHEY/DTQILNQTSAN RIYRIKIRLHQDQVRFIPGIQG
30	6210	A	30	2	301	GEQKNSLGPQKGPQVNPFP*EGKG CKPP*GPGFRPTGPGGGIPFLKKPKI TSSSSSPVTPPPGQVPEKFLDPGGG KLLGYPPGLQAGGPS*ISSP
31	6211	A	31	30	407	TRKVLFPFCPIPPPPPKQVGI*GLGPP ARPA\FSPRAKRKK*SKPPSPFGLGTL KKKGPPSQKPGFGPPFSTPWKASSPF/ HGPPSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS
32	6212	A	32	2	421	LKLYKRNOKARY*EETRVVCVCICI* RVCV/CVCVCMCAAYMWCAWVMC A*CVS/ACVCRCVSLWGCACMCIYN VFCV/CMCVVCTCTCICNV/CLCM SVC
33	6213	A	33	52	467	SVQVCFHVCIIGACMHVFCVTHVV VCTCVYG*VSI/CVKVCV*VCTYR*V CPRLLVCL/CVCLM/CCVCVSVCV
34	6214	A	34	3	1031	WNSDTEGRGRGTSRDLPLSDFLPPGG LPPRALALRANGEOTRTOGGHAGGP CCNHAAQQLTPSSQDEGGPLGLGQA PLILST/VEAPPMPASSWQDSQNLGPG MNISIWGGAFPGHPSSGGNLSAPRTP GGLGPPLSASRPHSPPRVAGAGEEGA SGLKTIKAGFFRDGQWPEMEQRAV V/GASSLEACEFYGGPGLRAVRQTVS CRYVGEPCRCQGLCLLSQNRTEEFGW GSPR*PGCCRPSSPG*CGKGGRDS YGP*RGKGGRR/G*EGQRPGCSAGL GSVASPGGC/QGPAWPHAEASVMEG PGSLIL/GLPRGEGHRHAPPHWTPPFI IKAKFSSCFI
35	6215	A	35	22	417	NQKRALSLGLGGRVG/SPGFPPLTPPL WKAKPGGSLRPV/SQPGAPGGTTF FPKNLNFPGGPPE/GPSSPEG*IGRFP* ARKGGLPGGQIGPPPHPGKNNPLF SSSSSSSSSS
36	6216	A	36	301	449	VIQIKKEEVK*PLFTDDMIFYLGKPEN STKKLFLKLINEFSKFAGYKVINI
37	6217	A	37	67	430	NIMVRYFTGAIY*CIKRQVTPF*FKLIH GTRNGKLPKKNENTVTEIVPEKDS TTSSPKDKPIYYLTDKILNKKLANTI QQYINRTVYHNQVSIAGPKG*FNIR KSNLM*SSNSSHHI
38	6218	A	38	1	347	CHHSQCLICVF/CGRDRVSPCCPGWS*T PGLQESTCLSLPKCWHYK/RWATIPSL KMLITIKFYFSQSLLPRRPYIYYYP HLKNSFFQLSLPLYFL*NGVSLVAQ AGVQWRNLGRR

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39	6219	A	39	15	468	QKKIARGRG/APPGYPPPLWGPPSSSP PGA/GF*PPPPKVKPPFLKKA/PSSSP GGGPPFSPPLGGKGEKIFLSPREKVP MPPKGPFFSPGGSSSSSSSP
40	6220	A	40	3	421	CWDN*ITTWKRIKLDLYL/TPYIKINS KWIRLCKTKLFLFLENIGVNLDFDGL DNDFLDMT/P*STATKDKIDKLDIFI KNFYTSKDTIKKVKRQS/TRK/ERVFT NHLSDK
41	6221	A	41	1	500	LRWSL/DSVAQAGVQWRNLSSILQLP PGFK*FSCLSFLSSWDYRCTPPRANF CIFSRD/MGFTMLARLVSN*PRDMP ASASKSAGITGVSHCAWLVPPLPEH P*K*VGPVL/CVIAWSSSHLQACMY QDRLPSAEPKGPRIEAQREQRMQSQ WERRQVPPTGIKRR
42	6222	A	42	2	414	FVSKWAEGPCGEGKV*GRGGESPA SSSSSSPPPKKSFLAPPKKVFSFHLV *PGGPLGPFLKPHPGFGPVWGSPPGK KPPWGEIGIFPSFSSPPGKSSSSPPG KPGPGPQGRGFPSTPGGGLRSHGR PVPN
43	6223	A	43	30	391	LGLLPPFFQRCPAQRGGI*RGSPAAYA LLHWLCCASSSSSSSPGLCLPVR GKSPTQASVMADAPPLTKLEHLGSTS DCCAGSKNFQPVGLLGSVGIGPTE QDHLAPWLQPPFQOSE
44	6224	A	44	1	514	VIDFCSAFAIILVVQTS*LFASLQKDN SSFRMLPQDCTESPFYFSQVLKPDLG DGSFPRDL*YVDDLLSSSL*LAC KEDGVDLLKHLAAKCHKISKEL*/L/ CKTQVKYLGHLIS*NKTTFG*RIQDI LHFPKPEMKWQL*GFLRHTSYWTP NFSLIA*LLHALL
45	6225	A	45	72	444	PPPFSPFGGPGTPISKVRGLGPEWFP GQNPVFF*NPKPSSSSSPFFVFGV WPGNPPYPLGGFPLPQFPPLPSGLGA KITLP/SPSSSGTLNLYLVNNKITIT KG*PYDPSFSPP
46	6226	A	46	51	408	QSIFGKEETRSTKGELGRRKSKTSRR KTTEIREELNEIDM*KSIQKINKTKTW FF/EKNKIDRLASLTKKKKEKIQESTI RNEKSSSSSPS/DIITGPTIEQKTFQTFY EVLSTQFIKL
47	6227	A	47	161	364	SMLSLRNRCYAVSFLRWSLNSVAQ AGVQWRHLGSLQPPPGFE*FSCLSL LSSWDYTYAPPLADFF
48	6228	A	48	1	445	APQFPGRRFRALCGSVMIGGVLCLCF YVSLNVRGCEYLLYSTCLLSICVT*/L/ CLCLFLFAVSA*ACL*ICLCLCNVC LCYSMLRSLCLICDQVILGVNSVC C*FAAEYSSSSSSSSLLDLYATSSLG VSENLHLFACMSFC

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49	6229	A	49	4	427	SWGPKRLPPLKNKPGPGVPPVISPLL GGLSSFFPGSGV*APPGYQGPPFFK/I TPKLPSSSSPPRSQFFGGLSPKNGVN PEGPPSINQNLGPPSPFWGQKK1FFSS SSSPYEPR/FPPKPNPHHGL*CCMRSG PHILLHTK
50	6230	A	50	68	423	PPLIPPPFKG*GRPEPLGPFSEKTPPAPP VKPPFFKKTKTNPFGFPAQPPFFFGG FRQKISFNPQGQGFNKPKFPPSS
51	6231	A	51	265	440	LKAKRAFTKF*HPFLKTLKKLGLGG PFFKJIRVF/DRPPAHFYLEGAKPGS PFFKTQ
52	6232	A	52	1	357	TWPLWITPGSIGIGES*KLIPIHTFYKP HLIFRQGGRMPEGKNSFSSNWCWVN WISVTHRRIKLDPPIHTIINLKWISDLN VSTKTINLLEKVGVR/LYDLGLGRCL LDMTPKAGA
53	6233	A	53	3	439	NQLDL/ETIY/RTFHLTREKYTFFSNAH KTFTKTEHILGYITILNKYERTHSI/G YYSE*PRHSINLGVYQWMNRKISWG YTYIFI*TDYNSSSSSSSPILLFAT*H NASSS
54	6234	A	54	2	372	PTLTPVPSPPLQMPFF/CV/NRPLPPVS HAHPGITLDDPPAPPASIPVDSTARS SHVSPPVFPPRPEHRSL*NPPSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSP
55	6235	A	55	3	322	GSHPEGGSPGRDPFGFVPGRPISMG RPGPI/GHPGREGPLVYP*GSRGFPRR LVFLPGTSSSSSRFT*SRLSSPWICR DPSSPPPAHPAQGGFPFPHSPCRS
56	6236	A	56	1	373	PRPGVQTPPAHG*PPVFFKIPKFPRP GGPPPYPSSSGGLAPGIPFPEGASL GPQWAPCFPPGGPKGNFFSSSSPS SSSSSSSSSS/CKLRLELSGEERGQK QDIRAPFPFPPPLFPR
57	6237	A	57	57	400	PGFPPSPPPQTKGGPPPKPSFY/PDSS SPFSPGGGPQFPNPNWGNFLPNPSLKS LGKPKKEEGGPPPG*NPQDCPPSS SATTLQSGSGRCPLTPRQGGKPPPV TAPCAATK
58	6238	A	58	198	403	RIMIQPRADFSLOTMDGKRNWNNIFK VYKEENYQPRILHQAKISFRNNGNLR *SIKRIFCQQNYLWKN
59	6239	A	59	2	248	TOPLILRCLPSPSYRFSNIPKIQVNF *EKEKSLKFIQNLKG*ITKTLIRKKK VDGKITPDPFTMYKYATVIKTVSWYQ

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60	6240	A	60	2	795	GWGTLGDSLEKGLLWPHGGAEWA PREKAHPQGGKGRPRAMHSSTPAV LSFHGEPMHGTASWV*F*TRGQPDHS PDHQGEPRGPYPHPKE*KTCKGLRP HCPDWGKPWPEORDAPLPRASADASS VPOAQHQQRPFVLSGHRQGRPSAK PGSPAPNKVAGRSRGHTPVPATSEQET SLALQALSGSMRQPPGHEEGNSMAG TPPS/SAGTPQ
61	6241	A	61	1	265	LLPSRWDFWRAPR/QHIFVFLVEPGF HLVGQDGLDLLTS*ARLSLKPCKWEY RREPLRPVTRVLTSSNDHCFLLPAVG SQQFQSYSL
62	6242	A	62	19	451	KPPGPGPPPLSPPLWGFSPVVPQAR GPKSPRVPGGKNPPSPKIKKFAVRG GGPPYSPF*K*KPPGPGPPPLSPPLW GFSPVVPQPGDPNPPGYPGERTPFP QK*KNLPLGLGAGLIPPSPEG*AREPA LTPGAGPPITKNPSSSSPVGP
63	6243	A	63	388	451	GTHADAAAPP*SPRSPALPSRSLEPPE ELTQTRLHRLINPNFFGYQD
64	6244	A	64	1	455	RKTDVNVCGVHNPQIANHLKFTGVQ LSGACQDIPSKVKGELI/HLIY*SQTA QCLVGFFGFWRHHDAI*QHL/REFRK ITRSSSS
65	6245	A	65	29	420	VPCRGWAVWTPPHRDTPPQATFLGS LDLPWWTDSRGLGFFTPYRGELKA WEEAAPQPGSPKPPPG*EQEMPPGGH SPSAPLAQQWGGSSGSLPLARP/SLP PLLPLGLKSCWALCAPAVGSAGCLLH RAR
66	6246	A	66	22	442	HAKLGTRK/WINIPCSYIGRLNITKMT VLFQILR*INAIKIPAGFLLVCMKVG KASSK*RRARLSNTT*RKEQG*SL*LL DIKTYFNVTISRWVLGQRQKNRAG* SS*VDLYICVLMH**VTMQC*WGKDL FFNKWSFG
67	6247	A	68	1	152	FFWIASIPLTPATCSAWWELVGHAPH/ GQPSQQPCSCQ*TPLSCTCPOGN
68	6248	A	69	3	193	RGKPTSKNIKKLIKLSSTKKYP*LDGF TSQFYQTFNE/NLMPILCKLFQKLEEE EILSNSFYEA
69	6249	A	70	592	1078	LEANMPGTRLSPAPASAPGDRRIPE GSPPPSARRLPLGSRKP/GPPTPOAGV ASEPSSSEHGVGIRRRP/SDGDHSDQRD SAPSGRSGVGVGRGGATKTGEVQAP AKEPLC*LPGTYVSYYPG/KSGGGLPA PRAP
70	6250	A	71	154	410	PGLVFLGPGPGP*DISCFQPKVFLYPH PGPEGPPQRGPIGGKGPNSGPDSP VGNNNRKGVGH*P/GPGVVPTVAGP KKGALLA

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71	6251	A	72	25	317	SNLMVHLKELEKQGQTKSKISKIRKE /IKIRAEIYKVATEKTIQKSSKCRSSSS SSSSPSL*LDKKRREKTQINKIRNEKG G*YHKNTKVIYGDYYK
72	6252	A	73	2	274	SVTDDLFIYIESPNDSTKNLINKFSKV AGYKVNIOKSVVFLYTNNELYEKEIK SSS/PSSSSSSSIKYLRRHLIKEVKNLD TLRTIKQ**EQ
73	6253	A	74	204	368	KQTVLEENRRETLQDMGL/GEDFMG KTL*AQAATKTKIDKWDICLKTYT*K EIINY
74	6254	A	76	268	391	TDKLAQIYMERQRTFV*DLYADNCK ALMKDINF*INRDTQC*CSWIGRLHIV NMSVLSKLIYRFNVLPNKSPNSRSSP NRQAG/CKFIWKGKGPLLPKQL*KSK SWRNHKKIIVIVNLKFT
75	6255	A	77	698	2107	LFECNIPSPPGS/AYPRTNVGLGPCRP TSEGSQVQVGAQFSS/RSQTGPGST EDHDAGWSEDTFRIKS*A*EMLIYV QAGSGPKGQTERNTVSTGERGRAGR MKSSGGHAGDLAGQGGEGG/PLGGDR GKSGSSEPGEEESVAYRKQKGAAPTPI LGSS/LGP*GLPPKGVNANPNNTTA*G GASARCGSGIWMASRR*/EAGPPCS PAGRLAALPGHARAPSSRDSASLFS VPKGVYGAAGAPWTLRREHLSQLIT* GWRAPRAPLSGVCTGSSGPKASPCRE SSGGWGHDSYSLFALGEAVGRLPTLV ADSSSSTGRGLR*DICLGRKKSQAPVF GQLLSWGESSSSSSSSSSSPH/EPP RAGGQCPAQELSHTPILLTLVSPFAS GEGCCCVLC*WQVSKSV*KEMEIG/V AGPE*TPRPPTCEEEGVGGIGVRA ACRQLSVCRGLTRRTYRCQTGPAPLA LL
76	6256	A	78	2	306	FFFLRQSL/NCVTQAGVQWRHLDLSQ APPPGFTPFSCLSLPSWDYRRP/PPR ANFFVLLVQTGF/VLARMYSIS*PRD PLASASQSAITGLSHRAPAQVS
77	6257	A	79	129	465	GEGSQIFPPGREG/PPKVVNGASSQ GKTNSPPFEERGITGSSSHPH*CLFLK KTGVPPGGPEGPKTPNLGENRPGPK GGE*RGGPMGPTQKGLFSPFGIPIR QKKMG
78	6258	A	80	2	379	DSLRFQLETSIWIQRSDVDFLYLHM PDHSTPLEDTLRACQHLHQEGKFEEL GLSNYAWEAVEICTLCRS/SGWILPT VYQG/LLTGKYKYEDKDGKQPVVR FFGNTWAEMYRNRY*REHHEFGID
79	6259	A	81	15	255	CQPPPPGFKANS/CSASSFPD*AGN*Q PDNPRLANFSYYF**RWGFTILARL VLNS*PCDPPASASQAGTIDVSHRTC P

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
80	6260	A	82	1	107	LFNGGNSLFNKRCWEWIPTQKITMD AYLIPYTKUNSEWIRDVTMLRN*NS* KRI*GKNFHDVFGNILGYDIKSKG KKLHYIKIENPHASKGHENEKATEK *KIIT/TYISDKSSSSSSSSSSSLTQL KKWTKD*NGGNSLFNKRCWEWIPT QKITMDA YLIPYTKN
81	6261	A	83	3	408	FFLRRSL/DSVAQAGVQWRDLGSLQA PPPRFMPFSCSLSPSSWDYRRPPLRPA NFLYF**RRGFTVLGAMVSI*PRDPP ASASQASAGITGVSHRARPIQMILMLIL SLSFQKMSLESFQTESSISYPNNLQWFD VD
82	6262	A	84	2	443	AFLWFPSPGGGGRGVPLFFGGGGYCN *GPPPRV/RGGGGKRGSSSGGKKK
83	6263	A	85	4	393	LDSSTIMAGDFSATFTHRGSNNRKKKT PRETEDLNSTNCS*DASRPLHLVTEK QTFLPVHRILLQKDSMLGHRSHVGL KRTAIQSVLSNHSRMLKLESITGENLE KSKT*KLSTTLNNQSVKKEITRE
84	6264	A	86	1	250	PSSPAWWSNRDRDSERE/KGHIDGEAE T*SERD*EKKDEQ*QDEKGRQSRDPE RQS**E*M*KRGRERMMQALGLISAL LLLDG
85	6265	A	87	106	453	KKGFVWVGAGAPPYFYFPFGRGGGPF LLIQGFKPLAPPKNPVLSKSNYPGGF GGPLIPPSSKG*GRKMGLPPKGSPL/S KPKFGSPPP
86	6266	A	88	2	1563	TKPGTFSHLIFNKAYKNFHLRPESLK MLQDSIQKAFDLIGLQGVVMTNAPK ANA/TNIE*DK*DLMKPKIFCKAEI S/VRVNTQPTV*ETVVTN*ASDKGLM SRL/HKELKEISKKK
87	6267	A	89	222	436	KGNFLFGAPAKIKGGDLGLEPLPSG LKGISCLTLFRG*KKRGPSPCPNFGF LKKTGFLHGGGGGQFQPK
88	6268	A	90	481	0	EWEKIFVNYTSDT*LIPQKHQELQQL NGKKASNLVEKVVWDLTFKKNEMQ MANRSMKKCSASLIUREMQIKTTVR* YPTPGSMAVFKRQ/NDQCW*GCGER KTLIHC*WKYELF/KPLWKTWRFLK KD*KIDPPYPNPAIPLSKENEM/CCNK HTCACVFI
89	6269	A	91	4	374	FPPATLGRVLASPLPROQLPLSVLVIL AVPGGGSWCPLGFDLRFPGGQPCGA SLPVSSTRACLFHHSLLYLFDRVLLC HPGWSA VV*SQLTAASTSWVKRTSH LGLSSWNYYRRAPP*LVN
90	6270	A	92	3	241	TFSCLSLSSSWDYRCPPQAGPANFCI F/M*RRGFTALARMVSVS*PRDLPAS ASQSAGITRVSHRTRPLV*CFN*ALFR

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91	6271	A	93	2	250	DHWGENREKERGDKERNKVFERRR N*RVREERTERKKERFQRGSEKEKE RESEKEE/EGKSKKEDKEEKREKEKE ERRRKGGE
92	6272	A	94	1	258	SGHPRRQEDCPTLQMGKLRPGEGQ*/ HHPELHSQ*ECEPCSHGRITYAYTPS GLPAIGTFCVSPSPSPSAPGS*ELPSA FVWASR
93	6273	A	95	2	415	YSFTNNNSIQKVNQEPNHHIYTY*VTN LMNEFTK*VKDLYSENIDETN*RLQK *K/SFLCTWIG/RIYIVIIIFLPKETYRFC VINISMSSS/PSSSSTEIQK/TILKLWVN YKRH*IIKVLNKNDAEAGITQPDLSIR YQI
94	6274	A	96	478	0	RLCNGPVLAHCNLC/LPGKRFSCLS LPSSWDYRRAPPRQLIFVYLLTGFH HVGQDGLDLLIL*SVCLSLPKCWDYR RDSRTWP
95	6275	A	97	3	434	ATEIKSIHGYND/RLCTTKFYNLDEM DKFLVRHKLKPLI*E*IDNLRWITSQ ETDW*I*QQSSSSSSSSSSSSSSSRP NGFTTESYQSFEKLIPIICKLLKIDKE/ GHFPLQL*GITQIPKPDYH/ENYRPI SLM
96	6276	A	98	2	432	GAAEIKSIHGYND/QLCTNKFYNLDE MDKFLVRHKLKPLI*E*IDNLRWITS QETDW*I*QQ/PSSSSSSSSSSSSSRP NGFTTESYQSFEKLIPIICKLLKIDK E/GHFPLQL*GITQIPKPDYH/PQENYR PISLM
97	6277	A	99	3	802	HENYSQECGSFLLAESIKPAPPFNVTV TFSGQYNISWRSYEDPAFYMLKGG LQYELQYRNRGDPWA/*VPGEMLSM DSRSVSLPLLEFRKDSSYELQVRSGP MPGCSYQGTWSEWSDPFIHTQSEEL KERWNPHELLLLLLLVIFAPAFWSLKT HALWRLWKKIWA VPSPERFFMPLYK GCSGDFFKWWGAPFTGSSLELGPWS PEVPSTLEVYSCHPSPRAKRLQPEL QEPAEQEEKAGVPKPSFCPTAQSSVIP TRCSRC
98	6278	A	100	81	433	SEPNL*FNVEGKGFVKQSL*ETGML E*ICI*DTCSQWEGLEDIFIMNLRNNI M/GSPASLKSFMIILYRPDLSVRTAA TQLGNL.NATGVIGPQGGSSQKAFFNC RRQC GG GYHY
99	6279	A	101	7	574	WVVGSPPEGPDPSRMVDNPSQRHPIL GORPAAAPQR*P*RSAGNPQRPAAP PPPLKKKHKQKNFPGMSLGRFTPEM FWEREPRGHPTPR/GIGPRHSFPRQWP R*NS*RPFPQVRDPQQRHLKYKSPD HPRNGQ*RTPSQIGKAPHPPDTPSY RTQTFPQTTPGSPINPRAS/SSPPP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
100	6280	A	102	2	214	RSGTR*GCAHCHHCFS AVIDILARAI R*EKDIKGTQIGKDEVKLALCADDMI LYLEKPKDATRKLKLLN
101	6281	A	103	61	450	ILCIFLSLWYFV*FCCDLYYFFC*HEV *FVFAFFSTLRCVSL*CLKFICIVCYCY KPLF*HCFCCVPRFWYVVL/LFFF
102	6282	A	104	165	510	IISKHTENTCAKIQHPFMLKR*QTEEDI IKL/YGKELHGEKQDTFPVPRGIWGC PLLPH/YLFNIVLEVLVR/STRQENIN GIQTG*EVKLYPFASDIILDTGKPKKQ TKTNSATLD
103	6283	A	105	115	443	LYEN/YRLISLMNTDAKIHKILANQVQ *CIKIRIRHHSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSPAYNKTTPHPI KLSSIGIEVNFLNLIKKQVQKPY
104	6284	A	106	1	454	LFEEKINKI/DKLLSIIRKKEDVQITKMR NERGDITADDT*VKSISSSSSSSSSSS SSSSSSSSSPLEIQSLKMKCHK*TK/NL NRLTISKIISKSTIKNFP/HPNPGSGGFIG EL YQT*K*/IYCFKLKIQEIEEVKTL SN SF/YEANIRIPP
105	6285	A	107	2	296	VGGFHNYANVELVDIAKRIPELALW AGWGHASERPKLPPELLCKNGVAFLG RVCPHHILGIGVLLGHSAGSDPLSP VL*SGGPFDFPHPTSVVRSE
106	6286	A	108	1	296	KRRFVLFSPRGGRGQKV*PFKPCPPK FKKIFCPSLQTGGDKRGPPNPRGVNF *MFGKTQNFPLGGGSGKPRPPGNPP PYPPKS/GG*NPQNRP PPM
107	6287	A	109	227	417	NHFPARMAAIK/SSDNNRCWCN/CG TTGTLIHGWWEREMVQPLWKPVWR LIKQLSTELP*DSEIP
108	6288	A	110	3	476	KRIYTNPTDNIIPNNERLNAPRLKTR PEHPLSL/HLSVVDLVLSA/IRQ/EKE IKGIQRKNKIKLSLFFVNSMIV*VKKN LKESASSSSPLSKNKP*GPRLNKPN VPFLFWPITPGAPKFNMRPFIKVQ WRAGGLGPGTIPFLKGGKPGVYPEAK
109	6289	A	111	1	367	STRGLGLPKCWDERSHHAQPNFLFLIF HKFHK/CSLVLFN*CIY/CSHFSIL*SRE EINYLYLPTFGAIDTKTGRTDVVGSK ASINIQVSFFFFLRRSLA/VAHAGVQ WCGLGSLQPLPSGCKQF
110	6290	A	112	10	347	KDKILKLLARI/TREKSOQIRNERGDIT TD/TTEIQKNKRL*/HNYVKNLIM*KK ILGTYNLPRWNHETENLNRPIATNNK *EIESVMKSLPSKSPGPDHDF*NYQ KIEEGRK
111	6291	A	113	3	257	DSLAVV/SNTLGG/QISVVISKGIPYY ESSLNVTSVV*VYMQFKKYMLYII SILGSIAGLRTS*ISAAASLNMVFMKEHL GSKHSH

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112	6292	A	114	141	404	EVNVDPLFAELLNGMLAMEDPGVND TILLALTIVIHGAGAQVDAGLPKNIIVS LTVAKEPTIHGTDSTVHP*SLPTPGEQC LFCRGSMHQ
113	6293	A	115	2	78	ISQRTHEEEEGLLYLILRFVTH**IKS VLYYHRNRQIDQWIRIGNPD*TD*LY GQVIYNKGASQISEEGLFQQLC*NN* TKTFCNTLIN
114	6294	A	116	231	409	KYQILLYNGDVDMACNFMGDEWVF DSLNLQKVR*RF*RPWDRGCCGGLGA G
115	6295	A	117	1	95	FSSGFLFLFCWMFFFFINISHLLYYLFI YI*IKYFYFQFVFLIRHCLSLFLITFF VAVFISGM/CLHF*LYPEFCHLISELF *I*FILFYVMCHLKMSEFL*INSHLLY YLFYFI
116	6296	A	118	3	380	SPLEPPPTPPFASRPVTRLKYWVALR GEVESVTHEKVPT*KLLEFSLHYK* KSSE*AWEWILRVWDNGGRNIELGQ AEFIASGPLSRDSAFNVAAQ*VKKG NSLFPWLAEIRLKKWPPVREL
117	6297	A	119	4	410	NWRSMVPFOAFATLAFPGMIPPPSP PEEVGPPGSSS/LNPGNGFIFGI*GEG GF*TPGSSSSSGPGPKFS/GFVGL*GG APLAPLCSSSSS
118	6298	A	120	1	403	DLKQNH**SKFTM*KAMTFPVTSKNI KY*KVNLTRDMQDMCTGNYKPLLKE IKESS
119	6299	A	121	66	407	ELVILNISIKKIPGQDDFTGEFYKMFIE EITSILPILFOKIDAN/NSI*TSIILPKS YRDIRKQSFSSSSSSSSSSSSSSSSSS SSSSSSKQLEFIPMEGWLN/*KSVN
120	6300	A	122	3	274	DRISLSSRLSCSGTILAYCNLHLP/GF KQF/SCLSLPSSWDYRHAPPR/RANFCI FK*ET/GFAMLGQGSLELLDLVDPP/ ALATPKCWDYRP
121	6301	A	123	7	396	KRGKRRRERVAILTTNKIDFKSKTVA SSSSSSSSSSSSSSSSSSSSSSSSSS SPNYIKQILTNLKREVDNNNTTVRDF HIPLSTMD*SRQINKETADLNYTIDH MD/LDIYMTFLSKTAKYTF
122	6302	A	124	4	416	DGSALSPLRSCSGVIAHCNCLPGRS /RFSCLSLPSSWDYRRPRPGAIFVLL VETGFHRVSDGLHLLTS/PPASS/F PKCWDYRRDDRAWPAVNQVRQSGK KMCTSPGME*GPRNETGEILCPIFLP NPDEACP
123	6303	A	125	3	358	FLRWSLNSVTEAGEQWRDLGAWFK QFFCLSLPSS*DYRHLPPCANFL*F** RRGFTMLPRMVSIS*PRDPPALASQSA GITGVSHGAWPEMIFNREPSGCKRA QKGQIKRNVPGLC

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124	6304	A	126	33	439	TGVCFFAQQGNNR*PNFGSKQLAPGG KQISCPTPPSKWGIGAPLPRNNFLPL IKTGVPVRVPAVLKLLKPGNMEGSAP PKGRVSKGKPPARPASS
125	6305	A	127	2	295	SRLNYKGVVLRQWCWHRDRYVDQ WT/RL/GDCTCSSLVYNKGTDV/GLTG KDVLF/NKCCWNR/WEK/MNLSSYFIP *TKINSKWIHLSTNSKNRRLQENGII
126	6306	A	128	3	408	EPYRQGREVIRGIEGKEAGHRGAAPG VAGMVGDRQRWGSGETESERERETA RKRERETVSQRETERESQRETERERE REKDKKRDREDEEDAYERRKLER*L REKEAAVQERLKNWEIRKDT*REY *ERSLKE
127	6307	A	130	598	1335	RQHISHVRMRQI/HSGQISYECQGCG RYFIQMADEFHRHEKCHTGEKSFECKE CGKYFRYNLLIRHQIHTGKKPFKCK CEGKGVSSDTALIQHQRIHTGEKPYE CKECGKAFFSSSVFLQHQRHFTGEKL YECNECWKTFSCGSSFTVHHRMRTW EKPYECKECGKRLSSNTALTQHQRH TGENPFECKE*GKAFFNQKITLIQHQRV HTGEKPYEC*ACGKTFRWGGRFILHQ NLPTQKTPVQA
128	6308	A	131	17	322	FYLANPG*NLVPLKGPPSSSPKRSS PPPPGRKPRGQRPPTPFQGGRIPL KNGGPRKG/RPRPNQP
129	6309	A	132	3	470	RELILKFRWDFKGPRIASSSSS/IVKD KNKAGGLTCPNFKTYKAAV/K/TV WHWHKDRHTDQQNKTESPERNPCIY DFQSSRDH/YDKDSLFNKRCRDN*IS TCKRMKLDPLYL/P/SSSSSSSSSLYVL RPKTLKPLEENIR*HLRDMGGRVGRP GIF
130	6310	A	133	1	406	KFRWDFKGP*IASSSSS/IVKDKNKA GGLTCPNFKLYSKAAV/K/TVWPH KDRHTAQQNKTESPERNPCIYDFQSS RDH/YDKDSLFNKRCRDN*ISTCKR MKLDPLYL/P/SSSSSSSSSLYVL RPKTLKPLEENIR
131	6311	A	134	182	434	GTKSCKCDCSSAACLRVLCICVCVS ELVCL*PCVYLWMVCTCMC*/CICVR VSRVCSVRVRLCSLRVKGKGGSPADT KPPFLRQ
132	6312	A	135	23	277	LWVALKNSDQWKSQWAQLLSVQP AGHFAQK*LGVDLH*FMD/SWPIAG LNENSQGLKEQN*KTGDKEVRARGM WTDLYKWADYE
133	6313	A	136	3	200	IFHVECPW/STRKFLLEISEFSEIIGYE VIIQKAVVLYT*NEQW*IKILKITYN KMKYIGANLI

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134	6314	A	137	26	915	EGGPRARRADGRRGPRGHRPGGEPG PGQKGAPKRRRRGRPPARTE/PPHAP HPTPHNPPTTHNPQQKTHPTPTDS SSNPPTTHPTTTTNPQNPPSSSYSPF P/PRHLSGEPFGSPPPVVK/SPAPGINF GGPIKKLLRCKHAEVNLDP.LKRPPSF SSPKNKKFATHERPVFHSYHL* T* TTF TAGWGITSAWKNSWWMRCLEPA/PP PRYSASFPCFWIPPPF* TMKHEAPRSI KDPPSPRGRAQEGEGFGPHFWEGYSL APCYSKCDPEELHPHALGVGETHRHP GPPRPAGA
135	6315	A	138	2	593	FLRRSLNSVAQAGVQWCNLSLQPP PPVFKQFSLCLPSSWDMRAPPQPA NFCIFSRD/MGFTMLARMVSI*PCDL P/ASASQSA/GITDVSH
136	6316	A	139	3	413	FIKNNGILLNNLFSL*HYILNNS/WP LFTLEHLSVVF
137	6317	A	140	102	1318	DEVSLSPRIECGAIMTHCSL.DLPGA QNPLSLSNWDYRCVPLHPKGERFF LFLFETESHSGAWSLCPSPSGFK*FSC LSLPSWDYRHAPTTIKLISVFLVEME FHHVQAGLELLTSGDPPASASQSAR ITGVSTHARWERSFSKKSNSSET
138	6318	A	141	3	298	RQSLNSVAQAGVQW/RKLSS*QRMF PGFKRFST/PSAN*SSWDFRHAPLLG* LFPNF**RQSFAMLA/KLVNSWPSSE PPTSASQSAGITDRREPQCLALH
139	6319	A	142	2	330	AQPRMCNELSQ/LYSKKANHPVRAW TQNMKRDF/SQENPQMANKHKERCS TSLANRETRMRATAPCQHPTTRTRVK *KT/GHSPKCW*GCGKSASP*GCKMA QPL*KTIRQFL
140	6320	A	143	1	421	RGGFGSGI*PPLG*PGK/R/LFFKKPK NCPGGWGGFFPSPGGLAQKMPLPP GGALQKNRIG/PPSPSGEP
141	6321	A	144	12	250	NFLGPRFPFPPPKVGGPPGGT/PSSPV F*TFLLKKGGLLF/CFR/VVLNPGVQPV LWPGPKLLGYKRGAPPPPKIFKGP
142	6322	A	145	2	327	SCPFPKISWLRVIYTLTSLFPFLSSPF/PF SFPLLSPFSFPLSFLSFPSPFSLPFL FLFLC*DRVSLCRPGWSTVAPSWLTA TSN*PSHLSLLSGWDYMRV
143	6323	A	146	1	186	TEWIRSHQPSFCYLQETHLTHNDSHK LMIKVW/RK/VYSANGR*KQAGLAVL MSDET/NKATAV

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144	6324	A	147	73	669	ARPSVELWPRPQCAEGPGARGPVGFINV FRPRFRCSLLTEITKCS/HTGIEPPFPQGF KGS*PTLS/HPPLLVSFVNSKRKLGL FKNLL*GGTVA*L*SQLLRRL**DC LSPGV*WHDLG/SLQPLPRFMPFSC/P ASPSSWDYRCLPPRLANFFVLVETG FTMLVRMGL/LIS*PRDPPVSASQSAG ITGVSHHAWPIRY
145	6325	A	148	2	236	SRTVTKIFKNNKAGGLTRGNS*GVY KDTVMQT/AHKDRHDQWNRTESPE/ PYIYISLLFDNGIKIQRRENSLFEKW H
146	6326	A	149	411	1	LSSSSSSSRYANWI*NHSPNIRHSQET YSQYSIDIKV*/IK*/WKCKSCKH*PK RKTGHTNIR*KLMSINRNKKGHYLLIK GSTHQEY*ANLHVYIPNNRALNY
147	6327	A	150	384	0	PKPPKVGGVFRSSSQARGPSPSP*TI GGFWGPPKFGFPPRPERVLKGGPGPL MGNWVFWGTPGPGVFFGPPVGERSS/ PSSPGKKPPG
148	6328	A	151	49	205	CSCVNSGELRRILAEDETFYQYNAE KTQS*QWLPRGGNSPVKAK
149	6329	A	152	479	0	LMFCFLNTGSCSVAQAGVQCYNHSS LKTQT/PGSTDLPASAS*VTGTTGMH HHAPLFFCFL
150	6330	A	153	392	2	SSSSSSSSSLNIQKLVMLFYTNSK*LE NEDFQISFKIA*KLKYLEIKLKGVKP VHCK/PLLKEIKHD/NK*RDILCS*VG
151	6331	A	154	3	259	KDCAQFLLSLFIHLI*PGCGWWRV/PS LPFLMKILPVETDKKPGQKQLQTRAD YLLKLLKKGLEKKGAVTGGEESTLP AGCFSGA
152	6332	A	155	170	490	MENNNETDLYLQRMKCECFVKRER NTKTVHWRKIDNLFNKWCWKSIST CKKMKLNHYLTSYAKNSKWTININ LGTKTIKLEIQNIYNLGLGNGFVYVT PKA*AT
153	6333	A	156	201	358	LMFIAA/LFIITKS*RQPCSSMGEWIN KLWYIYTIAYTSVMKRNTEVCDSR
154	6334	A	157	205	421	KRDPPFAPRPEGQ/WPQFGSTE/PPPPG FTHFSGLTQGSWTYGPWPPGVNFL EF*EKPFGTGTQEGILTRA
155	6335	A	158	561	0	SSSSSSSLKLDRLYVNTQRRKKNEA NLQDLE/DHRANLRVIGLKEEVERIGE RVETSLR**QNFPNPEKGINIQVQEGP RTPRRFTNTKITSRHLIVKLKPKVEDKE RILTAAREKEQITYEGAPIHLAADISV ETLQATREW

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
156	6336	A	159	175	410	IMRTVCLVVFVSYLLMPQGAALITLSLSPILVICIFFLF*KDNKTYKPLASLT/K*ERKRKKMQITISIGNEREVINAAP*/VH*KVREYYKTHCAH/KFNNDLKKGQFHESHKLPKIT*EEIINLRPIKSKSTEYVISSSFSSKKENPKPRHF
157	6337	A	161	413	0	PPPFYRIFSSPQEKTIKFTYPPKKPPPRGCSPIPPYFVWGPGGKKFLPPGV*K/PPHSSSSPPLLSPSPFSSSSPPP
158	6338	A	162	1	506	FFFFSREGVSPCCSGWS*TPDLR*STHLGLPKRWYDQV*ASAPRQKCVCVSLKAGSSKAVELEKE*/ANSTWL*SIRGEHHCWAWSQADVFCVLEETESGSVTQAGGQWCDLGLSLHPPPPGFKRFSCLSLSSWWDYRRAPRPFANF*KYF*RWGFTMLVRLVLNSWP
159	6339	A	163	1	256	PARYPHFGGQGRPIPRGGDPPGPPGPPGGTFFPPKPKIPRPGS/PSPPQHPHPPGLGPKKNGLTPEGGPSRRGP*PPPGGKGQTFP
160	6340	A	164	71	417	AFLLT*KKLIKFNLIKIKHFCSPRDTIKKINK/PTE*EKIFAACI*GYVCRIVKELLSNQOPNNPLQK*VKDLNR YFTGRK*IVNQHMKR/CINNISQSSSSSSSSSSSSSSSSSSSPKKWPMPNPAWNRNC
161	6341	A	165	425	17	GPPSPGVSSSSSPRGKE/GPPGAPPQKGGGGFGPKGASSSRGKGNRSPQPPGEGGKRGPAQR/PGENLGF*EKRGGSPGGPGQVGTQ/GPRGDPPP/EGSQGGGNTGRDPRPGDPF
162	6342	A	166	5	385	VLSRPLECSGATSAHCMRLPPGFTPFSCLSLPAWYIFLSFYF*PLHVFFIQSAFS*GSI*LSLVSLSKSPV*QSLPFIWGLCDHLHLIRIIHVIRFNSIILLFVWSVYQLFVSPFPLLLFFWNN
163	6343	A	167	2	328	WNKYRIDQWN*IKSPEIDPIYSQILDMCVPREKE*FFLTNDIGTTACKTMLKDPFLTLAGAKINTKLT/DLNMYS*KT*V*IFVTLGLGNRLMDTLKASATKEKT
164	6344	A	168	553	1245	DQEP TSSGHTMLHFGAPLPCVNCTLA WVAERETLSLHLPCQAHGRRLKSI**TNGLFSDSPKAGGQRESS/PFRAPDGRW*WREEAIRPPGPKHAPVRPLLRPS*RRRNCESAYVSPRPDPTI/SRDPRNWPRLPGPKPG/PAPHEADPGARPWPRVGR/PLAGPASNPQVTPPELEPHPIPSNPSPFPTPGPLAPS/RPKPS*VSAPEPSDRPPSPGRVGRP
165	6345	A	169	1	321	LVQKHFIKSNIHPTTKLTSLIGI/QG*NFLILLKTTTHIKPTLSIIFND*KQKAFPLRLGTRYGCLSSSSSFSPTLEILAGATGQEKEMYTTDQKEDI*LSLFADHITI

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
166	6346	A	170	1	383	LFLVETGFHCVGQVLVSNS*PHDLPAS ASQSAGIIGVSHHARLPCFFK/MHPPIPS QSLKMAPSIHGDPGIFGASPRLPAPGC PFPSPAGRSRCLSL/SSSPSLGSLPAGSA
167	6347	A	171	39	358	DPWPLFTPTFNINPKWIPDLNLKAKTI KFLQKIKKGVYLSNGVAGGFFQASP RKQ*P*KDKIYKLGFLSSPPCCKKAN KKINRHATNWEKLF*KDVSDDKDLVS RI*KDLVSR
168	6348	A	172	36	298	QISNKDGRGKESQPSIFMNTDTKNP SSSSSSPQKYIF*IHCKKLRFPNMQ GSFNV*KSISATHHINKLFFCTTAYES TILK
169	6349	A	173	2	366	CFNLI*RNCELFEQLGEYKFNALLV RYTKKVPQVSTPTLVEVLRLNGKVGSKCWKHPEAKRMPCAEDYLSAVLNQICGLHEKTPVSDRVTKCCTEYLVNRRP CFSGLEVYETYLSQEGNV
170	6350	A	174	3	325	LRRSL/DSVAQAGVQWRDLSSLQLPP PGFMSFSCLSLPSSWDYRRLPRLAN FLVY**RRGFTILARMVSI*PRDPPAS ASQRAGITGVSHRTRPKRYFSNPPTLIN
171	6351	A	175	79	380	PFLKRGPPFGPOLFGQFPNLN*WNPV PGFKEVFVWLNPLNKWEKGGAPNPS NF/CFLSKKGVSPCGPG/WAQT
172	6352	A	176	440	0	STIYGFGHHQCLWCS*HRC*S*HCSL KQSYPSLLAYMVSIIQ*DGWVTGLLI FNLIR*COICSDCCSKIYSHKPSMRV LITPHSHQSLKLSQFNMCKLCVKWRL MVVLFCLSLFPNRLGH/CFS
173	6353	A	177	3	247	EHFRIDHMLCHKTSLN*F/ORMEL/PM FSDHNGMKLDINNRRKFG/RIQNM/W KIKLHTLKSPMIQRESHRKIGYSEIK AKYII
174	6354	A	178	214	487	KSEIMSLKKN*KKIYHN*/GFIAGM RGWFNTQKSINTIHSNNEGKCNFMIS IDADKACDKVKFFP*TLYQLGKEGK SSIMKARYEHSTA
175	6355	A	179	2	292	ALNPPIKRFWAGAGPGGFSPLSPPLWG PKPGG/PPGAPSLNPPGPC*ASSPPKS FKFLSSPGG/PGPLFPPIRIKENFPSP RGLGPP*LKWAPPFF
176	6356	A	180	3	391	ATRTDGKVFQFLNAKCESAFLSKRNP RQINWTVLYRTKHKKQSGSEIEQKRT RRAVKFQRAITGASLADIMAKRNQK PEA*KRAQREQSLSGAC*REGKKRL RKALLKRIAIGLLAKPTKGQHSQK
177	6357	A	181	27	365	VLQNLKPLQTPDLKPKCLIFFYNAT* PQYKLSGSK*PENGTFNFIQLDLDTSCHKMGK*SEMPDVQAFFYTL/DPSL VSGPSATHPKS/SLSLPPVSPVPT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US91/09,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
178	6358	A	182	103	330	CLFN/KWC*TTN*KRIKLDPLCAQYTR INTKWIRHLNR*/I*THKESMDKFLCN LDIGKGLAMTLKLETIKEKIDTI
179	6359	A	183	I	295	RARVQKAQHNIENSNPAYISIKRIIHC DQ*/GFLGIGQWFKI*KSVRII*SIST/L KENHMIISLDGE*VFDKLQYTFMIIFT GQAAWWLMPGSPITLGG
180	6360	A	184	17	241	KGIEWEKIFANHVSDKWFIQICKELL QFNNNKKPKILKWAKELSRHFSKENI *IANKHMKRCST*LIREMQI
181	6361	A	185	2	399	VKNLY/WGKDSLSFKWIWEI/WISICR *VKLDPYFL*HSSSSSSSSSSSYRT MKILKEKIGELQDSGVGKHFLSNTL QAQAAKAKVKNWD*VKI/FCKAKTII LKIKSSSS
182	6362	A	186	17	245	GG*GCSCSEL*SCHCSPAUVTSKTLT QCKNPOF*QVV*NI*IPCLLLDSEFGL FLPKSYCYQCKVTLQCSKSL
183	6363	A	187	2	356	EINKIEGRGTIEKMNKIKSWFFKKN/K IDKPLARLTCK/HKTQITNVRNEWDI STDLIETSSSSSSSSSSSSSSSSSSSS RTQLT*EEIE/QLTHQNR*QKVESVIK NLPTKKISRP
184	6364	A	188	4	353	EDTPQMTTPIYGETIFNKGANAVQWG VFSQWC*ENWTSCKGMKLDHAHSS/ PSSSSSSSSSSSSSSSSSSSSPERE KLHNIRFGSDFLDVTPTQATKEKNI KQDFRKILKLC
185	6365	A	189	68	341	TGKGKISLGPKEITPDN*KLQLLPPRPQ TPASPPRPSFNGPRPP/GSIRTN*QTPS GARSVGHDSPEKRAPSPHEHAPTA GPPLAHAPRC
186	6366	A	190	1	254	LRSRRLSPRLAQHDENPRPPT*KKKK LAGCGGTGCPVSPQSWEMRQENHLN PGGSGCSEPK/SHCTQAWVAERDSH LKKKGKDS
187	6367	A	191	123	400	VSET*FC*CWSDQPRIAKDVICFHA EDFTDVVQSLQLDLHEPPV
188	6368	A	192	2	380	KEHNSMKVIYDKPTATGKELNTFSL RTRTRQGCPLSLFLFSRVRKIVLTRTIR QEKKKGIQIGKENVILSFADGILYIE KPKDS/SQNLLELVKEFNKVG*KVIN KQKLVGVDMMAHACNFTLKG
189	6369	A	193	358	0	HSSLSGKELEFVAKS/LLKKTSPGSFT HKF*QTFKEITPILHNLQIKTKEERTL PSSFCEANITLISQSD/KDNKITNQRP S
190	6370	A	194	I	301	ENYRPSFMNTDAKILNKILANQIQCC SKRITHRDQVGLPGMQGQFYI*KS NPFMRVHHISRLKKR/NHMPISI*GQK SI*YPMIYEKKQKIGLPGN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion
191	6371	A	195	160	387	EGGRKKRYQM SKLKW/DRI/DLLSKY VYFQETESIINNLPK* KAPGPDGFTVE FYQMFT*HIS VICNL* KTEVEGI
192	6372	A	196	2	260	PPGPRGESPPARYILGP*PPP/RFFPVGP EGFYFPFPPGISSRPFKRVGFRPTGP GPSPPFFPKKSLLSGAGGPPWGTGM ELCFQ
193	6373	A	197	115	294	EFLNYDCMVLFCF/CFSEMESHVAE AGVQWRNLDSQPQLPPGVK*FSCLSL PSR*D YRIIT
194	6374	A	198	235	399	FYLLIEMESYSITQGTGMQWHHPGSL QPLP/P*FKQFSCLSLKNWDYRRVPP VPK
195	6375	A	199	3	355	DKTHFKIKATKRD/EGHYMMTKRLIQ QENITIVNIYTNTAPRYIKQLLDLK GEIDYNSSSSSSSSSSSSSSSSSSP ETSDLNCTIDQII*T*DIYRIFHPAAEY AFFFIH
196	6376	A	200	3	343	MGCCFSLILFFDQK*IFMKSNLFF FSFIAHSSFFDRLVHCHPG*SAVANSR LTAAPASQVQA/SFSCLTLPSSWDYSH APAHLANFYFVNREGVFPMPWARLVSN SWPQVIRP
197	6377	A	201	3	211	ETPSLLK*KLGHDRHL*S*QLLER LRQENCLGTGLGGRGC/SEQRS/RHCTP AWA/TE*DYVSKKNKQT
198	6378	A	202	36	441	LMPKQSLYLTLAYFLCKTYHSLGDR ARLHLKIIIIASNFNTSFSVMDKSSS/H EINKQTTELNTMTNMPDLIRIYKT/LL PNNRRIEFFPSVHRIFRLYNHKE/GIN KLKKM*IVLSIFSPHNGMKLEINNLRK QEN
199	6379	A	203	3	341	KYLGINQGEI/REISVYIGNCKTLMK EI*KAINKWKDIPCS*T*RIIVKMSL/ PTLHKAIYRFTAIPKIPMTYF*EIENT VSKVMQNHKRP*IAKAASSSSSS
200	6380	A	204	3	349	HFSPCIKLKSKWK/DLYISPE*TMNLL ENIGEMI*DICLGKDILGKISKAAQAT LDKWEYLK*NH*SSSSSSSSSSSSSS SSSSTAKGLISRLYKENSIAQQRI NFEMGKR
201	6381	A	205	2	299	TNNPIEK*TKDLNKY*DTQMGNKHK KGCKCTL*VMKEM*IKIRYQYIHRV/V KIQNTNTTKCW/*GCGAKGLIHC*W ECKMVQ*L*NSA*PFLKKMKHITL
202	6382	A	206	2	340	RGRASHQGNIPWEKESEWQALSPRSF H*WDVSYSR/GHNC/MCWVQ*RKSTP LPQQSGS/LIHLGLGKGVLPVHL HTQLGAFSQRELQC*DAHIDGLPGTI* GDCTPTGGAL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
203	6383	A	207	32	649	TDILKNYKTLLEIKDLNWKWD/PCS *IGRLNIVKMAIPKFIHRLNTPIKILL AIIAEIDKLLVKFMWKFQGITGKNV GKIE*PYTARGFKAYYKAVVIKTAQ YKNWHKERYSRM/WNKMGEFQK*TP SIYHQVIFKEGRTIQWGKE*SPFNEW CWEKIDCMQKNEAGHLGHTRHKKR LGTYFTPTCKVKVSRWFKGLVLRKK
204	6384	A	208	3	393	VFPFAPSPFGSGPPGKPSRGYSPFSE KPPRPFGGHGGERTPNLFGGPGQG GSWKGPKG*GGPFVSXSPLTNK*P PGGAK*AKKGPKGASSSESWGEEGI GSEK
205	6385	A	209	1	391	LEVLVRAIKQEKETKGT*IGKEEIQLN LFTDNILLYVKKNTTEERNPLKIYLMN EFSNVAGYMMVNIQKSIIVILYICNTQSK NKIKKNI*FIIIVSKRIKPL
206	6386	A	210	30	536	VQWCDLGSLLQPLPGFKRLSCLSLPN RWDYRCPPPCANP*FLVETGFHHIG QAGLKLLT/S/GDPPTSASQSAWUTGL SPRARP
207	6387	A	211	23	307	KGFMTVKVFPYL*TKGP*GVFLKPS NPQLVGIYHPLVLPQ/VPGLPGGT KFPFGAKDKGAGPFGPAIKGLTGP GFLTGLKNWDVPRVKGF
208	6388	A	212	396	131	SRIKAN*IHQY/KMISYCDQVGF MQG*VNIQKLIHVHILNRLMKSHVN FSL*V*KA
209	6389	A	213	1	402	ENETKKIPLTIASKIQLYRLIKLAKEM *NVVSENYKTLKGKIKYLLKKWKHV LCSWVERLNIWMTAVPSNWCRLNVIT VKIPAGCSVEIDMGILK/FI*KCKSPRI VKKVLSSSSSSSSS
210	6390	A	214	28	384	KIPPPGGGSPSLFSPFPG/KP*KIPPPGG GGPSLSPFPGGPGGV/PQGPVF*SSS STPGKPRFFLTSKNFPGVGFG/PLFPPS PGGLARKMGKPSSSLFPNFQIFSPSSS PGGSSSPFSSSSPKVP
211	6391	A	215	1	384	QYHKHDSKRKI*YIGFIGI*NFSS*DTI NKLKKQGTDWENIIAKHIFDGPISII *KELSKLNSKTYELLVLFFKWTAKL NRYFTKR*MTNKHMKNASLURKMH INTTI
212	6392	A	216	159	616	QVAWSLFLVWVFFSRQSLTLLPQAG VQ*RDILGSLQPLPRFRVFCLSLSS RDYRR/GDHARLIFVFLQNFMTLARL SLTSGDPSASASQSAEITGVSHRTRPL SCF*SCVWVMLKSYFL*AIAPCR VGLQFQP
213	6393	A	217	148	431	KIIEIDRLLEKFIWKCTDLRYPEFVLK MKNKAGTFTLSNFKSYKSSRMKGL WSYHNKHIQWRSR*PSNRPTLYGQ LFFSQMMLKQLDIGM

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
214	6394	A	218	1	177	KPPFTLFTVGGIGFSKPGSFPGRGEG LHPGPWLGIIIPAPTKG/REGAKNPGP PPG/IKPPSSSDRLPPHVEKSPAPVPG AKGSPG*PPFTLFTVGGIGFSKPGSFP GPRGEG.LHPGPWLGIIIPAPTKGGRG QKTRAPPLGKTP
215	6395	A	219	3	359	SLNTNI.TPFTKIKSNRV/RDLNMKHK TIK/SLEDNLEGNLDDDELKGIFLDITPN KTSTRRTDKLDLSQIKHF*PMKDTG KRIKK*FKD*EK/FAKCISDNLVFKY SKKH*PFINKGTNDP
216	6396	A	220	298	586	TNTAILPKLIYIRVNAVLIKISA/TFFAE FHRLLKCMWWSKGTGKTKIIFYQK/D RKMLKESEVT*WDFKTYKAIKIQ* YLYKCRRAEQWNGTESR
217	6397	A	221	58	383	IRKYFELDKNDDTTYQNL.CNPGKAIL TOKCLALNANIQKEETSQINDLSFYLA/ELERRKLNPN*/RRRKEIIS*VEIKK IEKRRKPRE/QINKIKS*FFIEIHIINKPLA E
218	6398	A	222	54	312	SQAQLQPRISPGSNDPPAPASQCSWN YR/THHHAQL/CFGFCRNGVWLCCPG WS*APELKQVACL.SLPKCWDYRHEP PHLAILIFI
219	6399	A	223	3	319	TMPIKIPAGYFVDLD/OCLKFI/WKGK GIRLIKIL**KNKIRGTYS/PNFKISYK AAVIKIV*YW*RRNRHRHQWNRIENPE IDPHKYQQLIFGKDAIWGNVNEKKAF F
220	6400	A	224	158	364	LPCKVLILISNISCKFFFRDYNCDLKIS DNNTFELLNFEFIDRKTPNPNPSCKY ALIQ/R*ILLECGSIGL
221	6401	A	225	69	287	WKKSPSPTKNTQIRVWVAHAPOFP GTWEAEAGELP*TPGGRGCGELRSH HCTPSLGNKSETGPKKKKKDNK
222	6402	A	226	62	312	WACIFLQTDKILKFRWKCKE/PQQIK LRMKRVGKLT/DFNT*YKVMSTK VVYSHRVQWKRNSVPETDLIYYSQLI LDKLIL
223	6403	A	227	60	393	VKDVTYENYKTLKEL/ERRHK*KDIL CS*SGKCNIVKMFILSKMIHRFSAIPV KIPVASSSS/LSRTSSSSLLNFLGNPKG PQKAKQVLSSSS
224	6404	A	228	143	363	GILVFLYMNNE*SENKKIPFTMV/SKK IKY/IINLAK*L*NL.YIENFKA/LLEIK DDLNNWRDIL*SLIGLKIQC
225	6405	A	229	11	344	SVITDWEFPLRLGTROGYLL.LLFLFN IAELET.LGKEIRQD/EIKGI*FGKEEVL FSDDLILYTL/DPKS
226	6406	A	230	2	212	VIDLHKENYKILMKETEGDT/NRKSIP CSWIR/INIKMTMLPKAIYRLH/AIPIKI PMITFT*KEKTILKYVWN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
227	6407	A	231	22	376	KKGPPPPGIFGGKGGFSPFFPKGGKK KGEKKIFPSPFFKASSSPPIFLPPPPKK GGPPFFPPFG*GFSG*IFKTPGGGGFP RENPPPLNPSSSPP
228	6408	A	232	1	715	RQSLT/SVTQAGVQWRDLGSQQPPPP GFKRFSCGLWSSWDCRRAPPRLAN VFLVETGFAMLIQVRLLEFLTSGDPTT SASQNAIGIIVSHCTWQKIFFKKGES SLTTNSETELADA*NSHGTMLQYPR PPREKRDVNVGPRCPEGTGDWDYSR RWFFPGPPC
229	6409	A	233	164	426	LNHGPLQLLQQITFHL/CFVETGSHSV AQAGVQWHSLSQSQPPGLKRSSH LSIPSSWDH/SHMPPYLAN*IFL/RGG VSLCCPAVFN
230	6410	A	234	2	852	FFFLRQS/LRTVAQAGVQWPDLSLQ ALPPRFITPSCGLPLSSWDYRRPQHL ANFFVFFLVEMGFITLLARMVSI*PR DPPASASQSLHCLYFEGTKLSWIFPS LLLFHYNYPKTYIH/WPMFG
231	6411	A	235	1	406	TFIKNVVGGALLNFKT*YKATVIKT VWSWHDGRHT/DSQWYGIESAETN
232	6412	A	236	11	397	SVITDWEFFLLRLGTRQGYLLLLFLFN IALETLGKEIRQD/EIKGI*FGKEEVRL FSDDLILYTLSDPKS
233	6413	A	237	237	439	KQTLNNGGRQVEPLFHTIILPACPPLD ALCYW*QK/RQIDQGNTPHKYSRLI FDKGTKTQWRKNSLFNKWCQNI*IS TGKKMNLDD
234	6414	A	238	2	344	ITPLHSSLGNRVLRLHLKTTTTTTTTKQ LYPSK*NGLDEVHKLFLERQKLPLKTQ *E/VTDLNLRPVTREDTEIVVELPAK KQKPNAGFTAIFYQTFKEI*FLTKSF WRILSHSF
235	6415	A	239	173	691	DTGENLYLFFLLLRHSL/HSVTQAGV QWQDHSPLQPGTALKQSSCLSFPSI WNYRHAPHTS*FFKFFVEM/GFHML QRELLSRGPPTLASQSSRTGMSHDI QPALRVSEGMQLPRALAHVHPKVELI SL*LLPLPESVTEMDMHGSWQDTHII RELWSKGHYYSRTKGPK
236	6416	A	240	2	244	WRDFKTKTVIRAK*GYLIITG*NHQE DTTVINMYAPKTA PKYMKQKLT WKRAV/DSKTTAGDLNILLIMDKTK QKINRV
237	6417	A	241	101	410	ILGDYKITWS*TPDLK*STVILGLPKV WDYRRKATVPHLLFFLSLFFFLKREH LTLLSKAGVQWCDHSSL*P*TIGFK/H IPP*SP*YLLLTGTHHCTGVF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,319,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
238	6418	A	242	1	340	ETGAYSVTQAGVQWRNLGSLQPQLP GLK*SSHAPATRVTDHRYKP/RMPS YFL*R*GFTMPRLVNSNG/PSDPSTSA SQSG*IIDMSHRAWPSFPFHQHSILFILF VYLLKATI
239	6419	A	243	2	300	FVKQFHSVAQAGVQWHNLSLEPPPP GFKQFLCLNLLSSWDVYRHTPPLANF CIL/M*TRGFAMLARLVNSRQVTHP PSASQCAGITGASHHTQKEIKI
240	6420	A	244	161	383	SCIYNQPIEFKKCAKNTOVGKKCLFHK *C*ENQILTCCR/MKLDSPITPYIKITS K\KDLNVRPQTVKLLVHIEGKL
241	6421	A	245	1	183	NWMSVWGKLNSSPYVVPNTRIITLNR SDLNIDKKTIRLNLNENIGKNYDGSV G*DFLOQKY
242	6422	A	246	116	362	INQKLVELQAEIDRSTIAKHFNVFLSI FEKMCQRQNY*KYRRLD*HS*/LNWTS VYRIMHSAIAKYTFSSSTYGTIWLGF VS
243	6423	A	247	1	368	IKKHLSGRAQWLTPVVPKHWDVRYE PLCLVNVPFILKIFL/RQGLTMLPRLI LNSWA/QVILLRWPPK
244	6424	A	248	104	351	QLKVKG*KNFHANNNQKKAGVPI*V SYNIEFKLTVTRDKEGGHYILMKQS IHQDITIINKPNNSVPKHMKKQLTDLK GEID
245	6425	A	249	60	345	ETKSRFPVQAGGQWAINFT*RHPPPP G*RGLSGLTLRRSGNLGGPPAPANF/ EF*EKGGFPLVAQGLK/LLEGDLPP WPSQRTGITGGSHRSQPEI
246	6426	A	250	110	403	DPPSSRGNNGGPEGNKKEGNGPLGGP WGPFRQKKRVF/VPGGSSSPQILKTG KKLKKNFSSSSSRKGS*SLKKGWG SFPPGGCPRFPNRTPLKK
247	6427	A	251	25	278	NIATYAICCKLTSTKTQWDRIVFNK LCLDN*ISACKRVKLDPYGPHTKIKG DAWDLHLRAEIKLLEENIGNVNLHSFG NSF
248	6428	A	252	3	252	ASEBIKENEKFLETHDNGNTTY*NL*D IGKAVLIGRFIALN/ALHQQQKT/LQIN NLTMLHKELEREQBTKSKNNRRKEII KFN
249	6429	A	253	1	136	TYYLSTIFKSV*YYHKNNRYREQWNR KENTENGIYDQLIFDKHAK
250	6430	A	254	228	378	VHHLIFMFVETMPNFYFCRD/KSFAR LPMVLNLSWAQALLP*PPKVLGLQ
251	6431	A	255	3	214	LIISLMSGSVKFL*ILANQIQ*HNRRN VHQPYPQCIPGMQRYFISWK*LVNRR LKBBNNMVISIDCGRLE

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252	6432	A	256	3	329	VLVHC/KLPLWFKRFLCLSLSGSWD YRHVHHA*LIFILV*IRFYHVGQQA IVDLLTSSDPPTLA/FPKCWD*DH/DGL SHPLLA*NLIGISKSTFAPILYFYKKS EKNY
253	6433	A	257	116	381	INQKLVELQAEIDRSTIAKHFNVFLSI FEKMC RPNY*KYRRLD*HS*/LNWTS VYRIMHSAIAKYTFSSSTYGTPS
254	6434	A	258	2	282	FFFLRWSEFALVAQAGVQWQGLGSL QSLPPRFKQFSYLSLSSWDYRRP/PT MLG*FFIF*WRRGFTMLAGLDWNS*P Q/CDLPTSASQSGAGIV
255	6435	A	259	2	262	SAGTQIPQ*WE/CRIVLP/FWKTVWPF* IPMPYPATPFLGV*PRN*COFPKAYI GVIAMLFIVVKS WKPFPCSSNCAFQT QQQFS
256	6436	A	260	2	382	KAEDGSQTPQODLLNLFKVFNNRD EQNKLDKAQRDRAKYQLPAVAICQS SHSTQGHKRPDSSKPPGCFKCGKEG HWTGACPHP*VPKSPCLVCQ/QDGH WKSDCP
257	6437	A	261	1	354	ETGSHSVTQAGVQWCDHS*LQPLP GRRKS/PALAPQVAGTTGACHHAQLI F/Y/LVETGSH
258	6438	A	262	264	616	VVGDYKYVVGHLPSPSRDFS*AR RGSSSMGLQKDRAGHSLGG*GQL GDFKLKPVLLYHSQKPLGTLRNYAK IILCLCFYKWNKA*MTA/HLFMA/YF IEYFEATVETSCSOKK
259	6439	A	263	2	302	SLCHGVYYL*CD*MFSKILQSID/SSYS N*FL/DSHFCLW*PLELQCQFIMP/HL CLLFVYKHARTTTHTHTHNYLPTH TLIHQVTVVLEGACFLAVTSF
260	6440	A	264	101	470	QHLPHCVVKKMKLARCPTPSSHSVI QAGVQWCNVGLLQPLTSR/YK*/FSH LSLRNSWDY
261	6441	A	265	26	383	ID*CEKGDQICFYDTLNKQGV*GNY LSHIAIFSS/PSPYRELHKGKLLKAF LKKTICLFS/PNILEALGRSIWQ/DK/ EIKNIQIGREVKLFFANNILYAKNP *DSSSS
262	6442	A	266	3	405	HPLFFGKFLKKFWPGPGPPVYPYP LGGSSSSFPQPPF*PLGPMGKPPFF* KNKN*LGP/GGGPFFPLWKGKVKKS LWPPGQRF*P*IPFPSSSSWGSSSPF LSSSSPR
263	6443	A	267	14	268	KKGQNVVGPDKSLPPFP*RPGRLL VPPPG*PLGHGLWAQGPPLNPWG VILPPFLGPPVPFPSKRGA*RPFGV VPPPAQ

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264	6444	A	268	125	547	MCMFSSQSIIEAHTLTPPSLKCLSLVL AGDMLPSKSHLSFAGVQWCDHSSL QPQTGPKQ*SSCLSLGGGWD/YRCM PTTPG/QFVKFFVEMGSYYVVQAG*G LLGSSDPPALASQSA GIUGVSHLAQPK PFIRNKVSSQNL
265	6445	A	269	83	557	DKWWDKWDISKSSCTAKETINRVK ROPTQWEKIFANYTPDKRLISKINKEL KQLNSKKTNNPKKWAIDL NKHFSK EDIQMANRHMKKI*STLLTIKEMLIKT TUKYYLIPFRMAIEKI*NKCWRCRE KRIVVHCWWRCQLVHPLWKTV*KVF KKK
266	6446	A	270	390	4	SSSSSSSSMILLDIKIFYRATITKTVWD *LKETYSPKEQNREPTNKNMQIYQG LIFRDAKNAQ*GRNVFCNK*CWKN* VFT*KKMKLDPYLLP
267	6447	A	271	1	396	PTRTTLICRFLTIPV*IPPAFLAKTDKL ILQFI*QCKGPRIAKTILIKKVVEGLTL/ PVMKTVWYVQIYKYLCL*DRIESPEI NLDIYGQL/IFDKDAKKIQWRKNDNF NT*YWDKGIDTHTRMKLNPLYL
268	6448	A	272	37	452	EIESVAKN/LIHPKTOGPEFFLGEFVLT FKE*ITPILYKP*KRKDKREMHLSKFH EARILQK*RSVYVSNTNEKYMPIS*T EI*RL*TINKPNSSM*KNTDY*PAFIPGI *EY*KVSTVYYINK*RENNLSVDTE NT
269	6449	A	273	3	116	IFFVLRLVYEELKLNLMGEGICSL/IE LLVQLAR*ICL
270	6450	A	274	2	341	MVSLKTASLKIOSQRQKNEAHLQD LLTENSCLKRANL RVTKLEEVE*KR AESLFK*ITENFPNLEKDINIQV*ESY RT/PSQFNPKSTTSRHLIPKLPKVN DKERILKAAR
271	6451	A	275	2	409	QKNYVR*TVTHKKAGVAVLISDKVD FKTKNGTRDKVGHFIMIKG/SIP*EDT MINRYVPNRALKYIKQKLTREL VREM HN*T/TITTIIVGDLASPLSIMFKSSVSM LIFCLAVLSIETEDLNISQI.DLK TDA WVTE
272	6452	A	276	7	342	GCSELRSCHYTPAWMTVLCLRKKK KEIILIYTGKSYECKEYGNFTSFQRY/ KRLTGKKSDDLRYSSSIQSHKRTHTG EKL*KCTEYGETLIALHLHLSK/HVSVH TGRWMV
273	6453	A	277	52	389	GKKKGKGPQKGARGPLFWGGPPSS PPNPLKPTQPGEGPLKGP1PPKNSKP RENFSKDS1PSS/1SRGPPSSPPPGGL KEGPPRKGP1PPRFPSPKKG*KGPPQ KFSSPP

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274	6454	A	278	82	392	KGGFTLGRPRPEGRLNPGNGNPAPP *GNPSPPPQITRNKGPA/RPGGGSSSS SSSSSSPPGGGGV/QNPGPKGTPSPGP PKGGG*K/GKPP/EA/GPTSSQ
275	6455	A	279	476	910	VSVLPLNKAPLRLSAT*DTGGKLRMS KTLSPGNWSFHWPCRRKTHHSNSV MIVSWKLYLGGTSTV*GILLVNMKDC GVLEEGFLSSQIFFYEMLMVTNRRG NKILREVDRTRLEVKQNRKIQSQ/LQIP MHSPNSPLSNVLFQ
276	6456	A	280	1	302	LPGSPNPLWSGPSSPLVFFPQAPRTNP LGPPGGLGPPNPFPFPFPFPFGGKGP PP/NKGFFLLKPPQIPNLPFFQNKIF*PP SPPKGGGPPTPTQTPGGPP
277	6457	A	281	16	313	ALGPGIPGFGQRPQPPAPSGLGAKAR ACPOK Y*PKF*NPSSPPQVRKSPSP/P SSSGGVKPPGSKKGIIISPLSPFGGGRPF LPNRGFRQREKKGFIFSKK
278	6458	A	282	3	514	INSLVIHLKELENO*QTKPKISRRKSIV NIRTK/IKIET/QKTIQRI/NETKSACFKA SSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS S/SSSSSSSSSSSSSSSSSSSSSSSSSS S/SSSSSSSSSSSSSSSSSSSSSSSSSS VISLPTKRSPPVDDFIAEPYQTYREK
279	6459	A	283	3	514	INSLVIHLKELENO*QTKPKISRRKSIV NIRTK/IKIET/QKTIQRI/NETKSACFKA SSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS S/SSSSSSSSSSSSSSSSSSSSSSSSSS S/SSSSSSSSSSSSSSSSSSSSSSSSSS VISLPTKRSPPVDDFIAEPYQTYREK
280	6460	A	284	2	405	GRVGSKILTPTSRTQSKINHKEEKPKI NRKEGILKIRAEIN*VETKISETKSW/F FKNFSKIGRPLAKLTEKVQVTNYRN KTEAITTDSPIKEVIRECEC*LYPHKC DN/FR*LJDQFIQKHLLHPASMKKLI
281	6461	A	285	1	288	ILCCPGSTGDWRKNEQFSQHHSWN FLSICKK*/K/VDTYFKLYTKNYSRLH/ DLNGSKHLQFLENRNIHPLKDVVM T*KD**ALTPIK*TPVLVYDT
282	6462	A	286	326	418	RGRGRISVGIGSANVLLTVNGS*TLLV DKTLYYTIASRYDHSNEDVDVYL*AL AR/LNYLLTVNGSEHTVGCFFI
283	6463	A	287	235	327	RGRGRISVGIGSANVLLTVNGS*TLLV DKTLYYTIASRYDHSNEDVDVYL*AL AR/LNYLLTVNGSEHTVGCFFI
284	6464	A	288	2	310	SGAILAHCNLC/LPGFKR/FLPLSSN WDYRHTPPRPANYFVF*VETGTHHIG QVGLLETLASGDPPASAPKCDWDY REPATVPGLFYCLKNKYRLLLSKNC

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285	6465	A	289	72	281	NPLKVPVNVGFGKDFLDMTPKAQLT KVKTDKLAYFKTKNFYTSKNTINKV KK*P*E*EKIFANHSDRG
286	6466	A	290	78	580	EEVKKMNVLKNVREKLVEKNFFVCF FETRSPSGDSQAGVQVWHDLGSLQPPP PGLK*SSSLSPSSWDYQHVPVPHRT/ NFFYFL*GRGLTILHRLVSN*AQ/CNP PTASQSGAGITGVSHHV*LKT*F/CMT FCFVLFCEFETESCSVAQAGVQWRDLG SLQLLPPGFKQF
287	6467	A	291	3	273	CLISKQC*GN*ISM*RRK*ELYLTSY* KLNSRLIKDLVRAKTTITGLEENIGVN FHDLELGNVFFKI*PKSTKKNRNNNN LDIILKML
288	6468	A	292	2	167	DLTPKV*SRKGKIGKGLDFIRTKTFSWA KDHVKRLKRQTDDWEKIFLNHISNK/ GLLS
289	6469	A	293	3	251	PPLEGQVGVPPRSGGPGPPGP/GEPP FPPKFKI*PGRGFQAVIPSPGAGP/GIP FTPGN*GSSNPILPGLAPAGPKRISPP
290	6470	A	294	1	357	KEVVIPTVSPCNLPVWPVQELDEFWR EAVGYH*VNQVETLAIAGSDITLLE QIITLETWYAATDSAKAFPIPKDH QKEFAVTW*C*QYTFATLPQ/V*LYSV LHDDMVCRNTER
291	6471	A	295	206	420	GFGKPPPLKPGV*GIPPPGPKPGGMA GKTPSPSS/PSSKKGFPLFPAPGRPGPN PGKKNPQLPGPRGVSPPN
292	6472	A	296	133	305	IRKSLKKILAS*IQQHIKMISHHDQAD YS*G/VQGWFDIHI*RKVIHLIITKNKS HM
293	6473	A	297	404	700	EGETWSCNTGG*ECDFGASLLGAEF* LSHLLTV**P*AGVQVWHDLGSSQPLL GFKRFSCLSLSTWDYRHSPPCPADF CIFNRDGT/HVQQAGLELLT
294	6474	A	298	3	914	EFGGPIFLVDPPNNCGGGPPSRGVFC KKGGPP/IGQGFPHNFKTSFLAHGVPP LYFPFGGPTTRGLF*SGNLGPPGPQW KTSSSPKTKQKNVGGVAPAPFSPILL GGDEKFTTSPSSPCGRPILAPLPFGGP PGYPFSSSSRPNVFFPPP*ISLGPPLFF* KSFSP/GSSGKPS/FOKRTSSSLFGPFF GFSFSPSGPPPGAPSKPSFWVGPGLG SPVPPFFRGQKFPF*KFLPPRV/LPLFSP FSVESPPFFFFSPSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS
295	6475	A	299	1	420	SRIPGSTISSNNNLP/PPFKDLNHSK STLSSPGCS*ELDKSEPPSTSSSRET KPCFAPQPKGQGPDL/PNGALGPPG*/ RGFFGLTLPTRTNGSLPPPGVNF*IS RGK/MGSPNRPTRPPQDPG*PGLTPRP GLNPKG

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296	6476	A	300	3	198	PPIFVPCQY*KS/VLGMWAPHVFSPL GAGASCFLVPSLRPLPPFKNPAFSK NPKLFRFPFGGP
297	6477	A	301	1	541	FSFETEFQNVAVQTGVQWQNLSPLOPP SPGFKRFLCLSLSRWDYRHAPPCPA NFCTLVETGFHHVGVQAALELTSSDP PASAS*SAGITGVTHHARPRF
298	6478	A	302	1	451	AVLRGKFLAISASSKKQKNVK*TI*QC ISSSSSSSSSSSSSSSSSSSSSSSSSKL KWKYKYSQ*NEKLAHETKN*FFKKD KIDKPLATKKRNKTQI/QIRNERGDI
299	6479	A	303	178	304	PLFPNLQRVRPGT*PWWF*AGNPAGP RYFRPFGGLASSPPGAGGDPDPGPPG LKKPKNPSSSSSSSPRYSPISRGLOELP LTPGPGIPLA*NSPPVSPPGKGRLPF
300	6480	A	304	3	399	HFNLFGGFNFPPKGGPIWFRANPP* LLTPVPPPG/LLKVSCKPPFGGPPFP FPPGVG PENFFNPGAQGSGLK/PGFL/PP SSSPGGQTKP
301	6481	A	306	2	381	PIAYGSPRRKRGKMAEGLFKMEINT VFSNLRKMDQFHETQRI/NRLNLK KFTLRHHNCONSKILKMERKK*HHI QDKPIKLSISFSAQTLQARRE/WK*YIQ STE*NKQCPRLMHPKLCFKS
302	6482	A	307	2	415	ASILPRAMYRFDAISIKIPKSFLEAETEM LTLKFTLEQ/WGPEKPKPSGSSSVGTL TLPSS/RSSSSSSSSSSSSSKHHRIDQ QHKTEHTKIN*YIYDQLICAKSIQWRN KTLNLKWCWDN*ISTSKRMTLDSYEI VDP
303	6483	A	308	3	285	NTPPNNSISTAFFSSSTHETYAKTDN MVGHFLKTNKFSITQII*GAFSNHNEI KLESNNKKGNKSPNTWKLNTLLN NPKAKDKISRGIQRIQ
304	6484	A	309	29	341	VDQNGTVNQLDLIDYIRTLNNGCGH/ YTF*SSHGRSTKVDHILGQRKRSQYI LKDKVIQWMFQDCNRKLEMMNRKI LRKSQNI*ELNIVLLDNSWIKEDIRK
305	6485	A	310	125	375	ISQIQIKYIGRNLTNQVKCIYKENYE SLIEIEDTSK*KDTACSFSGRSYIVKN /AILHIAIYSFKMPVLFHHRNRNKTEN RHS
306	6486	A	311	1	329	LYEN/YRLISLMNTDAKIHKILANQVQ *CIKRIRHHLGFIPNSSSSSSSSSSSSSS SSSSSSSSSSSSSSSPAYNKTPHPFI KLSSVIGIEVNFLNLIKQVQKQPY
307	6487	A	312	2	228	FFFEIESHSVTQAGVQWCNPGFKRFS CFGLSSSWDYRYAPRPAHF*FLVE TGFFYYVAQAGLKLLSPGDLPALAS

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317	6497	A	322	3	141	CIRNCVSPCCPAFLTPGFKRSTCLCLP KCWDYRRATSPGP*MLILC
318	6498	A	323	2	2493	GSQRDICTPMFIAALFTIAKRFWKHPK CPSTDE*IKBMWYIQSMMEYYSAPKKK EILSNVQ/SWMNLEGIMPSEISQ
319	6499	A	324	249	443	AILPKLIQKLNITPI*IPAGVFTEIDNLI KFTGKYKGPRIAKTFEKE*PSG/GFI LAEFKTSK
320	6500	A	325	167	432	RGENIYDIGFGNDFLNVTPKAQTITTT KNIDKLDPMKI*N/FCASQSSSSSSSS SSSSSSSSSHISNKRLVSRMCKELLQ FNSNNGSAA
321	6501	A	326	2	332	QKICKAPKNILVAGSHFFKTLYSVKN *ESPNNRNTTHLDTAA/VQNFSVLVD FLYSGNLVLTSQN*MTVAYLQTSSEI/Q TC*NFTIDA*IV*RLNISIKSEVPW/S AVVDYNN
322	6502	A	327	1	630	VLRNTNLAQEIIDNLR*/IGKEIN*K KKLSTKKSPGDDFTGEFYQTLKEELI PILHK/LFKKLEEAGTLNPSFYEALMQ KQSKTSQENYRSLFINMSSSS/LSSS/ LSSSSHTNMKMIYVGGVDFIPRMQG WFNI*KSLSIYIYINKVKNENHTIISID TSSSRSSSSSSSSSSSSSSSHFFSL INSIFKK/PTDSIKLNR*RLD
323	6503	A	328	15	268	EKRPKKKEECLQNP*NSLFW/PFLKVI GLKGETEREIGKKVFC*GLITENVPNI EKDFNIQVQGYRTPSRFNQNKITLGY LIIL
324	6504	A	329	192	560	ICVQIFDFWGIYPEVELLDLTI/PVAM AGGNIVLDITSKADSLSSSTQASDVIT NQRSIATTNLRDGGTLLGGLTDY KNTS/QQSGVPFLS*TPFDSGLPSSRS VDSNEESTLYASVQRQ
325	6505	A	330	1	248	AITEYCG*FYANTLNNDDEMDKLLKT HKLSKL/NEEIPRLNKAIPCKEIESIIRK LPTQKSPGPDGTFGEFNLIF*EELTPIL
326	6506	A	331	38	294	YWRRKDFMAQWNTTENPEINPCISY QLILHRGTDKNIPWGKDGVENKWCW ENEIYLCA*RIKLDPCASPYIKLKLKIK NLYVRNY
327	6507	A	332	162	460	AEMDKVILKFIWNYKGLQIAKTILRK KQVEGFIPLNFKYCYCKAAVTETGWC WDKDRYIGQWNRIESPOINF/HT*SQY TENPLFSKCCRDNWMSTCKLGGI
328	6508	A	333	242	434	NSHISELICDKDKTDTH/WGKDSLFN *LCWENW/CLELDCHLSKWIKDLNV RPEALKLLVEDIVE
329	6509	A	334	204	402	SKLPRAKFGPKFFTEKGLPKTYGRGP NPKDSDPFFLEPKIMGGPGAQ/NWK KGKKGPLETF*KKR

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330	6510	A	335	2	249	PRVRGRVGLNVKHKTIKLEKNLYEL GLGKDFLNTTPK*QYIK*QVDFKFIKIK TLCLAKD/T**KYTQVTAWEKIFANPI NNT
331	6511	A	336	2	395	FPAKKSLGSPGIIAEFYQTFKAKPVAT LLKLIASSSSSSSSSSSPRGK/ETLFPNP F*GARGPLFPKAKKNPFKKSS/RPI/S LEKILAKTPPKIPKNFFSPPL*KKFFLG PGGFTPGNRGGPTFGKKTGGKTL
332	6512	A	337	15	396	WKGPPTRPYSINSADPLYPCPASQPL GPGGFP/GSPASSEETAEARPPGQAE APWRPGPARREDPSAGADQGWAHG TPDAPRKRCAPGGVRSCWLLICR*PE ARGQHGPAAATGVPEALGDGLPAVV
333	6513	A	338	2	401	RAFLAKTAQAWLGFQSRGPRLLPPGP AAGSPRCYPV*GIPCPHPPGLEDRSV YPCW*RRQPGIPVSPAQSISVSLFSP/H SELGPVPDPLAS*ESCFPSSP/RPQLPV PRLGP
334	6514	A	339	102	377	RYHKKCSNFQTSLHKWC*NNWSTNC QK*INQIKSNPDLSTFKINSKWIELN VKCKSIKLLLEDNIGENLH/ELGFVNFF F*DKSLKNQNR
335	6515	A	340	211	161	GFLFIHMKSYHWHTEIILLPPFQLG*G QGKCMMLMPL/LFSIVLGVVRAVRQG KEI*GIQVEKEEVKLSLYANDMISYV
336	6516	A	341	3	444	RRQSAIRGGRRAQTRNARSWH*VRG EGGRPRGDRG/SRTKVRTRNSRRDER RSEAGQAP/RGAEGITGKRGKNSGR DGGGRNTPRSSSSSSSSSSSS
337	6517	A	342	25	153	SPELYLH*YQGLIFFHKSAKAIQWQK NSLQKMWVDNWTFCVCK
338	6518	A	343	3	348	KL VYVVDLYLDYVGVVDYQGGNRH TVIQRQLCFALFMVRHLYGITV/FE DYLYATNSDNYNIVRINRCVQVIFVR *LQVHIIG/ALCISPDALPSVSTLACVV DPYGMVSGLDRV
339	6519	A	344	74	403	KRNLAWLWPPNNGGGGGQIGAHGAP NPLG*GNPPPPPPGEGGPPG/PSSSPGE NFLGKGAWRGAPGPKP/AGPQGTG GPNPPKGRGLRGPPSPQGESFLIQGP NPKKLF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
340	6520	A	345	2	1019	EQDLPGLSISCGSQVSPDIFGASATP ASPHPPQGTSKDDDGLWGVRAEVGGRR GRSRGGPGATPGASPATPSPSARAR PGLEPEPAARQPSVAARQSRAAEGAG GAAGRGSAAGPLPPDAALPGAVR AAACGAAGAGDARAEEQPLGLPGA AGRSREPL*CEGRGGTAEKVVPDPL RPGGERVRG*GGRAAGRVRESG*GA PLTSVPAALSGLVNVRPSKRLFRDLVS L/PAGAGGTGSECRAGQGEISPAATGSS PAPNR/SPPGPGPDMITLCDPETLFYES P/PPDPMGRSAPSTSTPAPFRGHLP PDTEAMGSVDPKDPWRASSYFCVKL FVRIK
341	6521	A	346	46	387	KPQLEFILGMQGWPN*KVNLPHYIN KIKEKPPSSSSSSSSSSSSSSSSSSSS RKQEQRRIFYLNLLEYKPTANVQTR Q*CP*PFSILKMLVSAVRQEKERQIN MKGRK
342	6522	A	347	1	363	ECTGPKIAKILEKKNNVGGPL/PNFK I*YKAPVI*FWLKVPIVPSAILMKT *YVYFKDRNQDEWYRLRVWKNISHY GQL/FSKGTKTQW*KSFLNK*CWNN WLFCTCKRMKLD
343	6523	A	348	81	585	RKNGTILKEI*WIF*NLPRKQTLNPEKF SGTFY*TSRKKIPIYLKLFQNEKEEA LYN*S*RQI*KIRKIVKQIQQ*LE/HH YQAEFVPEYQGSLLMEEKDHISKDAG KKVW*TLAAIDNFFKINFRKLGVENF FNLSIGYKKPTTNILLYAEL/LK*FPLR L*TRTG
344	6524	A	349	2	378	PRLCIGAAGVI*RPAPVPSDLGSLCLGV ASGSKGGGGNPAVGTVGIGGFGPCP RIPGAPCEGMVPSALPRPPTYDTLPK RPAP*PALQESGRLFRPGTPRIPGPPTK APWTRFRLPFSLEHESQG
345	6525	A	350	2	357	KWGTAKSPPTLHP/GPPGEAPAPVSV DSEPSCKGGLPRDKPTKRKDVVAPK RGSLEK/ELGPPSPGAPGGARGQWP SLCGP*PPORTACRACSPSPSA*AP AGGDQSCHPGGPKIP
346	6526	A	351	2	361	SILWFQHQKIA*AKR*RKGGREVGR A/ERMKERETKRGGRKCGCGGGGK GREVRKGGKEATQGGGRKDRQPR*L KSLYNVYTPRDSL/VWQFRQLIRRPKL FSKLGPICLIFYPCYTS
347	6527	A	353	3	250	DTYATYNFAFTACKDSVSTT/I/HEIM MYLIYQHRISPNVTSQGEHFMKTV MQ*THNNEIHWPNIVHHSEAAGVIE **KGTL
348	6528	A	354	1	298	ASNFTSFSVMDKSS/HEINKQTTEL NNTMNPMDLIRYK/L/PNNRREFF PSVHRIFFRLYNHKE/GINKLKKM*IV LSFISHNGMKLENNLRKQEN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
349	6529	A	355	18	32	TYRYIDQWNRTES/SRINPHINS*LIFS KSA*TI*WGKADSLFNKWR*NNWISA CTGMSSSS/FSSSSSSSSSSSSSPVRR A IRRKISVILCDRLRGNDLDTTPKHKQ *KDRIHDI
350	6530	A	356	1	351	VSMIVTQPSNFSNRNTGNTGKLLKC EECDKAFKRLTHLVGKIHTGRNSHT CE*YG/KNFNSYTLHRRKAFILHKMA H*SKHKCTAINMGLHLIQH*RVSP**I QYKCNDCPKSA
351	6531	A	357	2	308	YYPTAIDVHQPTAKEWVKARLYKK WSWDS*VHPRGGPYLPYINNSRW IKYLNARPQTVKIPEENLNKNTITLGF RK*FMTKSSKATATKTKIDNWDLI
352	6532	A	358	1	451	PPRKNLPFGKN*PKGGKPGPKGREP GKVSVEFVGGRNPGGFLWKS*P*T LGTFPEKSPGTGIF*NPANPVRVAPVIP KGPEGEKGGPLGPGNPSPPGQNGT PLFS
353	6533	A	359	8	392	SNINRLKVKWGKITYHKNYKH*RVG FYINI/STK*TFKTMIREKDGYSIIIR/ PHLKASKYLRQNLTELKGEID*SSSTV GDFNI/PLSVTDRTYRQKISKDIKYL N NTLSHLGLADVYKTPNNSKWVL
354	6534	A	360	3	325	FCSWFRNKTGVPAPRLYPGGMGLFGI GNWGFEPFPLVLNPLKTSSTSSVKLP VGPGLTQPGSLGPLFLPLGELGKN*I SPGGLGLR*/PFIGPLRCPGPGAGPPP F
355	6535	A	361	2	328	KLNNLLNNS*VNTEIKAEVSSSLEI NEYEDTTYQNLWDAKAVALKGKHV S/QNTFIKKLERFKKVSN*QSNFVPGK TRKEHINLKASGRK*MTIKIGDLFVLY FVLNG
356	6536	A	362	25	159	LCALSLVRDVEDYFRAVLQDERSE RAFK*DGPNVVCSISS/SDVDYDFR AVLQDERSERAFKLTRDAJELNAAN YTVW
357	6537	A	363	1	381	QGHYPGSLQWPVSRGPGASGSPGRGP VIFVFFVEKWVPPGPGGF*LPGSN/G FGPPGPKGWG/CPGLAPAGPPFFL* PLWSSSSSSSSSSSSSRNSVPSSSSSS SSSSSSSSSSSSSSSSS
358	6538	A	364	2	653	LGTPHCRSPAPCRGAGIDLGAAFQLS CPGCGGPGSAWNSTAPHGSPWHPA LFAFAPGHGGAGSERARRGSGALSPGG QRPGRLLGRGVGSGSVPODGVTPGWA LLEGFPHWSSSGRSPAVLRGPDHPAR RP*/ADLEPLPAVASVHKPLPEFPGP LRPPLPALDPGGAVSLFPGQCHVCT CGLTVWPHPVRTQPPLETQGGSRWP QEGEVETDDQA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, ∇ =possible nucleotide insertion)
359	6539	A	365	2	231	LKNKAVITKTA*H*QKNTDQWNRK NPEINHFFYGGQLIFDKDAKNTM/WKR /DSNFNK*CWEN*ILTCKMKQLIPISQ Q
360	6540	A	366	2	371	ENETTNIVVKFLLEIIQYRLPAAKS DNRAFTSPAQSVSKALNIQQLKHC AYQPOSSRQVERMNHLLKNTLKL/T LK/TNSVN*VSLPLALLKLRCSTSYQA NFSPEIMYNKAPILPKL
361	6541	A	367	3	331	TMPIKIPAGYFVLDL/QCLKFI/WGKG GIRLIKIL**KNKIRGTYS/PNFKISYK AAVIKIV*YW*RNRRHRQWNRLENPE IDPHKYGQLIFGKDAIWGNVNEKKAF FWGVG
362	6542	A	368	3	364	NIALDFEHKMATGASSSSLEKSYEVP DGQVITIGNEWE*/VPEALFQPS/MGM ESCGIQETTFNSIMKCDVDICKELYAK MVLSSGTTMYLGIADRMQKEITALAP SSMKIKIIMPPECKYSV
363	6543	A	369	3	358	GFGNPPPGGAGSPPRWGWTPIGSRL GSAPGRGPLWQKEKAGPSGLG*RK GKTSSSSPHLGIHG/ERSPCWRRGLFR PVHRERRGARALVAGFLSPSPDCSS SRSLWATPGAASSLSI
364	6544	A	370	7	372	RTLTKKHTANLIN/GERLNAFPPTLG/ TRORCLLLLLLFNMVLEVLASATR*E NEIKDITQLRKSNGENK*IRHTKKENT QLNPFADKKMIYVENPKVIYQKNS*T NESRIVAGYNVNRNSIV
365	6545	A	371	322	1198	HPTCAGGSTPMDPLTCCRHAVDSPTA HSLDTNPNRWELEWGMRRGSETV GLRRVVPPLASYPGTSSSKILGYSSPP PTPTTHSYLL*GRDPS*MMRKQCTKG GKDREGTCRTHKAHTGPHLNPLPPR STSPQPLCPHIWTPSSSSSSSSSPRGS LAHLSRTWVPPLFGGSFRLLPL/PADL QC/GLGPVQSLWP*DTRENLPPIHRTY *FPGRQGLPTEAVHWQREAGSWQ WQLLCLGRGVAPSPFVWEVGGKNLG LSLPSCHSPCRYCLNTPSLSGCGCHP ARFLRAH
366	6546	A	372	1	126	LPTKKSPGPD*FKEELIPILHKL/F/HKI EDKGTILHNSFYVVTI
367	6547	A	373	3	541	GQEEPEGRKKGGPHGSKPPGTGKVM D*GGRG*QIQAFFPSLLFQPSALPQGPQ PGLCAQNNLCAK/VQEEENWNERLGS YSPRERPKCNPORGKPRQPIQEESPL RAEETRSGPLAQAPPLGLLGVSPA QKYITWWARRPAPMQAPARQGP VALLREASMAQSHFQAT*PGTGQT TS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, G=Phenylalanine, S=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
368	6548	A	374	1	245	GGGGEYSKIIAIKTALKNTIYLGILYIKIDVPDLYTKNYGTMLREIKYLEK*RARPCS*TERFKIVKMSIL/PNLIYRFNTI
369	6549	A	375	208	411	ECQVSTVGLGLCLALSIVHLAHLCSVCVCMCC*AREGLDLFICAGKGVYTCVCMWACICICLCMSLCLV
370	6550	A	376	35	590	GQPCGTDMPDAGKLSPEISEFFPPR/PGRGGLSGSQPSGGTPGRPAPPSPVCKGSGPKL*NPERRRHCGETPLPASRGWPFKVCSCLLPVQPHRRPGPAGPRSDLRLLSAGALAGSPFEHLPAYRSAPGAIVCKVGGQLRAQALPLDFSLGSPAPPPPTIPFTRSSQSQRAGNIHPFLVILPETRPC
371	6551	A	377	1	481	QTLTLLHRLSECSGTISAHCNCLPGSSDSGTTASPVAGSTGKHHHAQLIFFIF/M*RRGRFRHVGGQCLKL/HGPQVIHLP RVPKVIGI
372	6552	A	378	16	427	IRGRVDPEFKRCSCLSLPSSWDYRRAIPCLANFVFLVETGFCPVGQAGLILTSDDPPASA/FPKCWDDRRDHCAQPPLLSALYPVLHTAAGTTLWKKEAVTYSPLIEEL*MLSYVLEKSKIHCLTFQPQGLFFFFCP
373	6553	A	379	163	601	IFCKGGVLPCCPGADLHFATSNMSFYYSRGLSRMTNKTETPMSTIPKGVGVAVWRFGNSECIFQELPLTLHHLSTMLASPIHSHEASANALVGRSLTVGWRSRGVGVSDPAAWLRDLKGCF*DKSHSVTQSGGQWCNLSLQ*APRLKRS CILSLPRSDWHVWPFLANF*IFCKGGVLPFAQGW
374	6554	A	380	90	433	SHPTMPYPLSKIVPTNSKYPETCPFS*SCMDIYETYEIFVALFAIAKL*EQVKCPLTEKGK*MWY*MEYYS/ALKKE TLPAKWTWMLDDFMLEHINQSQDKK*CMIPLVSG
375	6555	A	381	17	371	TQMTFFAETEKFILKFILDSQRTLK*PK*S*SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSQPS/E*/MPHMYCQIIFITKEANSLKGY*QFFNKWS*KNVTS TGKRIKLN
376	6556	A	382	3	402	WHPPSSSERVERMNOTLKSHLTKLVLKTRLSWTKCLPIALLKVRTVPQKEVGLSPCEMLYRLPYSHFTVDIPIFELKV SFSRAMYLVSLPLPSKLKAF*YRCRPLEFFPAHQHPGDDVLIRSWKEGKLRPAW
377	6557	A	384	2	353	VCVFKNNDGKASVFKAIWY/WA*RRS/VKVGWGTIKSPISPHIEG*MMFNKGAKLTQ*CKDSFFNE/WC*ENGISTCKRMKWMGPYLP*YTRSDSK*IKGLASK/PESKLEGNRGKIKHDI

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
378	6558	A	385	2	333	LCWEYFQILIAYLEIHKKSYLSGYKIYVHISVAVLYTNSTQAEQKIPPIAVKIKYLRM*LTKEVKDPYKENVKLTLLKEIIDDKNKRKHPCSWMGRNLIVKMTILPKA
379	6559	A	386	206	541	KNIRIQKPFRCRNP TG*SLKRTWKCKGP*DSQNPNIILKKRNKNGDCTL PQFQNLFLKLQVTTYSNRHNQWNRIESREINHIYIDQLILPREFRKKGWLFNK*CCYN*KYVC
380	6560	A	387	15	624	IVSEWKHYIIEELISEGKVVKLEKTTYMAPIGKTGTWDSVKHTTRKEQTGDVAIVPVLQRTLHYECIVLVKQS*PPMGGYCIEFPA/GELIEDGETPGAAALWEL EETGYKGDAECSPVVMYMDPGLSNCTTHIVTVIINGDDAENVRPKPKPGDGEFVEVISLPKNDLLQGLDALVAEKHLTVDAKVYSHALALKHANVK
381	6561	A	388	3	368	MEKRPNIENRILPVTNRNETGPYQCEIQDRYGGIRSPYPTLNLGLYGPDLPRYPSFTYYHSRENLYLSCFADCNPP*EYSWTINGKFQLS*QKLFIPPAQ*KIN*GLYPMGKTPNMFTGQM
382	6562	A	389	3	210	SCIYNQPIFKKCAKNTQWGGKCLFHK*K*ENQILTCCR/MKLDSP LTPYIKITSK/KDNLNVRPQTVKLLVH
383	6563	A	390	314	613	INGIIQTFFSPSSILDIHALRPHRGQIEVAFRFRSLSDHHPSEIA/ESDHVYGSDLFGYVFCEKNW*HDPCLIPSTSTESH RFCDRVQDAYTLRCCPQV
384	6564	A	391	3	370	TQAGITGFGCIRHLVTRASFNSGKAGIVVISDPFFDLNMYVMFYQDYDTHGKFHGSIAENGKLVKGNPTITFQE*DPTKIKWGD TGADYVVGSSINFTMEKAGTHLEGRAKRVFISVLS
385	6565	A	392	1	474	DLKNRKRGSSTANFYQAEDRI*KLEDGQFENKPEQQNEKIMKRSEELRKS WYSIK/PNIYI/GRPRGEEKEKAVKTLIKKMTQ*FPNLGMEMNIIHEAQTE*IQKGLEQDIIVKMSKIKDNYRIFKPAREK*LITGKGA/PIRLADSSSETMQAKRVR
386	6566	A	393	39	376	SLPASSWRKAGPSGSPGPAQAQAFAGPGKPSQGS PATKWQPPQDSGGQAGRWWQFQAGDPS/AGGRG*WPNPPGCLGKQPGSPQARQLSQA SDRGGH*APGRVRA PGSO
387	6567	A	394	36	206	NVIQSSWIGGLNVKVPILPKVIYRSNAISIKMPVFF*KIQKYIQ*FIWNHQGFQF
388	6568	A	395	3	359	TRAPGANALGPPWL*GPPPI.PWLSSCPRKPE/PGQAPSPSVTEGK*VPIRDPGLSSRISPPHQ*SPPKHPSAPLRSPHMLHRRSAHSRCLINVKCLQKNKHK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YKPFSQLCKNSQN
389	6569	A	396	3	374	KERWL*LRHSVVWSAADGLTGNS/G NLE*GWEPGGKI*KRVMINSYQGTQ SVRVFVSHVNDACILSAEALNNQV DKMS/R/SISSATVSLAQANEQSSYP SVR/GSRNEGHAWAQSHRLPPVK
390	6570	A	397	15	370	SRIETSQLDRKST*KTKNWFFERINKI DQ*TSQENRRREKRKDIRVR/NEREDS TICLTIDIKKNRKCHE*LYANEFNSFTL NDRFLGKYKLSMLIQEIN*VKSLST KEIEFVKKIL
391	6571	A	398	6	238	WDVYSR/GHNC/MCWVQ*RKSTPLP QQSGSISDHKGAKWGGPFTGTPLHT QLGLLPEECSDAHIDGLPGTI*GDCI P
392	6572	A	399	2	381	LVGLSIRVNHLDAPQIFRQRFQGY QDSPGPREAVSQRL*LCRLWLRPETP TNEQILELVLEQFVAILPELHTWVR DHPHENGEEAVTVLEDLSELDDPGQ PGSLR*RRKEVLVEDMGFSRI
393	6573	A	400	1	301	ETGFHSVNPSSQAGMQWRDHASLQP RPPGLKPSSHLSLPGS*HRCAS/LPGQ FYFL*RGGLTMLPWLVLNS*AQ/CDPP ASASQSVGITGVSHYTQPVNF
394	6574	A	401	388	390	PR*VIDLHVKSKIKLKENIERNFHILGE GKDFLD*TOQTLIIKDQIDKLGFIKII/ SLKYTIKKNVEDATN*EKIFTVYTSDE GF
395	6575	A	402	1	520	HLSPEKNADDMVVVRWFRSQFCPAGF VYKGG*ERTEEHMEEYR*RTTFVSKD ISRGSVLVIHNITAQENG*RCYFQE GRSDYDEAILHLVVA/GASGS*GLLRSR PRSRK*NPKPACLKLESTHPSQRLGSK PLISMRGHEDGGIRLECISRGW/YPKP LTVWRDPYGGVAPALKE
396	6576	A	403	3	368	KALRIAKTILKSENSTYMPDFNITFKA VVNKTMMWFHKKDREREQSS/VPRL MLVFNKGINGMKWRN*SLFNKWCW NNRLT/CGKMNDLPYLTPIKANLR *IMDLKIKAKNVKLEVVIRE
397	6577	A	404	3	417	NAQWITGIVYTYGFETKFLQNSVKSP QEIRD*ESDNGRVSLLWFLLL/VVMSV VSCVGA VLWNKKYGDWYWKEDSSS QLVFDILVFIL*QYLPISLLVTMEIV KYIAQAFINVDQDVHYKVNVSHTMA STFNLSSEL
398	6578	A	405	10	394	KVPPPFQGLGFGNPNRFFPPSSSSPF QKNPQASSSSSFFPG*PPTLKKGND/ PSSPPGPPKGGKPRGKNPGKTPPPPP WAPPGPGGKASSSSSRDRVSSSSSS

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						SSSSSSSS
399	6579	A	406	3	405	RLWCGWRNRHLGS*NRVENPETGLH RYAQLIFLTKVQKQVGGQPFNK*CG GTWAPTGKT/MEQPPKASSSSSSSS SSSSSSCKM*NIVFFKMGLENLWDH*AK SYEVRTKA*TIKGVVDKLDFFIKKHFC YGKN
400	6580	A	407	1	245	GGGGEYSKIIAIAKTALNTTYLGIYLI KDVDPDLYTKNYGTMLREIKYLEK*R ARPCS*TERFKIVKMS/LPNLIVRFNTI
401	6581	A	408	2	376	SCCIKYIFIGFNIVFWLLTFVWHCI* TCPSKVAFLGITFLGIGLWAWNEKG VLSNISSITDLGSDPAWFLVGGGV TFILGMARCIASLRQNTFLKPCSVVL EIIIVVELTDGALAFAFKD
402	6582	A	409	3	711	VVSLWQAPIGESQQRPLGFWGKALP SSADNNSPLERQLLARYWALVETEYL TMGHQV*TM*/ELPIMNWVLSDPSSH KVVYA*WQHSIIKWKIDRA*AGLAGT NKLHEEVAQMPMVSTPATLPLP*PA PVASWGVYPD*LTEEEKTKA*WFTDD SA*YAGTT*K*TSALQPFSRTSLKDSS EGKSSQWAEFRAVHLVVYFAWKEK WPDVRLYTDSLAVASGLAVWSGTW KKY/DWKIG
403	6583	A	410	3	361	KIHLQICKQRQT*RR/A*LRHIKILLE TRNK/GREVEQKPGRAQQQASPWK PGRRQWSNVNLNVPNTNN*KPT*IFKP VQTALKS*GEIKTFDDAQIKAF*TSRM A/LKEMEKEILEAQEND
404	6584	A /	411	595	606	FYLKPTFGWTLFQ*GKGSSPASRVHL RFQELMKLEKTPTTEHVIWVSRPLNSS KIQSVK*VPKP*LIPHVLPTIILLQVHP T*PKRPLPGPLLVDEGPTALEPPTSIP SASRKGSAGAPQTSRMPVPMASAKNR PGTLDKPGKQSKLDQDPQYRQYVLP
405	6585	A	412	185	404	HLKHPFLELATKVTISENLQIFPA*SC SA*HLV/ELLCIESKFKDADDEEKASLQ KSIISITALLTEKDAELE
406	6586	A	413	34	629	KGVRNSRFVRQKCLFYIDLPTVNLQV NYYNLRNLNLSKSLNTVNIKSMISLY SSHK/QFOK*ILKI*FKVVSDDRIKYPG KINLTKYV*DCYTENHK/PLLEIKED LNQ*RDIPCL*/ISRLNIVKRKIPPKLIYI FKSNSDKNPA*NFVEIKKLFLKCIWE MQRSKNSSNNLEKNKIGRLILSDIKI YCEDRIIMIVSQDA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
407	6587	A	414	3	373	VPGPCSPGPP/GGPGASGSPYRGPVIF GFFGGKGVPPGGPGG*LPGSNDLAP LAPQKGGVSGISPPGPPSSSQPLWSS SSSSSSSSSSSSGNSVPSSSSSSSSSSS SSSSSSSSSSSSSSSS
408	6588	A	415	3	375	SPWETIKAYSLPIGTSTKKAIEIALA*A LMLGKSEALTLYRYVSYVPSVLHAC GATWKEKGLFLNAKNKEIQY GTEILA LLWAVEMPRMIAVVLCOQDQEGGL*N NTGWLTLADTTAKRAVLEGRG
409	6589	A	416	128	805	GERRGRSLA*HYEGREKIQLRRCET NRLKQOQLLEEVKCKDAVQLSIFELRH KITELEAKLNTDNEGSEWKTRYETQL ELNDELEKQIVYLKEKVEKIHGNSSD RLSSIRVYERMPVESLNTLLKQL*EEK KTLESQVKKYYALKLEQESKAYOKIN NERRTYLAEMSQSGSLHQVSKRQQV DOLPRMQENLVKTGRYNPAKQKTVS AKRGVPVKITRPNHLP
410	6590	A	417	2	387	RNIGLYASCKTLKKEIGS*IDILCSW IERP*ILLKROILPOI/VSYGNTIAYQIP IWF/FIETERMILKITGKNRSQTANTI LKPNKVGRLALPNFKTYKATVIQTV WSWHKDRWYGFFCVPTQI
411	6591	A	418	109	388	CCTGEKLETFLLR*APRQGGPHLFDN VMEVLANAVRYEKEIKGIQNGKKKV KTSLFPGEIV/YAENPHKS*PKNSL/ KLKSDCSKVNIQPIAF
412	6592	A	419	2	393	PEGPPSSANPGSARGPW/PLPGDKKG VRPPAPGSGRPPPPFGQKGFSAALLAPG PGKCSK/GGSRVQKSPAPPLP/SSSSS QDGGK*EGGDPRRSHSCHPLAGWQ L*GSQSPSSHCW/WQPPSCRVTQCSWE GN
413	6593	A	420	210	376	RLTTWSWQGY/GRTRILLHCWW*SD RVEPVWKTVGQLLKMFLNLYLPHDPA ASPTVLQ
414	6594	A	421	334	404	GPQQCLLTGWIRRVNLGVHA*SYPG AAGSPAPWSPGASPLRSQSRTPPSQ/ PPPL/PSLALAKNALARASPPAAQD/S PSPSL/PGSP/ASPGRQASPGAPPSAS NGT*WGTC*PLCASVSPS*K*GP/RTV PPHGMDEPGQRGSCGTGGA
415	6595	A	422	123	373	YSCLNRLFIKRCQFMFKRQTIQWEKI FATHITTKG*YSQYKQKEFLQNDKRKT INPTEKW/AKEMTROFTEDTGMICKH RKRYLVP
416	6596	A	423	1	417	LKEIID/ENFHSARDLIDVQISKAPR*L SRKSIAEQLSYHIIRL*KGPMKEIKKSE REKHLVYKGIPIRLIDLSAETLKPKR E*DAIFKELKEN/VQPRILYPVRINFIN GEEIKPFTGKQLTREFVTT/PAKQEL LK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US951,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
417	6597	A	424	29	794	NPVSTKNTKKLARRGGGRL*SQPLRR LKDEKGHEAGRRSLQ*AKMAPTPAW APE*APSQEKKKTKAQWITGIVVYTG FETKFLQNSVQKSPQEIRD*ESDNGRVS LWFLL/LLVMSVVSVCVGPVLWNKKY GDIWYLKEDSSQHC/G/YDILVFIIL* QYLIPIILLVTMEIVKYIAQAFINWDQ DVHYKVNVSVHTMASTFNSEELQOV KFLFSDKMGLTLCNVKTF/K/Q/CTTAG VIYGATPSI
418	6598	A	425	1	792	FFYREVKPSLVFDCKILITEIPKES/NR VLQITRELSKMLAYKVSMKLSILFILT REYKKVKMFPNIVY/NNTKYSRINLM KDIYDLYTAIYPSTAALKYRYMCNLQ NIARRN*RPPLNKW/W/REE*YSWIEGL VYKILVFPKQIYRFNASPNKKSPLFN KLIPKFP*KYKGRRISQTNLGR/LTQD LKIIYKTTLKNIVWYWYEVQRLLP PAPQSAPIPRTCWQLSPSLDQGLKGA EEGLTWDGKGQSGTEITSGLHPLPLSTF G
419	6599	A	426	3	214	LIISLMSGSVKFL/*ILANQIQ*HINRN VHQQYVQCIPGMQRYFISWK*LVNR LKEENNMMVISIDCGRL
420	6600	A	427	3	538	RQAWRP*TAPPQKAEGPPEH/PPWG* R*VPQEEPPRQRAEPVCHPYSLMVP PWGDSNQANLRHPIRPSVPHVPM*L*G AEAPRNQELPHSAPOPTWKALVSEL LKPEsqCPTPVFLSSGHTAAVPSGTGR KLARHGHPPPGTSQHLATAPPSPST A*KAPSAMWSEGA VEATNYTDWT
421	6601	A	428	1	498	SVVVCLFLSPGITSHTYVPMIFKIGAK KVVHWWKSILFKKWCWRNLISTCRRM KVD/SVTPGAKMNTNWKIDLTPSAE SIICLKENIGHTF/YDIRLGNFWDMT PKA*ATKEN*IPWMTSK*RHFCASAN TVN*VKR*PMD*EKIFKNHISEKRLLC VIYKEQLELN
422	6602	A	429	3	428	VAKVFLSKKNKIGRNPYPDFQIRIIE PIVTKPPRY*HNKIYVDRWNIKSPKT TSYIYSEFNFNKGAKNTQHWGNNSH FNKQCQENWTSICRRMKLDPYFLTY AKIKSKWIIDLNL*PQT/VKLL/EENTE KALQDIALGKDFS
423	6603	A	430	62	449	VGNIIISFLVHFLWISLQGGHGKLFNSG SLFICFFVFLVFLVFLRQSFVAVTQAG AQGYNPGSPQP*PPSFKRFSHLNLPSS WNYIGHVPPMPAKFFILLGDRVSM QLKGW
424	6604	A	431	56	443	VGNSRSFLVHFLWFSVQGGHGKLFN SGLSFLICFFVFLVFLVFLRQSFVAVTQ AGAQGYNPGSPQP*PPSFKRFSHLNLP SSWNYIGHVPPMPAKFFILLGDRVSM QLKGW

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
425	6605	A	432	60	232	VKDVTYENYKTLLEIKGDI/*KDILCS*SGKCNIVKMFILSKMIHRFSAIPVKIPVA
426	6606	A	433	1	374	QTLWRKRAVAVAALSVSVRVPTMSLR TSTWRLAQDQTHDTHLIAGDEKLDIT TLTGVPPEHIKTSTVRIFVPARNNMI.S GVNNT*RWKMEFDTMERWEN/PLMG WASTADPLSNMVLVTFSTNEDAV
427	6607	A	434	1	356	TFFKKNVVGGLALLNFKT*YKATVIK TVVSWHDGRHT/DSQWYGIESAETN
428	6608	A	435	359	95	SRIKAN*IHQY/IKMISYCDQVGFITLG MQG*VNIQKLIHVIIHLNRLMKSHVN FSL*V*KA
429	6609	A	436	9	369	KFYKGKEVHCITIKGSI/HQ/EKTLILNI YSPNNRAKHLKMMQKLMELKGEIF KFTIAVGDF/NTSFLVHSSAGRSVN TVDLRNTINQYDIIDIYIIKYYLQTA*H MFFPSFYRTYSKIGHM
430	6610	A	437	3	359	FFLCLCKPYIIGRVNQANCLTPNLQLO HNFRRLVLCANHTPEVKGFGRFLRRN LMETEISGRVRNMELVKIDWPVKVW HH/L/NRLLEAHSFSDVSGIRPVFLSCP IDADG*RVGTTDLW
431	6611	A	438	392	0	LFVLVRVIKEDKENS*SSSSSSSSSSSS SSSSSPLYLGGKKN*RI*TKKL*FELISN FSKVASNNKINQKSLAFYANSEQFEE IKKVILFTIATNKTKYSGI*ET
432	6612	A	439	20	314	PLTSPQTLLEIREFIPKRNPTNVNNS NPLVHFQILLKHKIHTGEKSYKCDK CGKAFNWLLILMKQKIHTREKPYKC K/KCGLAFNQSPNLTDRDKRIHTKEKP YKCE*CVKSFS/HFQILLKHKIHTGE KSYKCDKCGKAFNWLLILMKQKIHT REKPYKCEKCGKAFNWLSNLTKHKK T*TGEKSYKCDKCGKAFNWLLILMK QKIHTREKPYKCEKCGKAFNWLSNLT TKHKKT
433	6613	A	440	41	509	DVSLAFSLLRGQRLGTGTGPEPGPGQ GLGLEPRPESEPSPPNPGELGPQSP GPGSGSGLGPPPPYPGAAAPPPPPYS P*LPPP/SPSPPGDP
434	6614	A	441	2	370	PWETIKDYSLPIGTSKKAEIALT*AL MLGKTEALTLDYVSVYVSVLHACG ASWKEKGLLLNAKSKELQYGTIELAL LWAVEMPRMIAVVLCCQGDQEGI*NN TGEVRLADPPAKRAVL
435	6615	A	442	2	377	VSPWETIKDYSLPIGTSKKAEIALT* ALMLGKTEALTLDYVSVYVSVLHACG ATWKEKGLLLNAKSKELQYGTIEL ALLWAVEMPRMIAVVLCCQGDQEGI* NNTGNNLADTTAKRAVLVGRG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,785	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, /-possible codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
436	6616	A	443	368	0	SSSSSSSSSSSEKSNNGGYRNGPFGN FPNLGRFLCLILRASWKILTWGENAW GGPFNFKPSFWVFFAGDGPWPGGGV VKGHGP*GGFPAPWGRV/PFPDIRG
437	6617	A	444	2	580	MIGQAGLELLTSSDLPAS/SFP*CDWY RRARNAWPSHS
438	6618	A	445	1	553	HLSPKNAADMMVVRWFRSQCFA GVYKGG*ERTTEHMEEYR*RTTFVSKD ISRGSVAILVRNITAQENGTYR*YFQE GRSYDEAILHLVVAE/RS/GS*GLLR SRPRSIK*NPKPAACKLESTHPSQRLGSK PLISMRGHEDGGIRLEICISRGWYPKPL TVWRDPYGGVAPALKEVSMFDAH GLF
439	6619	A	446	1	354	AVPRALTGPQSKVFPQLLP/SPPCL AVPHSSLPSPP/P/RP/SLFPLSFPAA SPSIP/RFSMP/P/PFPPEPSILFLLP* APIPLPYHRYSSPQGP/LQVPADEV
440	6620	A	447	27	366	QPVPCESSAIVTVLATVTHQQQLP /PPPP/LPPP/HPPPSPS/PHQQHNN NPQPRPVSTSCSHLGL*GRVPPF CPSKRTVGGGLGLWPPQVGSAPAG PHPGSSCIN GSAPGFC
441	6621	A	448	3	279	FFFCSERVLP*PDWSPGLKQSP LLSLPKCWDYRCESLQLVTVNYV LTKSLNLNTSKAMDNF/CLKSPL QPEKN*QKKYSGVSQLRKPNM
442	6622	A	449	3	252	ASEEIKENEKFLETHDNGNTTY* NL*DIGKAVLIGRFIALN/ALHQ QQKTLQINLNTMHLKELERQE QTKSKINNRRKEIKFN
443	6623	A	450	3	251	ASEEIKENEKFLETHDNGNTTY* NL*DIGKAVLIGRFIALN/ALHQ QQKTLQINLNTMHLKELERQE QTKSKINNRRKEIKFN
444	6624	A	451	46	667	RGWKTYQAHVSMQIGADGHN SGVRQAGGIQKASWNYDQSA VVATLHLSERVSA*AAIWGVY FYGTRYFTEKLLLLSVA IATENNVA/WORFLPSGAYCS APGKRSFLTSPPTCMQAF PFTLSAFLWFQGNLPR LVSLSLFFVLCLRVSKCS RVLPVIGIGVLLTQLSD TLSSLVWSASHEHA AELVSMDEEKFVDA VNSAFVSLNLP S
445	6625	A	452	2	307	PLGSRQILTCTAYGIPQPTIK WFWHPCNHNHSEAR*Q QSVTLTTFKYF/CDTW N*DFLMDADGNLHV GCTVYLRQRLSLP WKVKVGSYSYSL LLNIPYHWTIS
446	6626	A	453	57	250	EGGRIFNFSFSEVILTL/PK PEKVVERK*SYQ PISIMNGDVKILA QTLVNIQQY LKRHHYDS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
447	6627	A	454	1	370	RALKIIR/DKEEHYTIKGSILKK/E/LTI LNIYSPSNRAKVLKMMQKLMEKKE IYKFTIA VGDF/NTSFLVIHSSAGRKSV NTVDLRNTINQYDIIDIYIKYYLQTA* HMFPPSFYRTYSKIGHI
448	6628	A	455	2	384	PLLGI/VPREMT*VHTNICTWIFIASL YIITPNWQQLR*RLTDRKPCPIHMMME HYLAERNELLHHTKWVAFKNISS SSSSS
449	6629	A	456	3	407	KALRIAKTILSQKJALTCSDFNITYKA VVNKTMTWFWHKDREKRETFNRNRP LMPRI/ISNKGIMKWRN*SLFNKW/ CWE*QITHMGKMNLDPLYLTPYIKAN LR*IMDLKIKAKNVKLPRSIYKRIAF TGCSGRCL
450	6630	A	457	2	214	VKDLHKENYKILMKETEGDT/NRKS PCSWIR/INIKMTMLPKAIYRLH/AIPIK IPMTFFT*KEKTILKYVWN
451	6631	A	458	2	214	VKDLHKENYKILMKETEGDT/NRKS PCSWIR/INIKMTMLPKAIYRLH/AIPIK IPMTFFT*KEKTILKYVWN
452	6632	A	459	2	356	TNQETNDNQST*YQSLGDI*YSWPVA KIIA VPAYII/ERSYTNNTLTLQLK* L K*EQMKSSSRMKEIVQIRAEINDIKN RKL/LEKINKVKNWLSSSSSSPHTLA NWTKKKERR
453	6633	A	460	3	251	ASEEIKENEKFLETHDNGNTTY*NL*D IGKAVLIGRIALN/ALHQQKQLQIN NLTMHLKELERQEQTKSQNNRRKEII KFN
454	6634	A	461	1	340	TFFKKNVVGGLALLNFKT*YKATVIK TVWSWHDGRHT/DSQWYGIESAETN
455	6635	A	462	40	291	AGEGPPPLFPPL*GVKGFFGSP/PPK SLKPP*PPGQTPVFFKKPKIVPGLMGP PLIPRS*KG*GTKTFLPWRGGVQFPPT FF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, v=-possible nucleotide insertion)
456	6636	A	463	39	1628	ISEPRYASLDEDPDI.GTQN*VMSDI.W A*PGPYFPQPS/SLRPOGR.TQLPAPG/Q Q*PPGVVGRGSPHSLA.VVSAPGRESRQ WDSINVSSNSEHLPAP*LFLAPLAVLR SLDRPSQGQQNQRP*R*GAWRNLLPG *RALRLTTCA.PNDLLRSFA*QGG/Y*C TTQWNEELERL*VSSGRILPPCGGQ TGRTRLCPWGGQ/QPLVCNIPHLPGKG LGASGGVGVPPSESGGCGSPGVYPSV KSGHGGPALCTGGLSLP/SQASSLLQA GPGPRPQQLGHSQSRGQLPAFPDPSP GWL.SLETSPSPFKSGWRE*WLH*RDR RVGDLQESKSGCQRPVPVAPTQPLGV PTQPPQLHLA.VLPSAADKVNNSPKTS QRGSDDQPSQWPRKVNPGALPGPYQ PVNLLRAPKLTDCA*GHLVTP*PVSPS *PS*EQSLLSQPLRVQP*GSSPHNSI* GGEPRIPPAGPCTHQG*/QPATQVPGG HNRCG/HVGEQP
457	6637	A	464	2	1582	FFFETESCFVAQAGVWGNLGLSPQ PPPGFKRFSFSLPCC*DYRHLPPRPV KFFVVL.VETGFHYLGQAGLELLTSGD LPTSGFQSARITGVEHPARP
458	6638	A	465	51	462	EQIPGLRNPCHLGPLPVAFDLAVGIAD LSGSAGQGDWQEGVAGRPLPPRAGA AHHPTGREDPHPR*QQVRVECLPPSP SAPHKAPRAPTGSCLFPLPRLSVVMS LPTPKGHPPQCLPLRPS*IPASVPPPP GA/PPAP
459	6639	A	466	70	513	YHLKWLYYLIEVP*FCF*K*ISSAEHT VKRMRRQATDWEKIFARDIPNKRLLF QIFKALLKLNKKTKQOQKEIFKMGQ WYKQAPYQRRHTDSKQA*CSFYVI R*LEIKMRVYHFIV/SIQNTDTTKCWPG CGVIGALIHCAWCKCAV
460	6640	A	467	1	1183	QPGPLAPDVIDLGEGETGKSEEAQWL SRRLTAAEWCLIPSTAAPTESPGICGS GPPA/PLPDPTCTGRRGPRGKVLGR* AAEGGPGFSLSVFWAPPAPGKGSRG PWCCPCHRYRPGHELAGLGRAGVQP GRRAAQHLPVGR/PLG.GGFPKAIAPR
461	6641	A	468	2	644	RPGCRMGPPEGQCGARHSNRSRSP KQGG.LRGGEPMILAL.TWPLSCGLTG AEGQGGEETLGERGVQGGQRGPAG LRÆGSGPRGPI*GPATSLP/NAKSGPN **SAASLFCRSGDSPNKLKTLTACHCF C*FPKIDTNFWRVFP*GSOPQGORCG KAGLG*EGAVPELGSAGASANRSGA G*SEAQPASSCPGEWHGTHCPCGTGG REGGRGCT
462	6642	A	469	257	492	DPIYVNVKWCWDT/WHTHRRKM*LAP YLYTPYTKRNSK*IMNLNVVRKTNLL EDKIGVTLCDLFGGNYALDMPKTQ* KKN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
463	6643	A	470	458	710	LVIKTW*WQDSGTFIKIDQQNRTEGTEIDPHIYGQMLI*SVKAV**EKDNLFNKRCWNTN/WNMQTGKITLAPNFIPYTKINLV
464	6644	A	471	229	261	FIWKYKGL*KDI*EOYTANYIALLR/KEDLHKWSDICGS*VEKLNIIKR*IVPKLTYRVNANPIKKTQQDVLVEINKLML*FIWKYKGLGIN
465	6645	A	472	122	494	STLDFYLYLF*GQESHVSVTRA/MECSGSDLGLKGDSPTASGSTRGLPGTHHHARLIFVFF**RWGFHHVQGAGLGTPGPQVIHLPRPQSG
466	6646	A	473	1	352	DEVLSAEFRLTITRQDIQTLNHLNWLNDIINFYMNMLMERSNEKGLPLVPAFNTFFFTN*KRPGYQAVKRWTQKVDAFSVDILVRIHILGVHWCIAVVDFTKKNITYYDSMGGINN
467	6647	A	474	32	378	DRSGLGKTGPNQTRPVTRIQDQNKPQQTG*DWASDCKTGPQAKPDKTGQ/RLAQTR*DKTYPD*IRPDRTGQDQAE PDKTGQDRTRLRGRTG*DRSGLKGTGTNTGQGFVNSTQT
468	6648	A	475	2	408	SNVSSSPVHIQNRGLCSGPFENNLYLVGGQTITTECYDPEQNEWREIAFPMMERMECGAAIINGRIYVTG/GYSYSGKGYLQSIKAYDPDLNKEWGNLPSAMRSHGVCVYVNV*NLQK*PSNHFFGRVYVKN
469	6649	A	476	1	635	FFFSEIESCSVSQAGVQWHDGLSLQPPPGFKRFSCLSLLSSWDYRHAPPRLANF*FLVEM*FCHVGQADLEPLTSGDL PASASQ SARITCVSHHAWAQN/SYTIKF
470	6650	A	477	2	293	SPFLGVGPLVFFRPP*LGNGGPKLFGGASSPTKFFF/PPPFKREVSPGPLPREQFPFRSCKKGPPVTPFFLAPGPVFPFKFKKNPGGGPKILVC
471	6651	A	478	1	184	CLRKKNKVLGIRLPNTVLR/LYTTAVVIKAM*YWKKNSHYQWNILENPQIKP*KYAQLILT
472	6652	A	479	1	256	LSKWIRK/QDPMCFVQDTLFIKYKATYRLKVNA*RKIYYINTNLKAGVATLISD/K/LDFKPRKVRDKES/YYLIIKGLILQEDITMQ
473	6653	A	480	3	214	LIISLMSGSVKF/L**ILANQIQ*HINRNVHQYPVQCIPGMQRYFISWK*LVINRLKENNMMVISIDCGRLE
474	6654	A	481	334	367	KWINQ*GLLINHWKCKLV/QPLWLYLAKLIISIFYNPSSSSSSSSSPKQG*QETCTRRFVATLWLAKHWKQOQLST*KWINQLGYIHT
475	6655	A	482	288	468	KAEAGGWLEPRSSRPWREAGAGQSPGPGVGRGCSEL*LCHCAPA WTE*D

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LASKKKKQK
476	6656	A	483	2	596	RQSL/DSVVQAGVQVHYLGLLHPSPF EFKQL/FSLLSPNSWDYRKPHHTWL IFAF/LVEAEFRHVDQANQ/CDPPASAS QSGGHTSVSHCTQPDYDITL/NFFFTLY SYFKGKL*S*VFSW*LIL*YSTVICLYS *NPATGCSFFWRWSLALAPTGVQQRS LGSLOPLPPRFK*FSCSLPSSWDYRR VPPRP/INCFINID
477	6657	A	484	1	241	LSPGFNCQAGVNMVTPF*GGFFPHFF FLGRGGPRPLGTPPSLKSKGGGSF*/PP GLKGVIYP*WGPTPPPGKKNIPFPNF
478	6658	A	485	161	371	KRNSTFPPAGREG*NFNFLEPPPF/G*R KFSCPIPPKKWD*RN/PPCPINWFPG KGGISPFWGLLTPN
479	6659	A	486	17	371	TQMTFFAEETKFKILFILDQRTLK*P K*S*SSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSQPS/E*/MPHMYCQII FTKEANSLKGY*QFFKNWS*KNVTS TGKRIKLN
480	6660	A	487	32	366	NTEISVYIGNCKTLMKEIFKAINKWK DIPCS*T*RIIIVKMSLL/PTLHKAIYRF TAIPKIPMTYF*EIENTVSKVMQNHK RP*IAKAASSSSSS
481	6661	A	488	59	101	LILKLIWKFIYASQNNFEKNTNKV GGLTLPDFKTYKASVTKTSRY/WM*N SKAYMEVHFILG
482	6662	A	489	1	363	RWGLGTTPSPPGFSNPGPYLLDPFAL L/QFWQGGAGPPQGGLTVSPG*NPL WFLAGGVPL/WPSRFWLKVQFLKEPF PPPHLENPTRPSSSSSSSSSSSSSSSS SSSSSSSS
483	6663	A	490	82	466	RELTSANLRLTRYLEFFETGCHFVA QAGVQ*CPFCSLQLPPPGFKRFSCLT LLSN*DYRCMPPAQAIFCMFK*TTGL CHVGQIAGLKLTTSSDLPSSASESAGV TGVSHCAWPTQYFHFSLYHLLC
484	6664	A	491	3	233	QLSSITIWY**KN/RIDQWNKAQNTSV HRKLISDKVTKTIQWSKDSLFNKECW NN*TSIC/RKTSLSALTLFTKNSK
485	6665	A	492	372	1	SFSSSSPGGKPPGGPKQGGEGFGFG*T NP/PPPRVKEIFCPTPPRRGNKGRGPPP QEIFGFLSSSGFPQFGYSSSQPR/SPKK TPCPNPPKGGDKGV*PPGPPKNPFWK KNF
486	6666	A	493	2	363	GNQKRAGVAILT*DKTDVYKPKIVSSS SSSSSSSSSSSSSSSSSSSSSSSPFKAP KYIKQTLIDPKGEVDYNNMIVG/DANT PLSKTDRSSIQ*INKETVELNYILDLIG LTAIYRTFHP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
487	6667	A	494	177	598	LSSTTTPOSRLIVQHLTLTYLFLFF*N EISLYHPG*SEVQWRDL/GSLQHPPPR SKQFSCLSLPSWSDYRHPHPLANFCI FRDRAHYNLHLPGLSNFPASSSGAA GIMGAHHHARLIFVF/CRSELRSHHCT TA
488	6668	A	495	2	388	VSFFAPGF*TPSPPPKPLF*KKFGGTS SSPPFFPPRPGVVRGGFPLGLAPPE*K PFPSSSSSPGRQKKTPP/PSSSPKEKK PPSK
489	6669	A	496	113	320	LPCKVLILISNISKCFRRDYCNLDKIS DNNTTELLNFNEFIDRKTFPNPSCKY ALIQR/*LLECGSIGL
490	6670	A	497	78	315	VPPPLPD/PLLFPTSPPLFVSISSSPK RKSR LAPQPGGQNRNLTPWNPMPGS GILRPNP/SGEPGTGKGP/APPAVIFGFL TKKKVPPCGPGWL*PPTWGAEPESNP LEPSPSRVRNPAPQFFGEPGTGPGPL PQLFLDF
491	6671	A	498	1	390	GWAPFGF*GKFWPGPGAPPNGSRPLG GQGGGFLPGPGF/QNPPGPGPLTPFFF SSSLFSSSSSSPPIGFWGKPGGGGS H*LGSSRSSSRGFIGTPT
492	6672	A	499	1	377	TFFKKNVVGGLALLNFKT*YKATVIK TVWSWHDGRHT/DSQWYGIESAETN
493	6673	A	500	2	361	GRINSVNLVLPKVFNRFNIAIPKIPAE LIIFLY*SPSSSSSSSSSSSSQSCIYN QPIFKKCAKNTQWKKCLFHK*CE*EN QILTCRR/MKLDSP LTPYKITSK KDL YVRPQTVKLL
494	6674	A	501	53	354	ADSSQCYIID*RDQYHPGILQNLTLA RYIVDMIFGPDK*VEITLALAIKMHML RGWK/IKHTK*EPATF*AFRGLDI/C/ GAHWIDPIAKCKLYATPTAKR
495	6675	A	502	1	372	DGFVVFDNSAIAIYGSNEELRGTSK AASHAVQASFADSNIGPPARTWVFL TLGIMH/HCG/WLYEQDL*PSFRQAFP NTNRWDLTWINQPVRAVLGEVKLC DKMAQLDAKLAQIQPKKDTPR
496	6676	A	503	53	591	SRKLLPPSPPHGSGQ*SQRTSPARSH WINPSPS/PTLQGQERPPPEPPGPPS KSSPQ/DTG VPRGTAAPGAQQHPPEE RRDHCRPGKS/SPSHAPNPAP/RPSN TDTWASPPNPIALPVHPPASPSHDP DQQSERVGTTRPRNSYRGTVAASSA LAGKTPRESSVVLWKEHWTKGFGSC
497	6677	A	504	1	378	PLGHQVTI*PELPMNWVLSDFSPSHKV GHEQQHSVIKWKWYIRDRA*AGPEG TSKLEHEEVAQMPVVSTPANLPSLLQP APMASCRVPYDHYAAER*FS/WALE GQAAEA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
498	6678	A	505	3	387	GVHWSLLRPGSLQGLCSGPLSCPG*R TP/GEQPSPEYPTPIPVHTPGGHAMY MWRACHPCPLQALPLQPPAPRHWHL APPQACSPSPVGMSSQGLSKILDTPVCI VRGRSGDSSPHQGVVWVGKSPAR
499	6679	A	506	90	271	YLLKTKYKDILS/PLQIGFTFSVPVAKT AELSGSSSILEPIISSGK*KFLT*HTN NCIQ
500	6680	A	507	1	354	LEDVAAFLSAVPKRGPSPS/PTDQSS SWELQPVCMSFALRI FLVRPPAPSH ASEGRPH*NSP*VGKEASPPRVQVS QLGTSTHRRPGVPVPAPEWPLAFPGTM PLMSAQSPGLSW
501	6681	A	508	1	401	GGSKSQSRSSRSRSDSPRQAPRSAPY KGSERGRSKSDCKYPOKPHKRSR SSSRSRSRERADNPGKYKKKSHYY RDQRKRSRSYERTGRRYERDHPGHS RHRR*GGVAVTGGKRP/CPWGVDPG WPL
502	6682	A	509	1	574	EALFN/ILEVLARAMN*/QKEMCKL KIRKSKIFFVDDMIFCVENHKESTKIL L*LINTSVD/VAQYNIST/NK/VEFSYI NNKQF*MKI*KHFHLENLK*EIGING KEVRNSYIGNLQTLDMV*KHI*RY NPY*CFGKINTVK*LHNPM*F*FNTPI KISITFLKKQKTDWERCSV/GQAA LKTPDLK
503	6683	A	510	51	353	ADSSQCYIID*RDQYHPGILQNLTLA HYIVDMIFGPDK*VEITLAALIKHML RGWK/IKHTK*EPATF*AFRGDL/C/ GAHWDPFIAKCKLYIATPTAKR
504	6684	A	511	3	329	QENLTKSTE*Y*NLNLLNFEWINK KIKAE*N*KDFE/TRRDTI*QNVVWVG RALLRGKRLVLTICIKLE*SQTNL TSHLEKLEK*KLTYPKASMAKIFTY EPDKI
505	6685	A	512	1	411	RDNLNVRSETMKVIEKNIKEKLCIDGL DKA*TLKAQRTKATIDTWH*IKLKSF CTAKETIKRAQQPTWENIFATYTS D KGLIYKELKQLSSNKPNNPIKNWAGR AWWLTPVIPAFAEAVGSGLEVRSLR PAWPTW
506	6686	A	513	3	587	IFCLYTGRIILL*LPKVIYRLNVIFIKP MTFPTEIKKFKFIWIHKL*IDKATLG SSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSPAQ*APEVSLCT*SQLIVNTIA KNTL*GKANLFNKWCRAI*IFKFRKI MLDPCALPYMKINSKDLNVMLSIM KLEKN*KMLYNIGRGKDH*KNMSK HRKP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
507	6687	A	514	34	368	GPASFFGGWFFITQSGAGFPFPPWP/PR RIGYGNPVPFCFNQNWGPTGKEKGI FFGFQLGGPFNPGPGFPRGQMPPAL PPQKPFGLVFCPFKTPF*/CPVF/CCPK K
508	6688	A	515	381	0	SLLWFCFLC*RFVKMLESVGL*FSLNL EKT*TLFLQVFWGQTCILFHMSLRH/ TPNPPIIF
509	6689	A	516	2	373	RLLGLQYALLVWWTTKE*HLLGGDP IYNYIESLLSYALHHITEDSRDYDTIKAF NAKGRDPLIGGTYMTLLNTACKLGG NRPSTVALWLVYSLTVECA*ASNHN CRTPDAAELCKLFGSCET
510	6690	A	517	84	381	SKQNKV*KK*KQL*TG YRKTMEKIN ESKS*FSKKVNNINKPLQRLTKMGK QRTYIAKISKNKIRNITTDSTTSIRRK VCKLYASKFEQLEGM/DHFL
511	6691	A	518	6	407	IGNQDEKACVPS/RKSQSSQGAELALT SA/PPEKCGGQALRGLARRAGRAVVG TPGAAAPAPNHPFDDL WSKPS/LQVPP PRPQTSPSGHSLVLRVPEMVPSPVP SPISPLGQHQPVLGTGRTPPV*ST GLVP
512	6692	A	519	3	797	SHCGGIPMPSSAMLR*SGSRGPWEH AAGHSMAAATCRHFNELEHEL/SPRL NSWHTQTRAPKYHELAVLSHSDTA GQEMEPFFAGSILGWLIATYDEDVL GCGNMCWTTVTLGLVTVTVCRSFIP DQHMVFCPEQLLRVILAHIHMYLMDH WQGNNAHRSQTRDEFALQFQYKPVFIL EELLSPIVTPLILIFCMRPRALEIIHFFP NFSVEVVGKGDTCFFCSKGGARS WS FPRDRPPTRTFCGWERSLSPNSGFPGQ PRLT
513	6693	A	520	2	167	GVEKSFDLRKGIDKPTANILHPSF SLMSEIRQ*/PIKPFLLNIVRKVLASAIR
514	6694	A	521	1	365	LQLINKFSKVIGNKINTQKSVVSIIYQQ RNF*KKSSSLVQFATFKKGKHLGIYL TKKLKDLSTEN*KTLLEIKENL/HKW KDIPYSWIGKLAIAIEPKTIYRFKGSV CKNKKPTFKLIRNCK
515	6695	A	522	1	134	TYYKSTIIKSV*YYHKNRYEQWNRK ENTEVGIIYDQLIFDKHAK
516	6696	A	523	105	396	PKFPFGNPGOPPRGGPGPKVVG/RGG FCWGQKAPGLQGP/PMGPTPSS/R*T PSAGALSSPHNPYGRGKGRGRNSLN PWGARGPPRGKPTGLLPGPF
517	6697	A	524	3	397	VKIKALGGPLGPSPREYGPGRG*VIL PLSLSPRGP*AYWGWKGLLQRGVTPP PGWAPCPGPSGRALFSPSKNRLPNL WFRTPPGLSGVPKKGKFGSSSSSPMS YGSE

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
518	6698	A	525	64	403	EKGVWSLWPGQKGRGPAPANGTLPP PGQKNPPA*PPWKPRHLGGGLGQKNR* TPEKGGSGRGPKRAPGTPPGSSSPTGF SSSSSLFNSPPPPGKITEAGGRPYRKL NDPGVEGGV
519	6699	A	526	3	218	YPSK*NLDEVHKFLERQKLPKLTQ* E/VTDLNRPVTRDTEIVVTELPAAK QP*GYPYGTAEFYQTFKEII
520	6700	A	527	55	418	FRGFLWSWQSSCLQGSEERRKPGAGP APVAAGHSM/AAPQQDGLPEAGL*P GGCAPGVGQAGRGPRPGQRRAGAY PHGQSPGCGAPGCTQASASGLLWG PGLCPAWPGDSPGRGLQNPGQF
521	6701	A	528	2	678	GLQSLGQVWNPGBTSGHADAPLSPG DVFGLTGRGGAGETSSSATSLPGL GSESSHCDSSLLGTWQSQGCMGVPR VGAGQMGACHLRPQGPPTGAGGAPL AGRPSGPGALDTVGRGSRGRSRGV AVHKGKGLGPSSRDTVGSQDPPAGD GSRQRGDASLVHGPAGPGCAHSGP GLGYSAAGSFLS*ASHSLA*TPVASRT GSAGPRPGLH*ALRPCSPFSC
522	6702	A	529	2	376	ENPEINPYIYSQLIFKMGAKTRMQKN E/CWAPYLYPYSKIN*KWITDDV/RP/N TIKLLKCRHKS*PGGHNVGF*DMIPK AQATEEKPN/WDFI*LKTP/CASR*SIK KMKRQPTWEWERFTFDKGFVFL
523	6703	A	530	25	366	NIATYAIACCCKLTSTKTIQWDRIVFNK LCLDN*ISACKRVKLDYGPHPHTKIK A DWDHLRAEIIKLLIENIGVNLHSFG NSFSSSQDKVSRCFVWRWAQWG LIVGSSSR
524	6704	A	531	3	353	YRHKAPNTWQAPSLRWICGPWAY QQLPAKWTGACVLTGIRPSFFLLPLQ QGKTLGCPVYNKILNKHQRNRDIKK DTQIEN*KDTDWLPRIQYGYPA/TA QDGLGYRTPIYMLNH
525	6705	A	532	137	417	NLQVSSCLNAEQNHLSASLSRLHRV AQVTPSAGTSTSGPPYAGCIGWHR*P LWRWNQHLRAYLSRLHREAQVTPPAG IWLHCPCWTPGALT DVC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
526	6706	A	533	2	1118	TGSEGPWCWQRSLGSLGVG*NKYHPGE DGQMOT*AGARGHKGESKASAGTGA GSW*GPPRQAGSGPGGPGSG/PGPLG TRTSCTHGEAPGSPSPGSRKLKVHL LRAICFPAAGCDVSPSPGGEGRGCE WDSLRAIWPGGCPKGRPLGVSEKRS LFRFE/GCPPAGCFANL/GPHRVCSER GFWPHECFGLGMFLPGTECAVGA VAPGK*CPAPRLGGWGAWSSSCS*E GGGSPKGPAPVPPAPHR*LLSP/PPGS QESHPRDQISVILFLGFI*RVQSPGLR SAHPPYRVGT**GQDA/PDGVVLLSA GQPLGR/GSRSDCPPPLQAQGLSPPP QGRLHSA SRPAVKAPGPQKT/GSSP*V EDDEAGGRCSLPE
527	6707	A	534	69	350	QVTLEGLEDAFFTITVRNQFVR*GPA SLLCGCFSL*VRNYSNGNCYHQLGSLN AMGIKESRGGRAQVAAPC/HNQGHH SYHNK*WSQSSNQNSLTC
528	6708	A	535	1	402	NPSPVRKEIFLPEPKRKKVAPAPFF*P GPKEGKPLG/PLRLRGIT*GTSSFPQPK SPSPPK*KQGPKRPRFKPNFQGG*KS QGLPSSSSPFFKPPNKTRDSS
529	6709	A	536	255	433	LDLGPHSV*PIEYKTIQTSPAPPKTLY FVS*CRFEYLFNF/DHTFEIHDDIEVLK RMGM
530	6710	A	537	7	392	FSKGIGRVTRDSTFKVYCDTE/RQID CYIWKGRITPEIYAHRLEREYGCPCIT RK/TKSC/RFERPLPLTRLTLHI*NIHV VQAS/MGKVIGVLQPLVPEDNTKLGIS EETFPSPNIPKSFVPAVEKGFLLDA
531	6711	A	538	16	370	EILELINKFNEFVGNKITP*KSTGFLYP SDERSKNEIKKTFLRTVPLKRIKVVRI NSTKEMQDSYSKNYKTLLEKEAK/ RKDISWLWIGRLSIV/KMAILSKLIYRF N/SIPNKTSTGFF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
532	6712	A	539	77	1673	PMLPCEYVSPPIHMSIRPGPLPTPCN LIGTLGPAAGSCQSPRPAPVLSPPAPSS/ DTEPTPLVTCLFLHEASVVFPGTASS EALPLVRHCCKGR*GYLVITFLGLIHC AESEGVWLILVPPSSHQHTPICERKEG GKEYLSP*QHSLT*GPSLQPLDAASQS LPAEHLRQSLPMD*LVFGP*GPEGLQ GSELIAQTLPCGPPNGQSRDHP*RP RPGLVTE/APGSASHHPLRGREGSRH MSKKPRKGRSSSHIPDASSETPAGSQ ATRPLWSHPTHARFPPEAGLPShLSH SLKILFS/GPPRPSPLSPQTPGPGISM MFMSPLFVSRDAREGGWDMGK GKL*A*SQGFPLAEGSSMPGWGCT GWPGPSG/PPGSSPLPWIVPDCRLP EGPLMGWVLPRC*EHSFTDGCLEEGN PALVHREQDAVLPCCPPGPA/SPAGCG AAYSGSSGPGSGGVTLLAQGWWSGS NALCSGSSRLGEFFRGGTGTCRWGPA SFVRKPLGPVGPSPMDVFSKQDMD KDDLGLRWKE
533	6713	A	540	1	342	RPETKKYPQNPCCGGKKFQRNFVPP FLLSRWGSIPKGGGPPLVKGFPGSS SSSQSLPTGGG/NFSQPPGH**PK*P LPPSENFPDV*GPPPRVGVFFWFFPTIL KRKISQ
534	6714	A	541	2	228	KESRLSFQKSISVHHHNRVNOKGHLIS VDTERAFNKSQHLFMRK/SLRKLAVE GNFVNL/NSIC*KPAATILEK
535	6715	A	542	25	277	NIATYAICCKTLTSTKTIQWDRIVFNK LCLDN*ISACKRVKLDYPGIPHTKIK/ WIRDLHLRAEIIKLEENIGVNLHSG NSF
536	6716	A	543	2	790	GNIDVREPELEDLTRYDVGAIRAHNG SLQHLTWLGLQWNSLPALPGIRKW RQLVHHLPHEASRLGTGAPESIGLIDL EVSKGFNELNIGNCV*CF*LNFSVNE TG/LLGVVYTSHLQKKECNSHISS YQPLCLPLPVCKQLCTERQKSWWDA VCTLIHRKA/VVSSKTKILLSA*VLP GI*SSCEDLICHVTH*HICM*ALNCVF RKQF**IELFRPGNVAKLRLVQHEI NTLRAQEKHGLQFALLVHWAECLOK TV
537	6717	A	544	11	133	IYIL*YLSL*YLNFNLLIIVGLFLVVS SPLISRRKRLYLQ
538	6718	A	545	111	376	FILFLEGTGH*CLGWNAVVP*LTAA /SELTYRLK*SSCLSLPSHWYRHSPP LLAN*KKKTVKTGALAMFRLTLIFW FPMILLPWPP
539	6719	A	546	2	383	RFSCLSLMSNWDRYRCMPPCPTNF*FL VEMGFHLAQAGLKLPLTSSDPPTSTS QSAGMTGM/SHHAQP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
548	6728	A	555	128	438	ESRALTRKLAPVKRKNINSLGECVINLRLINQIVLPVHPVVPNPNYLLSSIPASTHYSVLDLKHAFITLHP*SQPLFSLTWIDP*PHQAQQIT*AVLEQS
549	6729	A	556	3	275	GRGSPHYSPFF*GVGPEGPLRAGGLGPPGA/PPGPLSKQIYPMPSPPVPPSRGG*ARRSP*PRGFAPITLGLPPLGGQNQARFCF
550	6730	A	557	2	439	VGHKCYARAPVCVEPDPSCAAPSPNWPVCV/GALFRQDSGGTTPPPAPRPFNWG/PPVFPLPPLKPGPCPSCMPGGWLLRIPNSPPAPPRGGPK*TPFSSSSPV
551	6731	A	558	1	308	RNRAGTSLSPLLFIITLKIPANTIKQGKERRTGRIGKRL/INLSLFTDNDCL*KIPKKQQQQKNTHTGKSNYS*VAG*KVN/SEKSIAFLHRSH*QLESEISKHL
552	6732	A	559	172	489	HDSTFITTPELKGHPNLSLSRFVCLCVSVCVFVVCVMGICECVSE*VSVCLCVRLCVTVYVSVCLCVCLRV*VCVCLC/VDCVCVREGLCVSACFDTRACSVAPH
553	6733	A	560	229	672	RPPPHRTAHAAKSNHGWVAGYKVNIKNQLLSYIEAINIWNLFKQFNIGNATAIKIPASYLVVPDKRIKFIWRGKVPEQPSK*GGRKTKS/GGVTLPTFESDSNTTAIRMVWDLNLRNPQD*NRIENPETDPHECSQLIFDKGTNASQ/WRK
554	6734	A	561	145	643	KVLGVTEHVFPFCVKGQGTGHQTSLSLDLSGP*GA/GP/GASSRSSPHSGLCPGN/QGADSPGCLGFYQAAEA/AADTAGSQGGS/GPGN/QGDPSPGCLGFYQAAEA/AADTAGSQGGS/GPGNQVP/SSPGCL/GFIPGCRGSADTAGSQGGS/GPGNQVPTLQ
555	6735	A	562	59	437	PWRLPT*PCRRFNHHCDPST/RGLSTPTSPGQRSPSGPTTF*PLMMAAPQQRHSWPRLPWPAQSPAQSSTAEGEEKGPWGVWPGNTGQ*TSASAAPCPGSGDNASPTAAGHLSQPWHAAGTGLVSL
556	6736	A	563	1	335	TKFDKHLKFFWKCGGSKPIK/SILSSQIGGPTL/PNFKFYHLPPVTKTAWGW/HRNKPIQGHKPEPTWVYVHIFNTGPKVHSF*RLKGLFNRCGWHRNGCWHNFFFWAKK
557	6737	A	564	11	376	YEKRVLSYIEAINNWNLFKQFNIFNATAIKIPASYLVTVDKRILKFIW/SRQRPRANKIGREENKVRGVTLPTFESDSNTTAIRMVWDLNLRNPQD*NRIENPETDPHECSQLNLCLCRAWPDST

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isolucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /-possible nucleotide deletion, V=possible nucleotide insertion)
558	6738	A	565	88	307	QEAEMGTACPALQGGRELSGEKAPPS HAANSDDGPHLLLLRSSWE*RNTRWFP S*SPGMDTGSRDGDGVPTPGAAERAP GEKAPPSHAANS/GWPTPPAPAKQLG APPPPAAGNRGSQGRCDNDPNPATP LWS
559	6739	A	566	3	368	KEIESVITNF*TTTKSPGPDGFGEIVQ TTF*KELTVLEPKLSKNIDEDGTTLP SAVSMTPPKT*QENHRPVSSTVSDA KILNGLRAN*NQQRTERIVYPGKMR WIPEMRQWERT*KSV
560	6740	A	567	1	208	SPPPAATFSLYRETT*KDFLHTPAPP LSCCLLGPRPTTVPFAPHS/RPLPGHR RPALAPPTLPPEELFW
561	6741	A	568	51	350	DRLRDEPLFAIVGQDGGKARLEKMA QQRGLRNMQFLPLQSYGALPALLKM GDCHLVEQKRGAAYPVLP*KLANIV SVGGNAVIADQAYTEVQLCET
562	6742	A	569	6	349	FRCYHIATVSKTSWCLHGNKHIHE*H IPETTCVYVHIIFNTVPKLEHLNVDGL FNRCWVHNR/WLAQLHSSMCRIMK LDPLCTPHTKLSQMN*NINVKAITINT FYEHGVNSS
563	6743	A	570	3	332	PTLPNFRFSLIATVSKTAWCWGH/NR HIHQ*HRPETTCVYVHIIFNTVPKLEH LNVDGLFNRCWVHNR/WLAQLHSS MCRRMKLDPLCTPHTKLSQMN*NIN VKAKPIPL
564	6744	A	571	1	422	TDSMAVPGDHGE/PGKPWRWP*DMP RTKPPK*/AGIIGMFHGGMAADIFS/P SSPEKVKSGPPGKRGRGEIKLMGTG PGVKEIFRPNPPGEGPKDKPAHPGK NLGF*KKGKGPVPRGG*NPGARGIP RDKPPKGVGKRG
565	6745	A	572	1	406	TVTRTTSKPRAYPWRLPT*CPCKRFN HHCDPSTVRGLSTPTSPGQSPGSPPTF *PLMMAAPQQRHSWRLPWPAQSPA QSSTAEGEEKGPVWVPGNTGQ*TS SAASPCPGSGDNASPTAAGHLSQPW HAGTGCL
566	6746	A	573	1	644	RSISLRIGRYEILPYLNTTPGPINRL NPSPQHRLLWP/PSNRP/YPPPPSHVP SWLP/PLLPLAPLPSPHRKLRSAPAFQ PITKPNAAASANP/SYVQKLPPQ*RL PHLREATTFSQRPDPLGWSWPTFAAIS NVKPKCSLHQSRRAPHTHTAQAPHPA LFRVICPPLPYVTLKTTTS*LTEPELR GKANKPSSATLYPSHPDVQRRNTNLY

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
567	6747	A	574	3	662	AATTITNSRSVPGDPQDWEHPGRRTT YGGQLQPNFRFYHIATVSKTAWCWH G/NRHHQ*HRPETTCVYVHIIFNTVP KPIPFEC/WNGLFNRCWHNRCCWH NLHSSMCRMRKLDPLTPHTKLSQM N*NINVKAKTINTLNEIIGVNPDFGL DSGFLDLTPQAQATNVEK*DTLGF IKVKTE/CASKDTSRVKSQPTWWDKVR AVQCQKDLRGRTVNLVI
568	6748	A	575	89	336	EQLPMPSPRL*PSPA/PPPGPW/PWE GRKPPSSSLQSLHPCAPAGPRPLLLP PLQPRPAPPYGPVAS/PKPEPPLPGPR P
569	6749	A	576	2	176	ATANKTONFEVVAQYQDFGLRPSIA YLQSKGKDVGGWD*DA/GNGEARPSN NDVVRVT
570	6750	A	577	1	376	DHLCCALQLTNFRFYHIATVSKTAWC WHG/NRHHQ*HRPETTCVYVHIIFNT VPKLFHLNV/DGLFNRCWHNR/L AQLHSSMCRMRKLDPLTPHTKLSY MN*NINVKAKTINTLNEIIGVNP
571	6751	A	578	34	304	APVPPMGPFSSPFLGLESQFAGLYPK WA*SIIFQKETFLGGPSWIGPRS GYPGPPGLPG*/DPLFS*NSPN*PG LGSTG*PGGTPFFFKI
572	6752	A	579	1	178	LDLHGIIYYKDIRHD*RGFIPRMQGW FVIGKSINVITYH/INRMKGNKHLISDA *KAFD
573	6753	A	580	1	196	RPLCYPPSFFKGKTPRGGPPPGGFPQ LQIPKNSPPRGNRCLYTPRSPLEPLG PRPPV*NQGH
574	6754	A	581	104	376	TNGGEPFGKPPPGF*KRAGGPGGGVS PPPQGGDPTRAPLRAQEPQLAETQN SSSPKGPFP/PLPGKRLRPGKVFPPNPS NGKPAQQGQFCGW
575	6755	A	582	5	600	NFPSRLGRGVHPYTPPFKE*GGKTG FGGLSPTGPNGEKPLFFK/PNLP GP/RGPAPIFPSRRVKHEKRL*PRG GRVP*TK/SPFP/GPPGQGRNCPS SSSSSSSS
576	6756	A	583	2	630	DCGRAPLPTGTTPRPPLPPRLDPS PRFSARLDTPPRARVAPKNIPC*RP GPW/LKSQDAPSPFG/SPGVSARGALL PPPA/SLLCPPGVFLPSPPFP*ARRV LPL/LGLK/PPTPRVFPNGGFLKLG HGPISPPGLFLRLALVP/PPLGHK GKPPFPSSSSPARPK
577	6757	A	584	313	750	KPLTMWNLNFQINIFNASAIPASSV VTVDKRILKFI/W*QRPRASKIG/GRK TKSECHFPPLRLDSYTHGIRMV/W* /WCYNSRPDQ*NRIGSPETGPHESQL FFDKGTNASQC*KDRFLNK*C*NSWT APGKKRFLTLTQGY

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,765	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
578	6758	A	585	3	292	RIRSRYPATIDLVNKCKAIKLPEDNIGEHLGDL*IGGG/DFLNHISRA*SLTQGM DKFEFIKDKIPYSLKDCVQKMN*QT TDWEKIFAKHLSNKRLL
579	6759	A	586	307	745	KPLTMWNLNLFQNIIFNASAIKIPASSVV TVDKRILKF/W*RQRPRASKIGREEN KVRGVTLNL*SLALSQQSGWCVM CYNSRPDQ*NRIGSPETGPHECSQLFF DKGITNASQC*KDRFLNK*C*NSWTAP DKKRFKLTLLTQQY
580	6760	A	587	1	431	LPPLPPGVPSDSW/CQPS*VPGIGPC PPAWLISIFLPHFFSKPF*LGFPQVFPL PPLLKRGPSPCKPGCLLK/CPPPAPP PGGQN*TPFSS
581	6761	A	588	2	357	PGGGPF*MFPPVLCQGP*PQGEFKPPFS EGAGPFFQARSLVSGENLPFWKGGF PPSSSPTSSSSSPKQNFLLPKPQSN GPILGPYKVCPPGSPFPAP/PPE*VGP QGTSSPPG
582	6762	A	589	149	466	PSPPGEEKPPTKPGQCPHLGGTLKKN PEGK/PFWAGPVFKSSSPKT/TGGPQI KAVWRKSSPCSPPTPECCW/FFPT*F LVPPGCAGGRFVKGPSPHPRSTGIQ D
583	6763	A	590	3	484	IYCPSLYNVRDWQKPGDR/PSYAD*T VDSPGDSPGDSPGDSHGDPDPGDS PGDSPGNSPGDSPGDSHGDPDPGDS PGDSPGDPGNSPVGAGASLAPAPPVS GADGACLSASGISSPLSKSNCSPPSSS LLLVSYIFISFKKKNNHNIKERYIDKY IYR
584	6764	A	591	179	269	QILSPHTPEKNMTDPLAPHPRGQ/QTD PSAP/HPQGT*QILPHTPGDSMTDPL AAHPRGQHDRSSRTPQGT*QILSPH TPEKNMTDPLAPHPRGQ/QRGPREP
585	6765	A	592	1	353	KSCGSRMTDPSAPHHRGQ/QTDPSAP/ HPQGT*QILPHTPGDSMTDPLAAHP RGQHDRSSRTPQGT*QILSPHTSGD SMTDPLPPHPRGQ/QTDPSAPHPRGQ/ QTDPRVPR
586	6766	A	593	3	251	ANTIKQKERRGTRIGKRL/INLSLFT DDNCL*KIPKQQQKNTHGTKSNY S*VAG*KVN/SEKSIAPLHRSH*QLESE ISKHL

WO 02/16439

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
587	6767	A	594	78	1459	APVGGKSQVRSSPKLGWEGKSSGLNPP LSSAPPASPGGKEVPSQLLKKPNQK SQVRLS/DPLRTGRASPAFFPKSRGGE GEPGSPAQPRASLIVLPPTQLRMMMLP LTRLLEFL*TGNSRPFQLQSLNSPCFL PS*LSPFKGG/HQFGKSGGTPSTPSY VCSSVSLDSVNLSSLTRVLAWHG CRGNCPCGCFPVITDPKILLGPRSPRSG GKGPLLARLPWVTNSHLGLPLLSL SFSLSPLFLTVH*VLWITPERMSQASAY HHIDPAHQH*GFALSPPLPVQSPFHP GPSPLYTQGYWSIYNNMVRPQCH*KSP GSHPLQOPRLLFILET*KDLLHTPSP/ APLFSCGLIGPRATRAFCPPQSPPLPG APAGKNCVHQPFLLQKELFWEGSGEP NLGPPPIILTSSCLSSPSVSSQAKSTC KSHYPYPRSSQNLTSSPDLNLTGSADTLS GASHTFYRP
588	6768	A	595	38	385	QWPWQSIRRHAFGRNGS/GGVTP/MP PFACESSPTAIRMVWGVDVNYSPA* LRIEDPETDPHECSQLIFDKGTNASQC* KDRFLNK*C*NSWTATDKKKELDLID FRPFTKSY*QWIMA
589	6769	A	596	82	412	QILPLRTPGDSMTDPSAPHPRGQ*QTD PSAPHPRGQ*Q*QILPPHTPGDSMTDP LAAHPRGQHDFRSRTPQGT*QILS PHTPGDSMTDPLAPHPRGQHDSFRP APHGDTG*QILSPRTPGDSMTDPFAPHP MGQDDRRFRAPQVTA
590	6770	A	597	1	422	PTPIPTP*PDFAHPPQSRPCPPPKTLP GPFPSPPLSDSPQTPPTNPSHTGPG SLTTRASSRRHRSHPRPLVTPQPP/SP NARLPSSSSSSSSSSSSSSSS
591	6771	A	598	1	135	IYCMGADGLQLYSSGKTQSLSVNVG GRD*VHAGTMENSVIQGGT
592	6772	A	599	3	249	ANTIKQKGKRRGTRIGKRL/INVSFLT DDNCL*KIPKQQQQKNTHTGKSNY S*VAG*KVN/SEKSIAPLHRS*QLESE ISKHL
593	6773	A	600	65	407	KVNMKNQLLSYIEAINNWNLFQNF NATAIKIPASylvTVDRKILKFIW/SRQ RPRTANKIGREENKVRGVTLPFTFESD SNTTAIRMVCDLLNNRPDQ*NRIENP ETDPHECSQ
594	6774	A	601	3	251	ANTIKQKGKRRGTRIGKRL/INLALFT DDNCLYKIPKQQQQKNTHTGKSNY S*VAG*KVN/SEKSIAPLHRS*QLESE ISKHL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
595	6775	A	602	1	577	QNKPSW*AEKKGHAHYGPETFSKAV/S YPPGGNNRSSAPPTTYTRQIKGL*AFIF RPAPPTKKPKKDF/PFSKTEGTFPPPF PKNFLPFYKRKANRVPISHNHNHVPF KKF*WLWYFPKSPPKPHKPKCYHQ/H VKFSPKGILGPVVPFSSSPKPKPSRKT VKPKVS*AIDMIPGUSHSSFFQKSITYCI KRTFEP
596	6776	A	603	2	579	GEINLPPLIFPRANPPK*GFKLGAPK DPPPKKTRFETPPPI*KPSSFQWQMS APHKKTIPSPYNTGPHLPSSPLPSFLF S\PPFPGGGLNPKGFLWFKKSYPPKS SSPPLGAP
597	6777	A	604	1	233	FRNGGSQVIDYSVVLSSMRKRILRDY LSRCLGCGKKISEILSPRADYVRRRL RCHSIRGAER/VVIDKNK*ELSDNHL
598	6778	A	605	3	695	PGFQSCRRKTTTASDPRQFPFRRP RKRPLLNAMVGLTAAERWIESGYVV KWMNQKIQFPDFLLAFKTFLLAILS AIFVMLAM*YVITPFGGWINGGIRTV LTAAGEKGLMYAMGLAAATAIDL GPINKAAGFVAFSFTTDHVLPTVARS AIVIPPIGLGLAITHDRRLTGIRLFAQL YPQGKTAMFLAFMGISEGAIFALESP ITAIPSYMVGAIVGSA
599	6779	A	606	2	539	FELQRKQAFRAPKPRGF*A/DYNPMIR VP/AASE/FKGYAPLEL/NGKVTARFL/ DGKTV*PTNQAQKGTGVV/LEQTPFYA KSGGQVADKGELKGANFSFAVEDTQ KYGOAIGHIGKLAAGSLKVGHAVQA DYDEARRARIRMNHSAATHLMHAALR QVLGTHYSQKGLVNDKVLRFDFSH DEAMTP
600	6780	A	607	1	550	RQQQQAQEDAQSA/RQEWVSM/LMD/R HGPSRLVFR/NPRNG/VKGFNPPELAP L*L/LPPQYQPAIKVSGIMGARKSAE DRARDMLYPERIQEFEGDTATWNN FDPVVEWLMGYLTSHRSQKVLVICA KAAALQLEQVLRERREGIRAAVFHE GMSIIQRDRAPAWFAEEVTAQVLLC SEIGYEGRV
601	6781	A	608	313	776	KPLTMWNLNFQNFIFNAAIKIPASSV TVDKRILKF/W*RQRPASASKIGR/K TKS/GGVPLPTFESDNTTAIRKGG*F AKINRPDQ*NRIENPETDPHECSQVI* DKEPNASQC*KDRFLNK*C*NSWTAT DKKELHLDFIPFTKTY*QWIMA
602	6782	A	609	3	561	RPPNTRTPTIS/YTFPGGPT/PPGGLV FKKKGGAWSPPNAPPGVPV/PTPPR WAPPKF*NSPGPM/ATSLSPFSGKF GGGPPRPVWVPPSPW*NPFPKNS KNIWGLRPAPVIPPVWEGKAGKFLP PKPRVPLSKIPPPVPRVGKTKPFSSS SSL*EIILLVASWRNGKRSRHLPRGK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						KP
603	6783	A	610	56	639	RQGRPRFPGVPSKDSGPOKRAPQCKT QPGDPPSPPGVKKGPPAGRRGPSP F/PPPGGGSGGGPQAQKLGPPRVPRG KPVFFSKSSSSFPQSK*TPIIPPFLGG*A RKKA/RTPKKRPPN*LKNPPSSSSGGQ KEGPFSSSSSPKLEAEPNG
604	6784	A	611	3	418	LFLPQEGSPRPPLKMSGKNHPPQGLG T*ENPSPGKGPGAFFPQTLGF*GEIR DLGPPPGVALKQVTPGAVSPRQDPRV HSPQPLSCDKKTPESTASD*PRPSPL QHLIG/PGPSFIGNNQLEAAKGHLGVL PSSFGF
605	6785	A	612	3	629	FGPARGPQSKDLAPELPPFSSSSSP GRGGPP*TPLLGPGPGKISLPQRGGST EFKFSPPPPRGDDKNNSFFKPPPKFF TPVFLGKIFGSSSSLGFPNPLGGDSS SKPVPRLGKNTLGGQKPLLPDPKPLI PPNNGGLAPKIPLRGGGV/PKKNFP SSSSPGSSSP
606	6786	A	613	1	635	RNRAGTSLSPFLFIITLKIPANTIKQGG ERRGTRIGKRL/INLSLFTDDNCL*KIP KKOQQQKNTHGTSNYS*VAG*KVN M/QKSIAPLHRSH*QLES/KFQNFNAT AIKIPASYLVTVDKRLKFIW/SRQRPR TANKIGREENKVRGVTLPFESDSNT TAIRMVCDLLNNRPDQ*NRIENQKQT P*CSQLIFDKEQCK/QW*KIVFNRRVD K
607	6787	A	614	312	775	KPLTMWNLNLFQINIFNASKIPASSVV TVDKRLKFI/W*RQRPASASKIG/GRK TKS/GGVPLPTFESDSNTTARKGG*F AKNRPDQ*NRIENPETDPHECSQVI* DKEPNASQC*KDRFLNK*C*NSWTAT DKKKEUHLDFIPFTKTY*QWIMA
608	6788	A	615	312	749	KPLTMWNLNLFQINIFNASKIPASSVV TVDKRLKFI/W*RQRPASASKIG/GRK TKSEEGHFFTRVDFTTARKGG*FA K/NRPDQ*NRIENPETDPHECSQVI*D KEPNASQC*KDRFLNK*C*NSWTAPA KKRFKILTLQGY
609	6789	A	616	49	632	FSQKGPVSPSPVPGKPPRPKRAP*LL PPENPLSPGENRGPPRPGGVAPPRIPP PFGAQSQSEFPFGN*TPPG*QG*PSSSS KSQKKYPRGIGR/PLFPFSGG*SRKN PE/PPKRPKPAIKFKKPPSPPTGGIKKEGP FSSSSSPKLEAEPNGLIWWFFHSGR/LP SPSPAPFLSAVEEVENPKQLLEGHH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						LLTL
610	6790	A	617	2	488	VSIATRVQDGIQSEGEILQACVCSAC GNCGMSSVRDSCLVCAKPSRGE*GV GEVGP/ESPSGRPFLSAIPSSQASCGP EHGEGARGPPGRCSFCFRVSSVSLAW NSGRFPGVFWQTTGGPRAVAESA/WVP QSPAGPPLMTGPPTNLGKAAGNG*K GGALVPD
611	6791	A	618	2	649	FFSAGFGGSPFFLPYRSAPRPLGKPLFF *KKIKPPAGGPPLYSPPSGPPSEIFFY PESS/PPPSP*NSSSSSSGGPKPS/RPF*A SSPNFCPPIFGGIIFGSSSPLFPSSSLG GNSSSPTPSLWEKPLLVGPQNPFRGF QTFFPLPWGFRPKNFPSPSSSFH*PK FLSSSSSGGPRPNLSLSS
612	6792	A	619	1	639	QKPPGPGIOPGKGPPVPSPGP*KVS PRGKNTPPPNFLFGPPNLF*KKNP SSSPKPNPFFWGPLFPSSPFKSSSSS SPGPF/GGGKPGGKPEPFF*FTTPKK GGWGFGKASSSSSSSSP
613	6793	A	620	2	250	ATPIKQKGESEAPRIGKRL/INLSFTD DNCL*KIPKDHQOQKNTHGTKSNSY* VAG*KVN/SEKSIAPLHRSH*QLESEIS KHL
614	6794	A	621	313	776	KPLTMWNLNFQINFAISAIPASSV TVDKRILKFI/W*RQRPASASKIG/GRK TKS/GGVPLPTFESDSNTTAIRKGG*F AK/NRPDQ*NRINPETDPHECSQVI* DKEPNASQC*KDRFLNK*C*NSWTAT DKKKE/LHLDIFPFTKY*QWIMA
615	6795	A	622	68	437	REKTPGQAQGSMLAGCL*RSRNRAR TFLLPILFNLLKVPAYPINQKKGR ASRHWEIKLSWLPDDNCL*KIPKNH HQQKTSHGTKSNSY*VAG*KVN/SEK SIAPLHRSH*QLESEISKHL
616	6796	A	623	286	361	QILSPHTPGDSMTDPLAAHPRGQHDR FSRPAPOGTG*QILP/PPHPRGQVTDSS AP/HPOGTE*QILSPHTPGDSMTDPLA PHPRGQQTDPSPAPHRGQHDRSS/PP HTPGDSMTDPLAAHPRGQHD
617	6797	A	624	42	645	FLFTQNGPQGFPGSPSGAPKPGPK\ KGP*G*SPGPNLPSPGKKRGPITPGK GVPPNTPPFWGPKGKGGGQGRGFVP PRGKRKSSSSSQKASSPPGLKAAPFI PPSLGG*AKKKGGPRKKNPPT*KASS /PSPGGQKKGPFSSSSSPKLEAEP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
618	6798	A	625	3	421	QALGNRGVVSRRGWRPGRWRGRGSKPKDRLPPAPRKRALVSVGVAERA VHEPTPLTHETFKALKPLGSA YADVEKSAQGIRELLDVAKQDIPDF* KATPLILK/ATAGLRLLPEKKAQR* LA/KGKEVFKAWLFFEGNDW
619	6799	A	626	3	387	GLLLRV*LLPLGVAPP/A*VWPLP*GVAPP*GVAPPLRSG/VLPEVWLLPLGVALP*GVAPP*GILLP*GLAPP*GVAPPLTSG/ILP*GVALPLSKLCMPLSQSSHSRSCHYLPQRCSNPDSGIACCLKTCLF
620	6800	A	627	3	433	LCESRSVQOMSKFKPSVITRVDYSHVSLGVKCSKEVATA/IRETILANLSNVP/VRNRN/RWGSQH*QHTVTP*KVTGC*GSVQGDPIPHPDILDTVSAPVPMKLG RMGYNCYHLARDRTS/LLGNFAKAIN*ATSKTCSLRTSTSG
621	6801	A	628	399	0	GPPSSPQGSSSSKFSGRPWVPPGAGS/RSPGSPATPGPQGSPLPFF*STTFQIGASPLSRPSPSPFPFPSSSQKRGQGP HASSS*TSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
622	6802	A	629	9	581	SSNCSSLLMSEVVECVSESVVMDGVWTRDLSSGRNRPSP/PSRQDSRQT PPGSECPWVGCLCTTPGGPQVAPAS* PPPRP/PGKKPGSLGMSSPSAKVGPVTSLPW/PPRSLGSLARTASPSRPPTAHPSAAPRTLWRTTPGKSP*SLPPGRWDPNISOVFPP/PSWPWKPSPAATRS TRRKPSGSRP
623	6803	A	630	15	434	SELPGRFRFRSVTNLCHEAWVPAVSSF CFGRVAFAGYPIFGTALIPCSGERGR/PWAAHLFLGGCCCLPKP*CLCPFSGLRLGCGPLDWSYLQLAASGAATAYSSFSAYCVFRILMGMTFSGILNSVSLGSPVEER
624	6804	A	631	171	438	RPKPOSTAGKPGKEF/PVGKKSFCKGPTG*LSFRGKKGAKRGNLPPKGGKG GPCPPGKEGAGTKGIAPPTRGSLGGKKFLKGERG
625	6805	A	632	84	433	LGDGDSEAE/PAQGRSTGVHGPWGP RQEQVTSFPPFHPACSTSPAGSGLSLLHGLPREGPALPA*ERSVLKAQQCSAGL*AVGGGGGASGQAGDRGCHIA*EAGRSPAQEEVASEGL
626	6806	A	633	86	441	AGSIHSPENKRSHPQAGSRLGAQRT PESWRRGPD/PPSAPSRPPPTMEPG WCPALHSRLPLPSSLQSTAGLRLLPSAENE*ITEPSITLPLTNCPLQGGKRGPKGRPGNTRPVG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
627	6807	A	634	2	2029	LKEHT/AWLLMEYCL/GSASDLLLEVH KKPLQEVEIAAITHGALHGLAYLIHSH ALIHREDIKAGNILLTEPGQVKLADFGS /ALSMASPAANSFVGTLY*LAPEVI*A MDEGQYDGGKVDIWSLGITCIELAERK PPLFNMNAMSALYHIAQNDSPTLQSN EWTDSSRRFVDYCLQKIQPERPTSAE LLRHDFVRRDRPLRLVLDLQRTKDA VRELDNLQYRKMKILFQETRNGL NESQDEEDSEHGTSLNREMDSLGSGN HSIPSMVS/YRQPEQQREQHAASHGA QSSSELVMMHDDDES TINSSSVVHKK DHVFIRDEAGHGDP RPPEPRPTQSVQS QALHYNRERFATIKSASLRVTRQIHE HEQENELREQMSGYKRMRRQHQKO LIALENKLKAFMDPEPRLKQKEVETH ANNSSIEVEKLAKKQVAIEKEAKVA AADEKKFQQQILAQQKKDLTAFLESQ KKQYKLCCKEIKIEMNEGHSTPKKE KQERISKHKENLQHTMQAEEEEAHLITQ QRLYYDKNCRS/YKQKIMIKRHEVVE QQNIREELNKKRTQKEM/EHAMLIRH GESTRELEYRQLHTLQKLRMDLIRLQ HQTELENQLEYNKKRRERELHRKHVM ELRQOPKNLKA MEMQIKKQFQDTCK VOTKQYKALKKNHOLEVTPKNEHKTS *RHLKDVRSVS
628	6808	A	635	1	416	FRAVRS LAVYAHDSPESEDGEAGIEA VGCAVDEKRG LVS DAYGDDDFSRIG GDEEGYDEEEDDNSEQSDHHS*TDK PEADDPLENSAQ*QRHPGLMKLMAQ LVGLRGQNNHILIMMRDVTQQPQLSL AAHTLHTTFH
629	6809	A	636	7	399	PRCPLLGR LPPPETKSPNPGGP/APTPP GQRGHRGVRAACRLLPN*PLYARIA APSVCVTW/PQAGVPRGPGSGSRPS LAASFACSSTHAASQSRSSPLCLAGP ARLPYNPPGPEHARRGRSRLSRPPPR
630	6810	A	637	3	401	MHILSPDIPWP LPRQTPVTALSHML AGSPIHFSYFYSSPYSLPVLLQTPSSAS GLPGFAPSGLHPDPSRPGA GAGPSAT ADPPNPLLA EYGL*P PHAQSSLPASPA SPA WLGPAQGPPSPRHLVLP LTPPR
631	6811	A	638	74	658	GPFRRAEVLARRSSEAAPSSSSSES LRNGFTPPPLPLPGAIAAILSCQECG RLPDWFRRAARIL*ASGDTAHLHSP GLTTSCLPT*ROGVRSKAGDPDAAAP DASASAAPAAALQASSRNRNRPGNR SPSAGTANGVS*ARPWQAGRRVPYR WPRGCTQCPVAGLGRGCGTKSRPDH EFWIRYVTRVQIAWF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
632	6812	A	639	62	481	RNSVPGRGIACAKALRQDCTWGAGG T/GEEAHVAGAE*GGER/GNNGGQGGD GAGHAGCPGPPGGLGL*P*GRWEPW RAVGRGGTGPDSCAHRHHVVGAVG GGTGGRGWEAGDHGRGTIVLVRAGN DQAGWGWKGNIGERWSN
633	6813	A	640	524	0	SPQGPFGVFPQPGVARGITPALGCPDSP G*GGPPP*PPSSGTPGLGPPSPAFFKF FGKKGAPHFTGAGLNL*AQGDSSSLP PPSAGIGGW
634	6814	A	641	173	416	GSWPRTCACHSSALHILSRYPQACK RTHNPVHMRGTGTQTPSPHSP*G SESPNDFPALLVEKLLQEHLEEQEVAP
635	6815	A	642	12	351	RWQSTGKDGFCGRNLGGWQEELAG THLSPKVATASEAGGCFLPEGSAPP*A GLS*DASPAQPPASAAKPPPGVPGPPH GEAHAGERPAPGVPAAPSV*VVSPAG LGAALCPRAS
636	6816	A	643	3	579	TRAQHYSAILRLFVEQLSHKTPDWL GYMRLVIPLGSHPVARYLQGSVDYRY NNFFQDLAWRDLFNKLEAQSVDQT PDIVSRITQYIAGANCAHQLPIAEAML TYKKQSPDESSQKFIPFVGVVK/V*F AEPSLVTTGDMDDAVPSGSGTLSSTP PSASQAAKEASPTPSSQTVTKRGLSSP SQCIASAKS
637	6817	A	644	1	491	QGAGGSWESPASAGAAASAAAGEAA PSPVARASQOREEESLQAQEQDEQE IPFRLREIMRSRQEMKNPISNKKRKK AAQVTFTRKLTLEKAKGEEDIAVPKF KQRKGESDGYIHRMQQEAQHVLFL SKNQAIRQPEVQAAPKEKSEQKKAK KA*VEAGGGG
638	6818	A	645	230	935	SFPLRLGLLNSCPDGVASCPGSSYPFRS SSLPLTLTLESGLLLGPGSLTGR/TGVL GADPYGLSPSRASTGPGGAPASRHGV SHRPPAPVPVGPASS/PGPVAAVA* RRLREAVRRGGVGEPRGWGARGLA E*GARPAQSELAPSCVSPIRETRCPS GKGTS/PRVASELGHHPVL*RPASA EAGNRGRGSDAGHRPLHRGVPRELP SPLSSPCLA*RGIKRCFCCKRLRSRS
639	6819	A	646	2	237	DAAPDLNSRVDDFVLFQDEVTRRLN VTNRSDAFNMQMTQRKGTLSVNFVS V/CGVCQEGKDLFLL*FCTFYPGISWY EFR
640	6820	A	647	12	390	GHPHGNCLGPQKADQEGEQWNKEA AAQEAACADTPDKGEPPTPKTDAPRA WHGKGFFLLMPAALAAGDQADIPGF W*WGGILKLIL*SPSSH/PPQARGPQM DLMSELTRRHEKEPIYESDRDGA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
641	6821	A	648	1	431	FRPPHPSNSRGF*EAKEPSPAC*NKIP NWPNRQV*HLFFMSSSPAREPNFV PQPKGGGIPGYWKPPGSKFESG* PPKEVGLTAPPRFGGRLEKPERLTPA WQKGSLFMGPPKSIQPGV*NGGKG KTGVPVNLNPLWK
642	6822	A	649	190	401	EKKAHWGPLGGGPKGDFGLLEPLPP GLKGF/CPDPPE*WD*GGLPPSPRNF LDF*KKGGFPFLAGVFSNP
643	6823	A	650	190	404	EKKAHWGPGGGGEGKDFGLLEWPP GLKGF/LCT/LPGKWD*GGLPPCPINF VCFKKKGVSF*GPGLV*NPE
644	6824	A	651	14	420	FLFIPINFPPPGFKVPPPCPVKPP*IF SPPKKG*KPPVGGNP/SLNPPPLGLTS SSPGSSSRPRTSSSPGWKRLGNKFA FKPHPPGAKPSSPSL*KKGEKRGKPP SRPSSSSSSSSSSSSSSSSSSSP
645	6825	A	652	2	439	FVPSWSQLSTSPTPVAAAASSLNHN TPPSGRLKEGALDELHILDPTRHQLLE ATFTGVA/SGSTGSTGSCVTGATAST NNESSNHRFGGSGSLTDESEKQLAL S*KDCACDGLTSAVGSLETPEKRHSE SSRGRPRHAYDPNDR
646	6826	A	653	98	412	FFWAGGGPPLPL/CLG*GGKNFVGL GRKKLGGDNPMAPPLGEKKGKSP/VP SSSSSPGPFPRGGSSPPPIKKKGASS/ PSPPPGGGPF*KNF/WGPSPTWSPPP
647	6827	A	654	2	550	KFKNLVPTLLYFNHYPKDLSLLSSPLI HCPYAH*TGPPQLHI*KRQIS*PAPP FATISGLPARP/GGTSQSASPGQIRPS K/PASVSTNLGSPRSADPAASSPSEV AGPPERATNFPLSPLEAEPSCGDPFP FGHKGGCYPRQISRSHSWRIASF*PH GQPLDTRPNASSPSPPVAR
648	6828	A	655	1	357	GGQRIFPPHPKGGGQRPAPKGGKT LGSSSSSSSGFPLQGQGA/TNPAPRG PSSPGLPKRGGPGVNPAPGPPNF*WP GKFF/PQGFWTSSSPGASFFLKRPKP PEIPGLPSFFYCQK
649	6829	A	656	2	424	YTIIVTTTSRTQKGPQSPVFDGVYN NSRMLHLFTAGGGSTCDVKVKNGT YEGIFKTLSSKVELPVDVARRAAEP TCGPRREDIVDTMVFKPSDVMLVHF RNGDFNYATKDKFTDSAIAMNS*VN GEHKEKVLHRWEGG
650	6830	A	657	1	516	GAARAQCGCNLPAPVWHR*GAADG WEA*GPNPPRASQFRGRDGLWSS RTQKKGSPG/RPPSVQRAGLGSPERP PKTSPGSPRLQQGAGLESQGGQPEPG AASPOGQKQPTPGSRQSTSSQSYSP SPRCQKPS*GGTKVFSGTRELLGLG VGP*YGGADPRPGPSIW

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/09519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
651	6831	A	658	1	421	PTLFSKRLRGMALLPISASSPSPKPTA SPPKLAKRLMREAGTLRSRER/P/QLG PGCLPGTGLPCPANVFSRPLPGPSW *NFWAQEPHPGQORWGPGRAPQGG PTVWPSCPVPVKVGPPSETLP/RP/PW LNPPPHGFQ
652	6832	A	659	418	426	YRE*VFVTHITDKGFISRIYKELQINEE KSENQKRRTAKAEKALQKQTVPSCLI NMKKYAVSK*VQIKTFMR/YWYTPIG LAEI
653	6833	A	660	461	0	SSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSRESGASVW SFPPPPVPVPSIS/QACSPDL*EEPLKP N*TSAFSGPNAPKAS/QPSGHGPACP P/GLQAKHPSPPCVSPAQLDPQGSR NRRPGFFSPVPA
654	6834	A	661	2	392	FVASAVGAGSGPWSAQEQFPFALM SFFIYNPRFGPREGQENKILFYHPNE GEKNEKITNVLCDIVQLTR*YL*A CL*RSVNSYNCCWRIVPNIFF*PL*TF SPSKPA*SLHTQKNRQFFVDPEENL
655	6835	A	662	1	548	SRNSHLVEHWRHTGQKPYKCECD KVFNRNNSNLARHQIHTGEKPHKCN ECGRASRECSGLTHVHTGEKPYK CNECGKNFRHKFSLPHYQRSHTAENP YKCNCEGKVFSVLRYLARHHIHS TEKPYKCNCEGRAFHKRPLMAHLVIH TGEKPYKCN*NKVFGRKFYLTNHE VVPF
656	6836	A	663	2	465	DLGTWLMASGRRTGEGSVQVFLQAH LCWSTPGGPPGQKSLKDTREKGD GRSRQAPPLGNGTLTPSPHREPLPH GGVORQGWGLPRCPSPG*G/PPAQT VALERTSGSORPLPKFSRPLGLSVLL SIIFKSSPLFRKYKVHEVVDGTGIRAC
657	6837	A	664	3	416	THEFQCRRLRGNGQLPCPSLWSP CNTCPAAPAGSPGGRGVSCAAGAST HVHTHPHPPPPRCCTP/SPSSPPGP/AA SLTMSSSPRAASLTLP*CTFLQEDM AQMLGPLGRPGSSPQRCPSLSLPMVS SCPERWMN
658	6838	A	665	26	437	PLPSA*AHSSGGNRRRAALGR/SPHLF LPPL*PTSGEEVRKWRNLPRFMIRLVP VTSQFPLGARPPRGEGAPPEHSQGS QARPRPSRLARSGRRTHEPLPTTW/W TVPGPQGRVALPNAPPTPTCSRAL PTKSS
659	6839	A	666	1	438	STTPVIPGTTSRGAACGQ*GGGQHH LP/CISGSWHAIGTSCGS*AWTWCRSS TATSTATSSLSWSICCTPISPPRAPS CWASPMSPISITSTSCPCAGAGAST RWCGSSCSSWDLACSCCWPARTTTS ACCASSLPATASSLR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,513,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
669	6849	A	676	1	387	PWSRPVGEPEAGWDYAQWKQERE QIDLARLARHRDAQGDWRPWLDD KAKSTLQDCSQLRGEPARAGSRRG PRSHQKIQPPPL/PP*WKRSGRASQQT LGGTSHRQQSPGQGEA\AGRARRWD MKE
670	6850	A	677	1	386	KTRKALIPDFTGATLAGDHSW*GTLF L*G*RTSPWSEPRP/PSYPPPLSP/CPAA PEAGRPKQRELGLTAFTPLSGPSS QGGGGRROPMSGPVGPQQR*GCG PAKPLGLHLLKGDITPLSMSEPLY
671	6851	A	678	3	378	CCLQETHFTYKDIHRLKGLEKPELLFF HTNRSQKKRAE*LYLMSGKIGIKII KRQGHYIMIKRS/VQYKNYVCVYLS IYLSHPHNTGAPRYIKQILSELKRDPII KKARNQTKTEKSQRESV
672	6852	A	679	2	411	HPLCFYADTLKDPWQIQLPASQHL SLGSPMSILGLAVGGWEQWNSRCHF VQGVTSCHLSVPI*\QPEDIKALSW NRQAQHILSSAHTPAKAVVWDLRKN EPIIKVSDHSNRMHCSGLAWHPDIDN HVLRLPL
673	6853	A	680	405	24	PGLKGRGPWANGA/PSSPG*RKSPG L/PSEEAAGTKGPPNPPQILDFWKKRG LTRWPGRAQNSEPMGTPLHGPCKGG E*RNPPWRAQKK
674	6854	A	681	99	378	GNGVWRPPKREGRGPIWVNGKLGPR GPPQAPA*PPREGGTTGAPLPQ*IFG FLKKNVPPNGQGGSPDLGTGPGT TPKGGNNGDPPPA
675	6855	A	682	3	453	VRSDMNSNPLDGRYRAPPAAPAE AGASSQP*SPPAAQASGKEGGENNAP LFQ*TPLPTTDTLTSVP/PRAPVPPSD RFLRSRPPGPRPSFPLRQGGGAPH* RGSSATPTPPA/SAPGPGVRSPLPRRW WTPIRLKKPWQKSADPSLQ
676	6856	A	683	4	233	FFLRQRTKQGCPLLL/VLAKAVRQE KELK/GIQ/MGKEGVNSLQGDIFICHY KEFTHTQEIILEINEFSMVTGQKTNIH* PVVQDN*IGENSHFNKCCWQKW1*TC KRMKHMIDH1H*K*QTEILEINEFSMV TGQKTNIH
677	6857	A	684	29	440	AAAPANPLLYTELALWPGAPHTC/ RCPSTSPSPSGALLELPPTTRCLISALIP APDRAQGCFCN*NRGRYQG*CGC CAGVSRAA*AGQAPGPCVPAEQWR WPRPSGPGESRRKTPQNPPPV/SA AVEFPH

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678	6858	A	685	280	800	KQLFVLARTIRQEKEIKDIQIGKEEEV KLLLFDDMIIVHLENPKDSSKKLLGL MNEFSRVSGYKINVHKLVALLYTNS DQADN*IKNSTPFTTVKNNKIKYLR IYLTKFVVLDLYKENYKTLK*IRNTN KWKHIPCSWIGRINIVKMTLPKAIYK FNAIPMKIPSSFFTEL
679	6859	A	686	387	1	LFRRSI*QSFQFKGCKLKNENCCVRFN R\NRSQQRSFKKCLSVGMSRS\SVRFG RIPREKQR\MLVERQASAMTVDSQI.S SQCPLETSNQLAMPGPMGSPPLDA VPSPLVGFSGQFPQMTTPRSPSLY
680	6860	A	687	56	533	GLITDPL.TSLIGCTFTKGKSIKCFVTL CQKYEPVRLARGCGTYHSNYNRAGEA *GSLKPSLL*LCM*ATVVHILEQRSET QSLKKNCDDLYISYKLNTHLPYEPAPH LGIY/PREIKAYIDKKTCTKMSVTTLF MVTKNYKLPKRCPSVGERINKLIYSSN
681	6861	A	688	3	348	PPLNWA PVPTPSLRPRPAWGPSPPLP PNWTPVPTPSLRPRPAWGPSPPLPN WTPVPTPSLRPRPAWGPSPPLPNWA PVPTPSLRPRPAWGPSPPLPNWTPV PTPSLRPRPA*GPCSTSPPELDSCPHAF PPSQASLGAVLHLPSTGLLSPRLPSV PGQPGGRAPPLPNWTPVPTPSLRPRP A
682	6862	A	689	2	264	LRTAGLTQRVRLFGLLKKLFQEKSSN RKEHLKGGGMSATMELATLSAFFGN *PIFDIPGRLYPVREKFCNLIIPDRREN TAYIQAIKVITMDIHLNEMAGDILVF LTGQLEIEKSCCELLFQMAESVDYDYD VQDTPLDGLLILPCYGSMTTDQQRRI FLPPPPGIRKCVISTNISATSLTIDGIRY VVDGGFVKQLNHTPRLGLDILEVPI SKSEALQRSGRAGRTSSGKCFRIYSK DFWNQCMPDHVIPEIKRTSLTSVVLTL LKCLAIHDVIRFPHLDPPN*ETEKILRI FKRL
683	6863	A	690	23	388	GNIGIDLANVFFPIVHQRQFAFRWQ GQQTHTFIVSPVCISSPTLCHNSVHGD LDYLSLPQNTLIGYIDIMLI*PSEQE VGTTLDLVERH/LRIRG*EINMPTIQG PSTLVKLVGTQ*HGACI
684	6864	A	691	3	428	ARDIGRDLGFSFSLSSSFLRLPRGPSLPL SLSFGSPPYSPPASSHKNSP*EAGPTL FPPTRECSGVPEVLMSTWTPRSVPG QSGQRRG*PLRPHSSQG*AGDAA/CTS LSCPP

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685	6865	A	692	78	1058	LSDKQRHELPGHPTGRPL*GLGRH LRGR/LS/AGTISIQVPLPKDSTGASKI PPKPHIVGI/QRSPDQARPLARHNPS\ RPVFV/VEGPFSLWLRN/KCVYY/HILR/ ADLLPPEEBGKWKRTPEEWELYYPR QLDLEYVRSG\WDNYEFDINEVEEGP VLA\AMCMAGAHDAQMTMVKWTQGL QETNP\ANLGPSPVVFPLRRVQGPGLP DILLQGWRSPPLPEDHP/EKEDDKPAS /EQQQG
686	6866	A	693	1	369	GRDALKSSVDAVKYFGKGTYTDCAT/ KKG*QLSGGSHLKENKYLIV/VTDG/H PEGY/KEP/CGGHLDEAGTSQLGVKS SRGITPDHL/EP/RLTYRTDHRPGTSGG DGPSRDQGAIPDHHPSGMSNN/VEQV C
687	6867	A	694	1	431	PHPEVGP/DTTQSSPVSISSGLTSDSYM VDSPVVTGVSQMAVASVMGSLSQSA TVFMSEVPNEAVCTMSSTAGPNQHL LSRDASQGLVLSVCTMGHKAFFSTG SSESLSMLPTNVSE*LVLSSTLVGGRK ITKTAMNFDPVYGG
688	6868	A	695	1	382	NTTSPYSVPVGVTRGIRGPNPCLDPA PFPFPFSAARAALLFTPS/PRPSAYPPRA PY*PARP/TTRGPRDPNYSRIQPRVRR PLSPPLPPGRERAR*ARVPFAREPRM RTPSPPWLR\AHQTTNQLNGS
689	6869	A	696	2	397	CPPSPR/HPRRGCKNSFFSGEPPGPYPYS SYPGHPNLLVPPVPRITISSPWSSCPFL PFTPGHPVYISTPVTSPQKL**TPSSH SFPPEV*VPRVKTVTYSP/PNVSP*S TLPSTPLLASPSLRPTVPVHV
690	6870	A	697	2	395	PEPSIPTPTSAAPSESPSELPISPTTA PRT/VHIFQLHSCARNGAAYWE*KDE *DIVFSLRDSIVQERRLAVKELTVSAG DNLITLTPDNEVELKAFVAPAPPVETT YNSEWNLISHPTDNQGEIKQGLY
691	6871	A	698	438	0	RAGANRVRFISYVFVYIKRDTTARGG GKDSL N*WSLTNWIYHM/RKNLKL DP*VIAYTK/INSK*MIGLNVKS/KTLY/ TLEENI*AYIYDFGGGHDFL/SWIQKA LLIKEKTEILDFTKIKNFCSSKDRSKRI/ NNKVGWEQI
692	6872	A	699	1	468	DHEKLFELILMEDIKFPRTLSSDAKSL LSGLLIKDPNK/RLRL*HKQKRQPVFM LELIVSFIH*WLWSTAENKFSVRISLG GGPDDAKEIMRHSFFSGVNVQDVYD KKLVPFVKPQVTSETDTRYFDEEFTA QTTTTPLEKYDEDEGMACMEWRSE
693	6873	A	700	2	233	VVLLSHPGA GRRSGCWNQGCPR*MT LMSSPLRMMMTIRKTAR/PYRCRMCS LTFYSKSEMQIHSKSHTEKTPHKCPH V

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
694	6874	A	701	2	478	QVEHYEFQTRQLELKAKNYADQISRL EERESEMKKEYNALHQHRTMIQTY VEHIERSKMQQVGGNSQTESSLPGRS RKERPSTLNVFLADGT/CTCTDRGQ ARACGGPLAPE*PRPAVQLQLPGFV AVPWSERLLPVAGVPRSLGREPLQA ALHGS
695	6875	A	702	32	408	LCRIKSVQVCFSSATVLDIGLLDVES*K LSTS/PS*LEKVLSPKVAGAVHLQFLT RKQELGYFECYSLVSAFIENAAKANE AAANSLLDIFCHYHRNCDLTGQLTRE PFILNDCCTNDLQ SILATRCI
696	6876	A	703	15	403	AGPSSPQ**YFCQ/YCDR/VYK/SATKR KAPIVKNHPEAELPPSIRKLRPAAGPGE PDPMLSTHTQLTGTLATPPVCCPHCSK QYSSKTKMVQHIRKKHPEAQLSNTI HTPLTTAVISATPAVLTTDSATGETVY TIDLLTHCI
697	6877	A	704	2	397	AGTSTPTQNPHPQHQLPLTPAAGGK VPELSA*LPPLPLHTT**KSGWTS/SPSPCP S/SPCSPANSFPQPLFSTMSMSIAPAPS PNDVLVPLP/PSPTPLTTPAPAPGSPADP Q*FSPLSQ/PSPTDSPDPGFCDDH
698	6878	A	705	2	849	TVLIVGRIAGVSISLSSIAATCVYIAEIA POHRRGLLVSLNELMIVIGLSAYISN YAFANVFHGWKVMFGLVIPLGVLQA IAMYFLPPSPRFLVMKGQEGAASKVL GRLRALSDTTELTVIKSSLKDEYQYS FWDLFRSKDNMRDPNN**DLTSLIFL YKHLGQPNILFYASTVFKSFGPQSN EAASLASTGVGVVKVINTIPATLLVD HVGSKTFLCIGSSVMAASLVTMGIVN LNIHMNFTHICRSHNSINQSLDESIVY GTRGTCQPTTLFRDHF
699	6879	A	706	1	400	KFFHEKACLTQHQRTHHTGKPSKCN DSERVLKESCLTPNQRIKTRLK/PREK NCKGNKCEKPFPEKLKHTQHQRRLH GKKNNGRNEGSPVQ/CRKSQLTQSQR AHKKIEKTYDCNKGESFCKKTDLR* HQSTHTV
700	6880	A	707	114	504	HRSDPCRCLPPECGLCCHKHCRDQV KVECKKRPGAKGDAGPPGAPVPSPT APHASCSEENHSYTL/SPGA*DWVP ASPCLDPD*IPTFLGNRYGPLPGDGP/ PSTASSKLDS*TSGLLSSSLPSPQS
701	6881	A	708	18	381	RRGPGSRVAACGVPAGQGHAAAPGHA GPWSGLYPGQSPSSQRLCEWGPAGG SAAGRSQDPAGQPPAGS*QSSSRPP EAAAPPPGSAQSGQPEPRGV*G*AGT/ TG*GGHVAVAAAGDIGHGK

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702	6882	A	709	2	382	IHGIVSAETIGHRGKEAWWQGGQRSTG GSECKGPGGGAASGDEGNAG*GAEA KGV/MHA*AKTSPGHTVP*GMGGGLD YPLQGQEQEPQGLNM*GLCKAGGSGR GDQEGA/GQRGQTSRPPAGVG
703	6883	A	710	3	601	QWKCWRPVEWLRQRYDSGEEVDLV KEADVPSAISLLRFFLQELPEPV/IPWP VYIFT*CSFL/TDYNNEDEFGRKLRFL LQQLPPVNYSLKFLCRFLANVASHH EEIWSANSLAAVFGPDVFHYITDVED MKEQEIYSRIMAGLLENYYEFFENEE EDFSSNDLSSITEQVNELSEEEEEDEK LEHIEELPEEGAEEKSNDM
704	6884	A	711	103	703	ELVWVRGPALLRCGW/WPAVAKSIFW VDLTLPGHIIWPEHLGPGSGLSWRLS WGVWPR*QG/MDRGGPSAAP/LLECE LPPEEGSGTNPIPTS GPRKQPGSGRCR ESRPHSAHRACQGGKHQNLPRNPSS TRPTQLPHSPFNSNSYPNTRFLFVLR QKSPITLSKGVAPRGVKDPPPPPLH PWSPPPWATACRPARGLSSQV
705	6885	A	712	2	430	RREVGPSRAAAYMAGTGSFLFGGVQ GPPEPVSVQVHPGKSGRLSGRKA GPRG HVVWPPSGDGGLSGTGTGPA GGEKP EDQAQLGHRGRAGTSGPGH*TGWA GMSGPRARCARGPRGQRVQTGAFS GR*KA*AEWTSQAGSSG
706	6886	A	713	2	396	IHW WENGKVFGMKCA GNSMGN SAG NPAGNSMGNAGNSMGN SAGNPAG NSMGNAGNSMGN SAGNPAGNSMG NGAGNSMGN SAGNSMGN SAGNSAG NSAGNDMNGT*KSA WNSMGN SAGSSVA NSAGSIWNSMGN SVWNSVRNCWG TGPRKPLA
707	6887	A	714	3	566	AAGRAGA QAPRWPGPRGYSRSGSPS D**RRPRDAPAAPPCPAGFR/TGDVQ GRVVGDWVFKVEICPHAAERIRPPA SAPAQPILSRA/C*RLPGKRESGLSSPA AQ*EQWIRLSSSLAT*LGSRSDSCSGS WIPREPRFASTSG WYSEDDPPEAVQE RHRRGPRAAGRSRLPRQRCPDADR N GPAAEMR
708	6888	A	715	187	429	PLKRLPSQVQPIPEDSKPWPASAPFM CKPHTLKPTPQQSLWSPHASGHHPLP PTPRPGPRQPRTYMPHRRHQITQAD SKP*RGCPPRS/RPIPEDSKPWPASAPF MCKPHTLKPTPQQSLWSPHASGHHPL PPTTPRPGPRQPRTYMPHRRHQITQA DSKP
709	6889	A	716	23	424	PSSEPVPPTGSGS/APPEPGAHLSPDF HPLGLTPPRPPTLAVLLSTP*AVWSLP APPAPRI RAGLLCACCRSP*APSLCA RGPVPRPRA*EATR VHQCMSPPPG WPGAPP

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710	6890	A	717	2	383	ACCSSFCPPKA*PC*LFRELCGAP*SSR NAWKTSIVSVLSFPVPFKQAILGT/PPF CRKQESIIRP*CTGCFSLWFRSRCLR ENERDEHNCVCESITATVTPRRWQ*S WQPDPGTKVLKKIQTHPTTV
711	6891	A	718	3	566	RVPELCSNFCLRYISC*TKGMIDLVIP DREGGSNSVSQDISRSATLADQPSWN RDHDDTASTRSGGTGPSSGGHLSHS GVNTSEQDGLDNSVASPSTGGDDDD PDKDKKRHKRGIFFPKVATNIMRAW LFQHLTHPYPSSEQKKQLAQDTGLTI LVQVNNWFINARRRIVQPMIDQSNRA VSGQTP
712	6892	A	719	32	402	STDLSMYPSSVHH*PLRLSIYIGSKDL NPCLIVH*PLHVYIHLSTDLSIYPTSVH *PVHLIHCPLTSPSIHLSSDLSVYASI YVQ*PLHLSHILSTDLSIYPSVH*PL HLSVFYPLGLY
713	6893	A	720	3	368	WVGVNQGCCYSPSYMDQPCLETVNR IKLYSESLVRYGNSPLYLYPG*DELP QVFARLSAIYGGTYMLNKPVDIIMD NGMVVGKSEGEYIPD/RVRKAVQFI RIICLSHPIMNTNYALY
714	6894	A	721	2	354	SPPFP*PRPRIPTLLPVRVQCSIPSRPQ /L*IPPFLLVSIPTPFPLIGLRALHSSP PAF*ATIPSHPPERSPRPAPRLSHQFG TRP/DLPPL*ARGPMARVPPAPPASPS SPSSSS
715	6895	A	722	44	570	CPAFRKQGLGGKSGQPGESSL*AFSE PKSAKQEGGQAPRAPGARSCTPPPA KS/ESPTAPVPI/ASSPRSSPGPSLRPTA APRALHRS*APLSGDSPRIQPGSGSGG DCPQHGGQKTPNAEP/SPRWRPRLRR DKTAPSSVCPSELAGPHQHGDLP SPKTA PPPPKAMPA VGMAA
716	6896	A	723	1	200	KDGRKRCVADVYCASDNHGCHECV NADGSYLCQCHEGFALNPDKKTC/SK *VTHCTHREIFA VTA/CDCHGTLS SID*QCHEGFALNPDKKTCTSKLHTH AHTEKYLLLLLW
717	6897	A	724	2	401	IQSCMCTSVCLCIPVDTCVHL/CDTC VCLCAA VCLHAHLCLVLCPLNEHL CVSGSACVSTCV*MCMPRHICTCLCL *LHWAASCLGCAQQASLKQVAMW RDSMSVSHLSPSWPCLSTCFCGKHR APEAGV
718	6898	A	725	409	442	LLPLKTP*HLPAVLSSPTDQVPADQIP HIRSSLTLLSLRPPSPGPIN*IPAARPT VSRTPLTRTSLTRPH*PGPH*QDLPDH IPPIMTLPGFDTDEAPLTRSPGNRLPVT RSLLTRPAVTRSPTR*PID*APLNRLL PLKTP

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719	6899	A	727	1	856	RPRGSRPGA WRSLLGPRLAVCPRARGRSEASETPAPAGARVLDTVRRKNSGSGQKEARGWKRSEGTDPSPRAELGFPPRTGVWPFSSRSRFGFSVKLRSLCLGPGAAA WVFHPPTTGAIPNSHLNATAHPDAAGLSPGPA/PSRYLTLPDPASMS*PLGAAGDAGVQHVGLSLLLPQGSPAQVRTTTP/DPAQAQVSPGIFSLPTQ/PSNLWTGPVAPPPTRRG/PTPPGV AQSLPTYAFVENRPPKHLRQALHSAQKAA M
720	6900	A	728	3	446	DDTCGDPPERPPDEGGTGTLRPAWGSW*VPGDWSG/RQEPAGKDVSSLDFFPNASDTCPHSKLPKKTQAPLTREAGKSGGGNEGLASESQNSYSGMRGGQGGGGEAGRAGRPGTALFAKLWGLESRGQMSESLPMQVRGKGK VAPVPEG
721	6901	A	729	268	597	RWVCFPLPSNSSVPHPQSHSFLIGERSLKSPISQDLDAFHSG/FQTCA/KEVLQYLSRFESWTPPREPRCVQLINLHAVA TQFLTPSV C* LQVPLSKGTGAPSAAGSAA
722	6902	A	730	100	401	THRAHVYTKIHHTYTDQRCR*AICVCVCRMPTCMCFCLQGVHVCV*VCVSPHGCVS VYK WVCMSVCKSACVSVCTCPCR/C/CMRLCVMSVCI/VHISASLCVVCVVCYLCVHV/CLCVSRQIC
723	6903	A	731	71	441	CGGRGVSVCMCMCARGGSCVVCVCS*/VYICVLT/CMCVYVFTCICMYVICAPV/CGGACVCMCGVCVCSVCLWRGIVHVCVCGVYLCVCMCM/LCPRVCMYLCMHV/CVCVCMRAC
724	6904	A	732	459	0	LCLILLAAAYTCACV*SWVIACV*VCM SKHVCEWA*ACVCMCVTMGKYVCEQVCKCECVSKHVCGREHVAHL*P WVDMEHG*VPVCVWV*ECVCM SVSMVECMCVSKGIFMCRVCTGSMCECGRMCL*MCEHFCTCLNTCVWMCIS KC
725	6905	A	733	45	423	LYKMFYIEVKLISLIKNNCKKEGSLKLLTVNNKKTNNTLGSWATDSS*KYKWLKHTKRHVTWFI*KNLQIRIMLKHHFSLIRFLIRISLSMILQSDNDFAGEKCG/E*STLIHCW/WDC*MPQL
726	6906	A	734	3	416	YTAAISECDLCVKTKRDLLEALQRAQDV/VFTRKKMSSDISLEKDNNEFLTEQLSEARINTLKSKLHDTRNSLREKVLV L*SVQKDL SQ/RKSGKWDYVEERISQLQHENLL LQQLDGAHKGDNEQEVINIQGCWLEN

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727	6907	A	735	33	775	VMGPAPAGEQLRGA TGEPEVMEPAL EGTGKEGKKASSRKRTLAEPKAGLL QPVKLSRAELYKEPTNEELNRLRETEI LFHS\SLRLQVEELLKEVRISEKKKD RIDAFLREVNRQVRVRVPSVPETELTD QAWLPA GVRVPLPKCPMP*ACFRF LAPKPRITVCEASYLSGQFSIRPDINV DVALTMPREILQDKDGLNQRVFRKR ALYLAHLAHLAQDPLFGSVCFSYTN GCHLKPSLLLRPQ
728	6908	A	736	3	397	AIQORTLLQDFSYDESKVEFDVDAPS GVVMEGYLFKRASNAFKTWNRRWF SIONS*LVYQKKLKDCPTVVVDLRL CCSVKPCEDIERRFCFEVLSPTKSCML QADSEKLRQA WYQA VQASIASAYRE SPCI
729	6909	A	737	690	1132	LPISLSSGDWICTFCRDIGKPEVEYDC D\SLRHNKKGKTAQGLSPVDQRKCCR LLLYL YCHELCIAFPPEGPASIPYYIK VMQKPMDDVSTVKQLHKHKLHLYQI PDDFVADVRLIFQGTVERF*WN*WK VVAQVLWQDTQENLEAD
730	6910	A	738	3	403	APWPGLCLPAW\WPSPSEKO*QVLL PHLPELAQNHEFYKNADVRRPFTYA SLIRQAILETPDRQLTLNEIYNWFTRM FAYFRNRATATWNA VRHNL SLHKCF ARVENVKGA VVTVDEREYQKRRRP KMTGSMY
731	6911	A	739	3	402	DILLWLQKLVSVLQRVGC PGDHLFLL NHILRCPAGVSKWA VPFIQIKVLHNPS GVFFHMQSLALVMSRVGN\HELSLCA A*EPSEKRPSSSGRGCGTWTVLVGKEG EDEVEPA SGI LLNEDDLVTILAQCRR FL
732	6912	A	741	1	410	NTCLGMHLCT* TGM*IRVCTCAFAFY V*MYTCVHA YM*LLMCVHMYGCM S VSVQLCICMHL SYNCK\HTCLE
733	6913	A	742	2	488	TISARAPPEQNPAASGVAVL CVFQCL CCMTLCCLCVCV/CSHSFSLCLSVSVC FFFITLCGFVVCPCACVSLAEYAL*T TEL/CSCMAA CLC*TS/CLCLCLGHEA GC
734	6914	A	743	1	365	PPYEELP*LSNPPV*TTGLVPVPRPTP PRNP/PG/SPASPLQTLPEP*PSSPPS CG*PPNAPAPLPPLSRYPHTPLGP*AR PLAKTSCDSLPPSRTPIITVPHLGHDS PQRGREGEEEMGE
735	6915	A	744	2	385	IHGVCSTRYLKHFCKINKYNESGWLLL IVLDKVGKEKRR/DEFRDSNSQLKHHM NESKVSMSALMSHRCRAEMAENQK* DLILA VAE LQCKLNSQPCRP S AVK\VR A*IGKEFCLWTPMPT S ALPW FSSLWP

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736	6916	A	745	1	389	NTGILYLKRIIEVIHKFDNLDKMNHFL KTRTTTCPA*NR*FNSMPMRKGIELAI* TLPRKTF/PGPDGFTG/EVYKTFKEKL TPILHILFQKIEEGIFTNSFY/ES*LLSS SSSSSSSSSSHYRPTILMNID
737	6917	A	746	1	377	NTAGAGPGHCGSGTSCRGHLLTGGAG QVPROFQGEIMGEPGRGERRERGVKR KGE*SPKVRGRGGAPALKTTKSRDKP *SGSTRHPR/RPLY
738	6918	A	747	833	1148	KYTRSQASCSLPRRLGRAGPTEELG MPTQEVAPLPA/MRLRA*VTTPSSRQE FLSGRTVVRVKLGLPLTEGKIVLPGG EGSGPHVCPSPWIIERTADQGVVAE
739	6919	A	748	1	372	GTQHGRGEQSGGVPHHRSDDSAHSG DGASVFITKIIRGAAAAQDGRRLVND SILFVNEVGVREVTTHSAAVEALKEAG SIVRL*VMRRKPPAEKVMEIELKGP GLGFSIAGGEGNRHIPGVV
740	6920	A	749	27	340	TEVGLRAIPGALHPPLPGI*PCPQTWQ GSSPLPHQELPAPKLLVTSPKPGSAA *E/PGE*GPECPGSSRR*EGSPAPSGEP LPLSSGAGGTVREGRGRTYITP
741	6921	A	750	83	429	RRGTLAQQAAGPQGEAELEKHVVTE HGSEKHPAAAGGKS* TSAALGKSTA GPTDAGEAAKILAEKRLRLAQKQDQ EEQERLDKEEQDRLEREELQRKAEEE RLRVEEKERKLEWR
742	6922	A	751	1	931	GQSL*PQL*SPGTEVGLSPSPCCGC/HL RGALCASPPGVSSSEHHWFQAEALP CWDPGSESSPRIPGCRELQSCPPPTAP SAHTQFPGLGAKAGAGGPFPSWAL PS/STSKPKKGAGASCYPRPHSALT PSS***AGMARS*DPYPQGPCGSSFLA NTPMAAPPELLPPPAKQKQAGQGAA PGQRLP/SSSGMLPASTGAQGLPGA GT**SPGQALPQLQAPFPFHLRFGVG GGG*RAPTL SAAQGMCSGRVVEANN PPTISPCS*RPGTSA GPIPQPGGPLPFH RGCFSES GHREVLDGFIATLL
743	6923	A	752	3	418	SSPLAVPALSASSLSRAPPAEVRVQ POLSRTPQAAQQTALA/SVT*WLRQ KGQGRPGMWPSLEALCSLFAARSTG SQAQSAPTPAWEDTAQIGPKRIRKA AKRELMPCDFPGCGRIFSNRQYLNHH KKYQHIIHQYI
744	6924	A	753	3	376	HDQRTLAAAAAAQQLFPPGITYK GDSYPVQFIPSTMAAAAASGLSPQL QKGVHSHPIQINRLKGLSDRFRGNLD TFEHGGGHSYNHKQIEQL*TAHPGQ/ VQKTKVSPKKMPSTPQPPCI

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745	6925	A	754	3	399	RKVFAGQLVNVVEVRWMLGPASHME TGCGLFTDLLLTYYRWAACVRCVSFG GVCCC*FHQCALSFRGLYIFFCSFL RPGFWKASCPPSCTSPLLVFNNSKTG DDQGGVKFLRKIKQLLNPALYCGRS EFPFR
746	6926	A	755	630	342	STLGVVFDPRGQSDWTKFRAMARL HKKTDDSLKYLAFMSMCCRVRCL PSKE/EYV*NFLLVSVKEAKITKIRKF PICLFYVKFQYVANSTCQ
747	6927	A	756	2	478	FLRWSLDLVARAGNWDLLQLPLPG FNRLSCLSPISWDYRPAAPHSANFSV FSRRGFTMLARMVVIS*PREPLCPATF SFLSYNPCTTGGDFHLE/DFCYFVFET GRNARISLQHPSPSGSLSTSASWDC RHVLPPLRANF*FFYRSGLLPCCPGW SL
748	6928	A	757	3	361	RPQEAGVRCPGSQLPGPPPKQADLPD AKDSPGPQPTDPPASEAPDGPSPER AAMNGADPISPPQRVRGAVEAPGTPK SLIPGSPDGP/AGKPNRPHGGAAR *SRGVAGAPPKPSPCI
749	6929	A	758	85	426	SFIKINCPTS*VG/PIY*NDVVGECS/PS SSSGK/RGPGGPPFAPS/PSQGGEGFG MAPPAGTKGANPRSKKTKPPPKPG GGGPKKA*GRGPPLTEPGEGGKNHG KRPLFRPGGAPG
750	6930	A	759	3	392	YTCVEGRSTVQLSLAGTTPPQ*PRFPS TPRGWPPWKGTSPPLFSAAPSPKRPL ELPRFSDINHLPG/AGKERGEGRNLS AVQTQEKVPQGW/SQGNPRALLGLH TGPIPEPPVGIIIVRPRPCISICSSR
751	6931	A	760	170	365	KRVSIINYLKTVKKMLGN*V**Y/IRR IIHHKQPEFIPRMQDWFIIISKSTNIMHA INKRIKIHII
752	6932	A	761	169	367	KRASINILKTVKKMLGN*V**Y/IRR IIHHKQPEFIPRMQDWFIIISKSTNIMHA INKRIKIHII
753	6933	A	762	1	330	IHGRYYCEQLTFSFTPLSLP*FS/SQH HPPG*GQFPLSWSPGSPYHPVCP/PP QYPREDT*EQ/GKSGVPVPLTALHGS HPPWQGSNPPCRPQGPAGAPSPPSL CFSRS
754	6934	A	763	2	443	FPGALALP*SHQAPALHCGSSPEHPFP SPN/SPTQKPPSTAGPPR/RPPGPPL LPCSGSTPGP/PQTPPGSGSTPGSPRL/ PPPGSG/SHPRITQAPPPGP/PQAPPPG SGSTPGPPR/PPPGPPRLNALAPPQD QCIAAAREDSIRAD
755	6935	A	765	406	142	SSSEIEKINKTKSWFLKINKIDKPLTRL RKMGEGSNKIRNLRGDITVDTEIQR ISNYEQ*YVNKL DVLKLLQI

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766	6946	A	776	1	398	NTTFLETGMRWAGRTGRQDTKRKL WGQEGGS*SPGLPGAYGGSPGLEGW PEQ/RAGTKSPA/PAAAPMGPP*GKDR *GLGCEMKPGERRKLHHGMDFSV/P ATAQVPREKWEPIGNKADPKGGPG RSSYGKTY
767	6947	A	777	1	510	TISSLAQKP/NKPAVPEAPIA*KDPVPR GKLSRRSRVHRGLPEAEDESCRAFPVL PKDILLPESTGPPQEQMKGAGAPAR GAS*GLPSMCSRSLTALSEHRTGPPG LTTTPAPPDKLGGNQRAAFKSGKRV GKPSPKAASSPSNTAALFVASSSTMT GSKTKETDPSVY
768	6948	A	778	2	411	HPLCFYADTLKDPFWKIQLPASQHCL SLGSPMSILGLAVGGWEQWNSRCHF VQGVTSCHLSVPIL*QPPEDIKALS NRQAQHILSSAHTPAKAVVWDLRKN EPIKVSDDHNRMHCSGLAWHPDIDN HVLRL
769	6949	A	779	1	489	EKTFCESHGKKSFCQESHFIEHRTCT REKPCESNKYGRSFQK*QLTNSQIMH REEKPHFEGKTLVKSALTDHQSQSE KKLYVCSDCCKRFRCHSSVLRVHQSIH T/GEKPYQCNGKS*AKSNFSHHQRT TGEKPYECKEKRFSRVKPNLTKHQK THIGELY
770	6950	A	780	1	396	EKTFCESHGKKSFCQESHFIEHRTCT TGEKPCESNKYGKAFQK*QLTNSQIM HREEKPHESGKTLVKSALTDHQSQSE EKLYVCSDCCKRFRCHSSVLRVHQSI RT/GEKPYQCNGKS*A*SNFSHHQKTE Y
771	6951	A	781	2	452	KGRIRSAHMPVPTNQGVVPCAAGS WGQPG*PEERAPSTPSDDFGSAEGK DLSAKSLGYGSGPSLGETGWEARGG AGRAGTRHRPGRSREGGCPAGAVTS TGIGEAQQP/GFPSWVILLAAAPPVP GPAAPYNETCNAAAAILHWAGNI
772	6952	A	782	4	431	PAGLLVGLNVIAFFCMKGEDLDSQV GVDFSMYLDKGNSKGTGD/GHIT AILDQKNYVE/ELNRHLNATVNNLQA KVDALERTNTKLTTELAVANRRITL QEEMERVKEESFYILESNRKGPKQDR T*EGQALFDARKLLK
773	6953	A	783	17	391	PPDQEGNRLYREGFFKEAAAKNYDA/ IACLKNLQMKEQPGSPWQLDQKIT PLLLNYCQCKLVVEEYY*VLDCSSI LNKYDDNVEAYFKRKGAAHAWNA QEAQADFAKRLDLPVLVPPVSR
774	6954	A	784	1	225	VLVLT/LGAP/CYAPALPSCKEDEYP VGSECLWPSPPVEGEVGPLLG*SWGR HVPPFWASDGLPLFCCLGSSPES

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,785	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
775	6955	A	785	3	411	QVPAPNPNPSPRIHAPGTGSPVAPP RLQQGG/CLSP.LTPSSSSSGL*RPHPQR VPGTLNR*GGRAQLGPSWAEGPSGRA GSKGGPGRTA WCGRRGSAQRALVG PGRGLPGEKGAPGYTSSAAKLG
776	6956	A	786	3	451	DAWARSIGPL*GVRVPVPSGGRNRPGE VRAELR/PDVPTVTPPEWAI VSDPSKE RPPSGDMGWWRAGPRGTGKGRPHSRV PRGGREGALCAPQEEELSPGIRHPFT CIPTQMAHQGPLSVFPPT*PATAA HPPRARHPPWEWAQESRAAV
777	6957	A	787	2	383	CVRVCLRCSCSEYFWLVCVACLCLYM FLGLCLSVCGW*SMVPVCM/CSWVFC GCVCVS*TPCMSKYRV/PASCWTTVC CGSMRPWCE/CRAHCA CETVGLGFG V/C*/CVCLC
778	6958	A	788	2	389	VSGCARLCSCEYHWLVCVACLCLYM FLGLCLSVCG/CLVIACLHGSVWFCG CLCVS*TPCMSKYRV/PASCWTTVCIC GSMRP/CV/CSGTLCF*DCGSRRLRCI* /CVCLCFCMGDYAMCCSMEMLI*VC VMFV
779	6959	A	789	5	396	SNPIPPCSQAQLTVPLHPLCP/YPYQQ/ PRSPIP*ISPVPHPHQPPQAYQLISES PSPKLPLPPWPRDIFKIPSPNFAHPCR YPFNESSPVMFYVPSALTLQPRSPHA LVPVIVRSP*IQPTVPHTPFHE
780	6960	A	790	1	397	EECAAKCEEDLEFTCRAFOYHSKEQQ CV/IMAENRKTIIIRMRDAALEFK*M YLSQCKTGNCKNYRGTMSTTKNGIT CQKWSSTSPRRIPSPATHPSQGLARN PDNDAQGPWCY/TDPEERYDYCDIPE CEG
781	6961	A	791	3	445	SPVRWNSDGLIPGVEPREMAAMCLG/ LSHSLSRYLKFSADKVDTMIVQAISL LDDLDELNNYIMRCREWYGWHPFE LRKIISDNLTYCKCLQKVGDRKNYAS AKLSEVLPEEDEAEVKA AEISMGT VS*EDICNLHLCTQGIE
782	6962	A	792	3	393	RPLKVRWNSCFWLLDALLQYTFYGV TPSILSHSVNRRQPPSGAGSVTPERM E*NHLHRYSKVLEAHLGDPK/PRPLPD CTRLSWAKPQPLNETAPSNLWKHHK LLSIDLKVVLNPNFRSNRPQVRPLSPG
783	6963	A	794	1	437	PRGPAPPDRGRASAPR*SPRRADAPA SAAARTGAPRRGVGPRSGASSGSRPR *GAGSPGPAPGSGRPPA/PEAPVHE APGEAQPPVETHLHQHREAHGDAAE ELPRVGGVQHGVARVAPA/PALGASP PPG*SASAPEPQESDAL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
784	6964	A	795	2	451	SKKRRIK*PSNRSACAPMKHMEVKL QTKRSLSSMTDVLVDRPAENVSVNP D*AQYMGGDPEVAQMICEF*IGLNH NGTV* CETLVY/HTINSFCESVLHN*T QNPAISPLDDMPNK/TASMGFIISQL SSGDTTINSIORIPALSD
785	6965	A	796	777	1504	CFYCLKIIHCD/HLE* RQQLQP/CLV HSSASF SRATIL
786	6966	A	797	396	0	IIFLILRHGFAVVAQAGMQWCGLGS LQPLFPFGRLFS/CLLSSWDYR* RQGF TMLARLV LNS*PQAR/SASPSPGPITD VSHCA
787	6967	A	798	10	495	LDTREVLVPTTPARAPVQPQSGSERPF LEGCGPPFSLAHAPRAACRAGWHHC RRGAWPFGVRQEAEP*PVLAPLGRK PWTTRYEEGGV/LGSVPLPRPPPSHA PGRTWNSGVHLQAEGLCEQVLLTQG VQAPAK/HPVLLG*ACFT*GALPQDR* SPLVCPHP
788	6968	A	799	3	276	LATVSPGWECSGAILG*TAASYPPGF K*FSCSLFSSWDYQRM/PRAANFU FLVEIGFRHVGGAGLELLTSEPPQPK ICDYRCEPTHPA
789	6969	A	800	2	365	DPVSO*APPPAPPSPASPSPWKMEQ ALAEHPSPSPSHCRKKEPNCLVLG VGTLTTPRPGPSSPSPLVPRAS/PGGSH QTCQSSSLPGEAVPHCQRVGGKNVD GIWHLKLSDSRVFPNS
790	6970	A	801	561	1125	PKSYLLKTLTSFQDGAASPLAAPPVR QQHRGKAPAPPRS*LSPLCNHQGEK HGKAPPRKSPTK*QLRP/CKMENKRT PNQRQPEELHLPAS*QPLPDSHPCSCP HPVGSFETQPWGKCGQWGLGPGQAL SGLRQKREEESSHGAGKGPQTQITG PSRQGPSRKGGSSGLPGLPHTPGASC QARLRLA
791	6971	A	802	172	565	IVICLOIKTTMYRHFTLVRLMAIKKTK NLW*GCGK/I/GKLTHCWWECKLVQ PLWKTV*RFLK/DYK*NHPYDPAIPL LGIYPKESKSVCGRDICTLIHAALFTII AKIRNQTKCPSTDEWIKETWYIYTQW N
792	6972	A	803	6	468	LRQAWHEGGAC/LFNRPKTLFEPTC GNGYVVEA/VECD*GFHAESYGLCCK KCSLSNGAHCSDGPCNNSTCLFQPR GYERRDAVNECDITEYCTIGDSGQCPP HLHKHDGYACIQHQDRCYNGECKTI DNQCQDICRT*AAWTDQICYEKLNTS
793	6973	A	804	2	294	POLKKNSFHFKRIEIVQSTFSDHTRV KVVN*SGKVNTM/WKN/NILLNNQW VKDEIRGEIR/FF/EMNENEDITYENL RYASKTMLRGKFKVVVNYYYKEE

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
794	6974	A	805	3	639	HASAGLVVVGSLLSNLAPTARGPYA PAWGPAGP*/APPANRRPSLGT*TEP DFTLSSCSRNRQKRHPADSEGPARD/ CSPAPAPWKGSPPRPPSHRLRPASGL PWDLRPPPPGCPPCRADKGSCCPW GTCSLP/PGQPLLQGPFFDMSITSA APRCPRLGLCGHTAGDGA*/APWGR GTPRCPGASPGCAILGSSLAWPWGMS LWRCGP
795	6975	A	806	1	395	GGCGHRA PGRHDAQRGGLGPGGAA HATGLPEAHRSFSKAHLPRADGPEAP QPQLLWGNLGRWPPAPVAHGRLRLSL NLRSCDNIS/RHGHHAHGQGPAPLG AGCFVL*QGGRPESGLHSPGAGWPQ VSLPL
796	6976	A	807	2	491	SFPKFKFMSQSVPHIYIQVKEFIYASL KFSESLHRSSTEIDMLRKRSTNLLLTR TLSSCLLNLRKPHIGLTELQIINTTH LEQAICKYLEDFITNITNISQETVHTT RLYGLSTPKDARHAAEGEITYTKLNQK IDEFVQLADYDWTMSEPEGKT*GYL MD
797	6977	A	808	50	394	GGSAQPCALASPHLASPVLTROPAAA GMPDGPAPTA VKVGAAATPLADGETE APGSPHCSSAASVSTFW*GG/SCPTLP CPKPSPLGLPLDSAAGCRWDAGWGTG SNCSE/E*ELPRH*RMGRRRP/CSPHC SSAASVST/CLVWEKLASCLLP
798	6978	A	809	1	438	EAVSPCSRIYWHVAAWENKDALPGQ KT*F*VDSDDQWGEYCCVFLPEPMGT ANIQLHGPPRVKAGKSEHINEGETA MLVCKSKSVPPVTDWA WYKITDSED QALMNGSESRRFFVSSSQGRSEL/HLW NLDMEADPGQYYPWNGTIFK
799	6979	A	810	2	1238	GGGGTACAPGAPGHPHTPPQSSSRPGH GGRREGEVERGA*GSWGTGGERGPG VGNLGMSSLSEQYKGQGRSGG/PDS *DGRQER*SLRTPGEPSCPPHPSLTPP GASPWAFQ*SGTNLPVWWSAGD GGVMAPGDDT*PGGVKG/KPGVWG *DPWHDPNLSLSSSTPPSPGS/QGES PHGLDWSWGPPVLLTGVCSSRAAQ RGARKGPSPPAIPISASLALVP*GP/PF SVPGIENCSLASSRDRVIQPTTYPPQ QATGPRS*MKLSACLTPEEAGQWLPR APCSLPQPGPDGVPCKPKSP/GTDLA GLSHPPQPCPLTTSGGLSPAGPPNRS LGAAVSGQE*YRAGGEEE*GASFVSD AQMWPFFQTLVSPSG*LD*LPPLPGP ARKGGGKFFADCMCDTVGGA

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800	6980	A	811	2	1044	FFFLVKFVFSKRFAMQGLLDPLPQLE TLERGPQGQLFQGGPGPTASQP*CA DIP LAPAVPPGVLT RSEMS PAMQSR KASAGPGVSL LQPCQGVSPWILLAH RRSVASQRRRRRSPSAEWCFSQAQSL PWLPTPEMTCWALSFPFGAGVGS SLPPPTTKPKLGL*LPSCLPSPSQP* LSHSTLPTGPQWHRSCLPPESSGHA PPVPVPMSTPASPSLGTGVFAPCCIV VVLGWG*GTCSLPSPHKMPALHLPPL WGAFEDPAASGVLLQDVRKSSAKR HPGQSLALSSGAPLLVPSAAPLETLET RRAIQSVEGGSGAPGLLHRDPKEP MPYLFNLG
801	6981	A	812	2	1729	IERLEVPLQNSRVNAHFNLFLRPNK EKIDFLLEVCSRSVNLEKASESLKGN MAAFKLNVCGLGLEDLQYVFMISSEL FITLLKDEERKLLVDQMRKRSRPNL CIKPVTSFYDIPASASVNIQGLEHQLIL SVDPWIRJQILIELHGMTSERQFWTV SNKWEVPVSYSVILGIKDNLT/KIDL VYILMAKGLHCSTVKDFSHAKQLFA/ VYVSW*QSSHRSFVRSC*MRCCFWIF IHTKLGQGRQERDRHPTL*VEYEAIW K*GLPDISLRQGITECVAFMLNWRE NEYLTLPVPAFLQSNPYVKLGQLLA ATCKELPGPKESRRATAKDLWEVVVQI CSVSSQHKGNDGRVSLIKQRESTLGI MYRSELLSFIKKLREPLVLTILSLFVK LHNVRREDIVNDITAEHISWPSSIPNLQ SVDFEAVAITVKELVRYLTSLNPNNS WLIQADIYFATNQYSAALHYLYQAG VCCSDFFNKAVPPDVYTDQVIKRM KICCSLLNCHTQVAIILCQFLAEEIDYK TAV*NLWQGPQSMAMMDSYYDL HVGMYTILGIPGLIFHPKRG
802	6982	A	813	38	445	SHGWDPSHGLEPGWESPGGHIWTQ MDPSSDASGRD*GEGAGLGDPRRGS EKPAWGRGF*QGPACPPPVSPRVPH DVSRRPTPWSQGLAH/RSPGP/GPL* A*RGVAVGTGSPAAG/HILPEDPAQR RGYGEDGGTV

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803	6983	A	814	131	1946	PQLTKTCADPTKIGTFARLSTLQIKSG SNPGSGPRGTGEGRAVGACCPMPST D*GPLLPHGGDA GVPTA WPRQEIPW NFLPPSK GIVASRRAGPEQAGSRGVP GSGNVLFTEQEECTVSFCKVLRYSVQ KYQNNDDKHGTHGI*RGADSVADGQ GPGWAEELRSSEGPRSP/RGHPGHCVL RTLSPMGCMA/RGA/PGSRLAPAPAP PPEPTAPSGRLCPGEHFLMEFPLCAH LSPSGGNVPVHCIRQRPVGLPAQWE KG*IPGSAVPRTLGSGVGLGPGRGS HVTPLGNKDDQPGSPPTNAWGAEQ GLTWALSPPE/RIVDGSHPGMSQHL* CCPTPPSSTPPGNGP* AAT/LSLQARG PHSGHLSTCCNVF*VQPLHALGHGAL DSL*CAKPPPGKVG/PPALGASFPGG* GPCAQG/GVPALAEARGP/PPRQAE VNSNGCPWEAEFGKQLVSKPMPSKK GQRSAP/SHDGLPKPPDPDWRAITDVP SVGPAPWPSLPMPPCLAHLTLRFMV NLRGALFGKVDSA*FWQQMLPTPPG PSWCPNP/SAPLSRGGCGAWPRPAAP SQSKVCPVLSVQSRHSRLPRKNSSE LISPPPGWGAMISDSLV
804	6984	A	815	67	506	YAAVSKLSADKCLMNRISYCLLNSEV LSSFQCEIPPGGFAMMDK/TL*FIWK FKEPRIAKTIPIKSKVGGGLTCPNFKTYY KATIMKKVR**NLESRNKPSHIYGGQLF FDKGAKIIQWKG/DSLFSK*WWDNW DI/APCKRMTLDSYFTFY

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805	6985	A	816	238	2673	VCRKERGCFPGQSGRSRAGRDCPS LPRASGNPQPLAARQGPAPGNSGSL WPGQEPVVDWPSSEGTVPDITQIEVE KPTQKCNRQKGTTPADTKFPSPCNT VL*IPK*NPWGEQSRP/GPRQHPGP KDM*QPLGEIVYIYSQTPKNILQNRN LQLR*KSVKSL*DF*QFLQLGK*GSRP *KLTHPAKGLATGHNG*PPSPACPG RREPPCNCGLGCPRSILRGSGRGL GKRRAGLTG/LMGD*DWRPAC/RG HPGLRHEGRMGDDKTEAVRQEGVG AGLLSTSPSCG/RESPPGALPPFAS VSSLTEL*GYI*KPLPRPATVTCPRAP GGRSMALG/PPPAPHPFRRGLCGTFQ LPGRGDCSSPCPGSAGKGTPTLLT PGLCSKSAGAGKGTGAETPK/PCSS VLKVGKGQISYRPA*S*GNPAPAVGC APPLYAAPGSLRGPRVRRRPATHI GQVQAAAFLEREQV*HPPGFLPFMQ CARST*KAPVFQQAASKRAVSNAYCE RKKNHYSYPSQGLQALEFFKPSLRG RITFSFRVSTRWHSGLQDHCALGV/PGP QEKADTVLRAIWPDP/PSLASGSPRA SAWACVGGVSGCSPGOGARAHKK KPWPSLGLSGNTTKAGKKVAGGA/P GDRFRGGGWVGLSSSQPGRSQAAA CSGRFCFWRQAGDT/GPPALCP/IFLP /GQLICQVPGPT*QGLAARESRAPQGG EGKPV*APSP*IPPPGSLPGTGVGG HMHARSRRTRTHHQEPTDIFLA/GP PAPSGCPSP/GAVSARTPQGAAG
806	6986	A	817	3	396	RWCPEPLSKPHGPPAGQL*PG/PSCEQ T/EPPSPVNVTVTHLRANSATVSDV PEGNIVIGYSISOQRNGPGQVIREVN TTTRACALWGLAEDSDYTVQVRSIGL RGESPPGPRVHFRTLKGSDDLPSNSS
807	6987	A	818	109	446	KTLLILLTLPVDLPALCFLLVTSHSQCL FLLFDCQPLWGNQGFQAALCSQK VOLS/PLQTEYRNKSEFLVGVVVDGE DNTVGCRLAMFKGGT*AIVAIPFVTV HIPQITQHAA
808	6988	A	819	391	0	SSSSSPGKGVSWFVTPGGGRAPNPK* LEPRPKG/PPSPGAKRIPGNPPKKE KGPPPKGPGKFLVFKGKGGAQPGPP GSG
809	6989	A	820	6	457	PAYAMLGTRAPASEI*TPPVTPSPDL TPSP*/GLPSPGGESLSPGLFGEVVG LA/G*EGSLGWRGPAGPSKLASSAAS WGEPMPSAQLPPSPACPG/DPGSPQ SLSPAGT/DDLPQASDGTGKPG/QWSAH ELGHTTPQPPPGKTQPRGTAAVK

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810	6990	A	821	3	457	PQDRAAQTDASSIGQGPAPG*PAHCPAR*TRTAQHREGCRHRGPQSGRGKAGHRPRCPCHPGS*TCSCPGGPATGSRGPSGRTARTATCAAPAAPGA TPGRGTGTPRSAARPPGRTRINELAPGG/PERPLPHGTARGACPRPSGQTSRHHGH
811	6991	A	822	2	1372	EAVELQPPPPAPLSPPPPAPTAPQPPGDPLMSRLFYGVKAGPGVGVGAP/PAVDTPSPSTPGGLCLPLRPQPQLQP/PVDA AVPGAGKKRYPTAEELV/PGLGPSQPOLPCQGVPRKTPQTA*DLLQARQPWRPRTNTTPRV/PVLEELGPEPEVPSAPNPPAAQPDDEEDEERAAAAVSSRA GPVQPKALIVE*VLPAVTIDFLPKGYTSLLLITDPGSPEDSGQTDPDNPGYKGRATNLLGTCCFHPVSGGRANCPISNPNP KFGCGGVGV*TWLVHPRSSKSEAPSP*GRGHRTPWEGGRWEHLPPMGRGTL PPTAFSPSPSRGG/PFRGF*GIRLSGGGPRTP/ILLGHIFLSFPRS/PAPLFTAPGL LPLTTAWFTNSHQLPSPHLPKVPRFNKATP*LA CVCRGKSSPS/VPPSLPHWE*P*RCGFPTTSSVLLCLSFPPRGKAG TLNSVPLDR
812	6992	A	823	87	437	WNSPLGPDLAASPL/WNAQLCGHLA DHDSIHRRIQRGFSFLEHVDKALALQP ENPMAHFLGRRRYQVSHLSWL*KK TATALLSPLRATVEDALQSFLKAEELQPGFSKAGRGYISK
813	6993	A	824	390	665	NHYQSAKWNLILKKCIGPLKRTKFL*VRQPKKSNSTEKL/EKKIG/TYRKAHS KSAKEHQETKPVKEEKVKKDYSKDV KSEKLTTEEKAKPNKKNPLDNK/GEF*TRTTEKGVDKDFESSMKISKLEVTIEIVKLPLPKRKMEDTEKMHRTPE KDKISLSAPAKKIKLNRGTGKKIGSTE NISNTTEPSEKLESTSSKVKQIVTGK VRRKVGTGTEGSSSLVDY
814	6994	A	825	1	445	SCEEPHANGPDL/CRESDLRHAMANC FEALIGAVYLEGSLEEAQ/LFGR*LFN DPDLRENWLNYSLHPLQLREPNTDR QLIETSPVLQKLTEFEEAIGVIITHVRL LARAFTILRTVGFNHLTLGHNQRMEF LGDSIMQLVATEHLFIHF
815	6995	A	826	344	471	SLYLPEMSKVIHQRLSKNESVALQE LL/VWRKKLFEEQRQDWH
816	6996	A	827	3	269	CRLLPKKEWKIFHPNGNQK/RGVVIV LIDKIDFKT/TIIRRDKEGRYIMIKGSV LQKDITLSIYPNTGKRLRYIKQILLEL KSSSNKIQ
817	6997	A	828	1	170	GGWGPFLPPPKKGVFPKNPPGGFFRP PLK.GKNFFPPPGKFGPPR/VFLRGP PP

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818	6998	A	829	3	366	TFGGRPGGGPSEEGGGPPLKRGGPR VFVKGPINGPGRGNPFYPHPGIGSGKK PPCPGGKGGIVTSGPPPPAGGPEGIP PPSSSPSS
819	6999	A	830	34	331	RVKPAGALKVKPGGPIPFQNSRVLKK FGKFPSPGVFKRDPKAWGPAFFPGW VFKPPFWAPCLSSSPFKSLVKSQTP GFFPMGKNKKRGGVFMFGK
820	7000	A	831	2	234	QKFFRPQPPGERGGQPPPPQGPSSSS SKKESPSVPOGGKRWGHFQSLQPPPS/ GGPKNSPFQPPPGVGNRRPPYPGL
821	7001	A	832	320	505	GRYMCSKKCGSMPLSPNKDLAEVSA/ QRVFASYSERSAYPVKDQGRFVDGQL PIPENSLSGLCLR
822	7002	A	833	2	450	GSTKFFQHHGLGVFETASLTTPR/WL PLRDPVPPKA/SKHFPALIKSAIKLLTP VKRAKSEQLHQGMCSNERNKRRESS PLGHKRRAL
823	7003	A	834	2	460	QFGRFRFRLTTEQVTKVCMRAWF KLHSPAQAPVSFTLQQAQLLLPNIL LNKGDKTSQPGIQQGLSKKLEALN QLVSEQLQLGNVPELSPPWNSP/VF/V VKCKSGKWRIVTDLRADNAVIKPMG AVQPGMPAPALIPKDWPLIVIDLKE
824	7004	A	835	1	294	FRWGRGLVAWTSNGTSCLPWGPVPS PWASVGSRWGGRPSSMAMAAAGSG/S FSGKKTVPDPPIRLSHGDQMQEKRPV PRPPVVLQGRCAVPPSPPLP
825	7005	A	836	3	438	HPFFQRGNKKKWPCKRGKPPPLKPPY FHGTFLLIKKQEGGDQFPEFNSPPRGP PPKPIGVLTPIQNKIWGGENPKKTSS SSSSSSSSSSSS
826	7006	A	837	3	404	KENYKTVMKRTEGDTKKWKDSICT WIGRTNIAKMSILPK
827	7007	A	838	21	231	AAIQQGLACSHSVPPATTPRAYTPV PPQLLVNRYPKLTLESLRQLRCARRF PRETGADCRHAGAGRQTK
828	7008	A	839	413	2	GNPFADPVSQAVRPS/SSSSSPAQL TLKFNIGTDFGVGEGPAAPSPGSAVP GTQPPQLSFEQSPDAGQIVVEVKPAGE QPLQPVNLNAVAAGTAPAPQPPPAR
829	7009	A	840	1	201	ADHSHSFYSKIGENRVSVEARYAGS NTALLFATLRLCLCN/DE/HKSGLRAH LGIVPFLELJHDKDSFA
830	7010	A	841	17	257	IWGEQDTFHSMKWIHLNVNHNKT KLDDNIGIKRGDLGVDNEFLGTTP KAQSMETIDKLDLFKMKNFCSVKDG EPBCW
831	7011	A	842	2	246	AFFTPPQLGVFSPPPPLKTSPPRP/VK FSSSSPHLRPPPKKGFSPKSPGVPFA PPLSSSLFPPPGVFGAPPGFFFKAPP

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832	7012	A	843	14	400	KKSPFLPGRGGPPLFPPLGGHSSSFP LQGQFKTLFSPRGWNPVFLKKPKYPSS SPPPLYSSSGGVGGGNPLYHSSSFPVL NPPLPLSPWGPCKGNPLSSSSSR
833	7013	A	844	18	221	TTLQPRLPPPYHTLPPPYHSTPPYTIL PPPDHHCCTPPYNHLAPPPY TILPPPYHH PTTIVVSSIQGS
834	7014	A	845	1	983	FFFFKTESR/SVAQAAVQ/VYMDLSSLQ PPPPGFKRFSCLSLSSWDYRHLPPRP SKFCIFRATVSPCWPGWFCWP
835	7015	A	846	1	331	AGEPGTEPPPLPQQPPMTLP/FAAA AANPGAPAAARAPPPVIEDKGPPLS RAPILRQRQTRAPGPSSADPRACWA PHFRADQKPLHLPLAFRLHAPAKWF CVLYSI
836	7016	A	847	151	427	MATNCLCSISQSATASGVPTTGAH HHTNFFLF/CIFETEACSVAAQGVQW HDLGSLPLPPGFKRFSCLSSWDY RHRLPHPANFCIFS
837	7017	A	848	504	0	PKVEYSGAIFVAHRSTRLLSSPQVSC LSLSSWDYRWSTTMPGLIFLIVET GFCHVQGAGLELVTSSDPASA/FPK CWDRHE
838	7018	A	849	2	136	RGSAARCGFCG/CGCGFCGSGVGSAD QVRILRCRFRSPVEAHTCKP
839	7019	A	850	3	456	GVWGIKPGPEGPGSKPKNSPGA.IKNG/ RPALEPKTLPPRARPRVALPKRSPP/ APAFFSLPFFPSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSPVLSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSQ
840	7020	A	851	3	235	AVEFRECKSNLEPLFEGYLRREAE CMEANSRLASELNHVQVLEGYKK KYEEVEALKATAENEFVGLKDGKG V
841	7021	A	852	3	378	GAIRTACELHSLSLQIQGVQI/GVFKSS AHPGMNEHSPARPHHGAGLGHEQEP GSDTGHGADAPGGVHPQOETHRRHRH GVQSHLCECPGQADSKTGRGHVGAS DWGLWGLGEMAKGHPQKLMIMLH
842	7022	A	853	1	241	SSEABFFCGTLVCTHEQDILQ/RDSY KSQKLLKKLMSGRQSCNWTGMM GTLRLWLFLFSVWSARCSLFTHSQ FFW
843	7023	A	854	3	278	GVQWCNLSLQPPPPGFKQFSCFSLPS SWDYRCVPPLRGNFVFLVEMGFR/L LVRLVFELLTSGDPPAFGLPKVLGITG VSHCAWPEVNNF
844	7024	A	855	3	922	TAPAQSPTRKGTNRETGPQSHQRRR /PNGNRGIGAPAGSSSPGRGAGAPP RPP/RRPPPGRCRAPAGGAPGGPQ PPGPGRPAGAAPPRGPRTPRAGPR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						RCPSPP
845	7025	A	856	61	438	VVREAPECEWFLPSGVGRGLGFLPPFPF PALYPGPFQLPRPPWAMLSVACAQC FPFLPVGSCPITPSEQSSWPASPPAS VPSCASGDPSPQRSRLQLTSGSTSPPEP KPDILRPLVGLFFLKKIS
846	7026	A	857	265	421	AYTENRKLRLKIKE/SRNKWKDRSCS WIGKLNIIKISILPKVIYRFSVTPNKL
847	7027	A	858	58	300	NPAPFNFNGAPIKKFFLAKFGVLNLVLP LKGPSSSSPFPKGGSSFPVFPFGDF PGPKNFSAPFPFGGWGSGLEPRGLPG
848	7028	A	859	408	1	SSSSSSSSSSSSSSSVAFLYTNNEQPE KEIKKTILFTIALNIIKYLRLTL/REAK DLYTGNYYETLLKETKEDSNK/WKAIS CSRMEMLNIVKMS
849	7029	A	860	3	360	FFFSDSKHSLYYVDFPEEKLSAGLGR RGLDGEPPCLGAPGPYPLWEPHAL PAPSEHPGCSIG/PGGGKGGRGSP
850	7030	A	861	12	301	HLSPRLECAMARISAHCNLRHPGSGD SPASAGVAGITGACHHAHLIFVFLVE TRFHVHGQAGLKTDDL/PASASQ SAGITSVNHCAEPSCPF
851	7031	A	862	375	3	SSSQTSFIQDIGKLPLEQHFGRCLKMEA LPYGEHGIIDSDSREEAQLNGGQLVE EALGELTQTTEPKTWY/PLSQNSENEL PANQPQPFSSQ
852	7032	A	863	1	83	HHHHSS/YHLHHHHHHHHHHHHHPMA MQTEK
853	7033	A	864	2	367	TFVEVSRNLGKEGRICCKHPEAQRMPP CAEDYLSVVLNLQCLVLHEKTPVSDR VTKCCTESLVNRRPCFSALEVEETYV PKEFNAETFTFHADICTLSEKERHIKK QTALSELVKNKPKATKD
854	7034	A	865	1	273	RGA VPCL/PPPLGGQWGIGPRAGISDS SSNPGGIPFFENTPKINPGGV/GAPGPP PPPRFGPGKSANPGGWG/PKKNPFP GPPPGGKKECPF
855	7035	A	866	353	0	SSSSSSSSSVAIILSDKKDFRAENILKD KKSHFLMIKASNHOEDITILLSVSVP NSRASKYTKPKL/TEQQEETE/HSVTV GNFSAPLTHGSTNRKLPDSSSSS
856	7036	A	867	69	342	ILYSLGRFLSFSFPAVSYGKGTGYFAVD AQLFCPR/HTYSKPDNSGRKHMYVV RVLTGVFTKGRAGLVTPPPKNPNHPT DLFDSVTNNTSPK
857	7037	A	868	182	389	GYPNPSPKPLPWGSGLWKGMLTPL TNPPLGGGVNPGVLSPPPKKE/TAPK VPLKRPPPLKGKKTLPPP

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858	7038	A	869	30	437	EDLGTARRDLIKSEELSIKHQRDLREA VGQKEDMEERITTLKRYLAGQREA TSIHDLNDKLENELANKESLHQEEL ARHLQELLEVAEQKLQQTMRKAETL PEVEAELAQRIAAALTKAEEERHGNIEE HLRQLES
859	7039	A	870	1	386	GPOQPHKAHPKEPGLLPFGAQNPPPP ARG/KLVPVADMHTRTGRGPSEPSLA RGTPGPGTMVGRGCPERQRRPQPRG HPAVQGPVWPTGSPQISSITREKLTP GGGSAICSHLPLSALEAGQTSRAQTG
860	7040	A	871	55	393	GCGLRGDGDGQVLRVAVPSTEEAGLL PSGPPQPGQVGSRASIPAPGPAQLD SGMLACYGAP/GVAAVTGSPGPGQN SGWP
861	7041	A	872	3	529	HYAAWQGRNEPIKLVKAGSAVNIP SDEGHIPLHLAAQHGYDVSEMLLQ HQSNPCMVDSNGKTPADLACEFGRV GVVQLLLLSSNMCAALLVPRPGDATD PNGTSPLHLAAKNGHIDIRLLQAGI DINRQTKSGTALHEAALCGKTEVVRL LLDSGINAHVRNTYSQTALDI
862	7042	A	873	197	663	CSPGPSHKEVRPGLPSSQLGLLPIFLS PATKLLLR/HGWNLTTPPAKWGGA GPGQGHHITSFLQELIEGEPGKWHG RPPRGDLGGQGI/VPRCPSPHRCRC TPAGRRHVVGPHMCMVGRLRGSLPT AGHCPRPLPPPSAPRIRICPGSQGKDN
863	7043	A	874	338	113	PSQKVGAAAPRKGPQTSSSSSSSQKRI FPIWPGWFLTSK/APMDPPPPWPPQRV GLQG/VAPPANPPKDFLMALFLKA
864	7044	A	875	91	349	TPYPPVRPKTKILLLEIIGQKLHSIVFV NDLLDMTSKAQ/ATKKNKLDIHKIKYF CTSQDPIKVKREPKSQKKI/AT/YISD KGLISR
865	7045	A	876	2	524	AQEEEEAKVNEIAFINTLEAQNKRHDV LSKLKEYEQRNLNELQEERQRRQEEKQ ARDEAVQERKRALEERQARVEELL MKRKEQEAREIQQRQEKAREGAA RERARDREERLAALTAQPRSYEEL QKKIQLKHDESIIRRHMEIQERKEKA AELSSGRHANTDYAPKLTP
866	7046	A	877	2	375	QGPPPEPPLGKVKQANPPKSSRLSP CPYYLTPSFLKNPKINPAFLAFLPL PWKVKPEPPYPKNNRRFHPKWPSP PTLATPPGPQKQTKTSSSPKLCSGEV EIWEGL
867	7047	A	878	2	153	IKISFPPTPSMLSGMMKNIPNVIPMLT CEWINMTYSIGIVATKVLFLPL
868	7048	A	879	1	282	RPAWHEVTNLTFGDVANKATLCSMK GCMRALVAQLKS/ESEDLQQVIASVL RNLSWRADVNSKKTIREVGSVKALM ECALEVKKVLPLKTFSTII

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869	7049	A	880	279	498	GWEFCSCCPCLGVAMGVLDLGGHWQ PLPSGFEQFSCLSLSWAYRHLPLCLA NFVFLVETGFHHVGGACLELLT
870	7050	A	881	1	126	CSELKSCHCTPA WVT\SKTALKKKIK RQPVQSILVHCRITY
871	7051	A	882	2	370	PFCFVVRDHEQPKIEISIMRSFCNVW LLPTFSL/PYLLSFFVCFRDRGLLCH PGL/WSA VGDIMGSLASNSGESRQIG FYLHLPSSWDYRQVPPQ
872	7052	A	883	21	378	DCVPFKNKNDYKAPVFKIVSWHKA RQEAQR/NRIESPEIYPHIEGQMIFNK GAKPTSSSSSSSFSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSPARPETKLE GNRGKKVHDI
873	7053	A	884	3	159	PIKRHRVTVWIKKQDPMVCLQETHL TCNGTLRL.KVKGWRKYSTTTKTEKSK R
874	7054	A	885	1	295	YKHVPPHAKFLF/SLVERGFHHVVQ AGLELLISSDPSPA/FPKCWDYRHE
875	7055	A	886	81	412	YNNSGEIQHSTHSIRTEIGNLANQQ SIPPNNQYNTYLLADHSRIKLQISIKRN FRNYKFTKNLNNILLNSDYNEVIMM TSSSSSSSSSSSSSSSSSS
876	7056	A	887	3	371	DGFTGEFYQ/SFKEKLHQYFKLFQKIE REGTLLNSFYEVISITLITIKDITKKEN YKPIAFMNMSSSSSSSSSSSSSSSSSS SSS
877	7057	A	888	1	454	PSMEHYEAQITLGMWMMYSVNKQOH AGAEFYALGKGDVKVCPCCGRRLT/ DWKPIEHPREQHA KWYPRCKYLLQE K/NQEYISNIHLTHSLESLVRSAEKN ASLTIRM DYITFQNPMLQEATQMGFS LKNIAHASADA WADA EVVPGFPEGSS
878	7058	A	889	3	412	ALEPLTGRKLNRRHLGRAPGRVQR SFGSRTLGHRRHPQRKGRGWOHPVP GRSRLPLSPLVPPTAAPDVSLHQVT MADRAAAERACKDPNPIIDGRKANV NLAYLR/GPKPRSLQTG
879	7059	A	890	3	133	QTKDENSSKSTFSFSMTKPSKE/SEQ PAKATFAFGAQTNTYQL
880	7060	A	891	1	436	RCVGRGTRGFGIRKSFVWPGLVPPVF PTPLRGPSSSPPRSPGFGPPGPFNNPP PPPSAQKIFSSSSSSPPRPPLGGLGRE FPLPPRGKVSPTVLPSS/PPWGPKG AV
881	7061	A	892	206	418	EGGFLFFPRVGGKDPNLGWWKIFPPG LG/RFSPLKTPRIWDWKSPPITPGNFC GFIWKGVSPPGACWHLNFI

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882	7062	A	893	4	391	YSGKEDNIVISDSSL/HHYVTHRFQYDSHLRQKHG/TLQNGNGKLVINGSIILE/RDLVNLKWDGAGAEVTVGITGETSLKAKGHMK/GRAKRS/PMFATGINHRKHLKSLVDLMQDASSTTWCLLSKFTHH
883	7063	A	894	2	425	RNPRVNPVRVRKYCENYMPILLTSYMGQSFLLKSTVTK/PDRYFIYQKLFHKENSGDGLIPRMQGWFNQKSI/VHHIKKSYGFS/HFISVDAFNI/LQH/PKMIKIFKDFLSISYTFYFK/KPIASILNGESLNAFPLRSELT
884	7064	A	895	2	447	RHSCPFGWLGVCGSAVLPL/IRPSQVLGGPCVTTTHRCRHGSLQLRAPGLKPSLCLGLSSWDHRRCT/LCPA
885	7065	A	896	3	472	GVPAAKSPSPVGPVRPNLSRAKIPNPQGPKYETPFFFKNLKLSRGVGGPRFFPRPGSFCPENPNPFGGSLNPDPPPLIPR/VVKRLPPSSSSP
886	7066	A	897	179	473	GMSKLVFQNLANSRMC/SLRMPGVQYEQPILNGLRDKASYVRRVA/VLGC AKMHNHLHGDSE/DGALVNELYLLRDQDPVVVNNCLSLLEEILKQEGGCI
887	7067	A	898	2	415	QAGYPASLSLSCPGLGAFAGFPSLHYSLTWPPAPHQRKAQITCTVIFIVWGVLVHLVIPPFVFMVTEGWNIEGLYYSFITISTIGGDFVAG/VVPASASHLFFCF
888	7068	A	899	100	451	IKLGLENKRGHLRAKECSASGSPFPNQAVLGKSRP/KARKAAAAMPKTA/VLAAERPKKAWGVLIPKKSTKRTPKAFAGGGCW/TKVGWSKVAKKVPKPEASKPKKAAPKTRRYKSTLKT
889	7069	A	900	3	374	RSEFPCCRFRHHHTPHTTHIPHVVYTHHTRTLGPHHTNTQHHTPHHPTQPSSSSSSSSSSPTYLHTYTAHHTTEH/HHTTHIPHVYTHH/HVPHPTPHVHTHHTHYTNPPRGTYTYH
890	7070	A	901	2	293	RHQTMKLLQ/ETIGETLQEIKNKDVLSTNPQAQAAANAKMNKWNHSSSSSSSSSSSSSSSSSSSSHLETA/YKELITRIHKAHKQLYRIKSSDDK
891	7071	A	902	3	454	IGRFTIVKIAISKAIYRFNAPPVKITLVLFKKIEKEIVKFGNEKTPQISKSLRKSSSSSSSSSSSSSSSSSSSSSSSSSH/NRQINNDRIEISGINAPIKQLVFDKGTNTLGGMDSPFNKWCGENWISISKTIKFDVY
892	7072	A	903	3	332	RSFALVPPRLVCNLAHCNLLPPGFKRFSCLLTLSTWDYRRLPPCANFFVLLVEMGFHHVGGAGIELLTSGDPLTLGLPKHWDYRREPLAARPPSNSTPLCPTNSTFA

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893	7073	A	904	1	269	TIRTRYHILHHCPPPHMPMP/PPRPMP PSSTTVLHHVHHHPPLHPPPPSSTTIF HHVLCHYPLPPSPCTAPSSIFFVIH WLPCCV
894	7074	A	905	2	421	THVCVRACVCMRVRIYACVCSACT CMCVCVHTCAPMCVCTCVCV/CLTC VDL
895	7075	A	906	135	272	TAPLLLGLRLSALSYPMAIALTLG/MF LHHHCEFTVFWAARRWLL
896	7076	A	907	2	419	GPPGWVPWGQEHLGSGRGFPNPGNS PPKKGVEIKGPSSSPKPPKVPFKFFF HNQQGPPPGFLGILEKKEGFVFKGP/P PPS/PSPPFPFKKFPFKPK
897	7077	A	908	3	327	GRRRREEEKRRRRRKQKRDREGRSI KGRREEEKRDEERKER/DREEEREE RRGKREGRGRESGCEKKRERKQER DGKQSRARGTEGEESVSKANSKKPPR MAINHP
898	7078	A	909	140	403	ILRGSKPLGPPGLKKEMGALG/PGKK GNASSPKKNTPGR/PGGAGPSSSPN PKFHPGENKPGRNPPGPKNFSSPLP GGRGPPGNP
899	7079	A	910	59	385	RDQREKTOINKSRNKRGDITLIAQKY QGSFETIMNKNTLTKLESLOKVS/SF SSSSSSSSSSSSSSSSSSSNKTESVI KSLPKKKSPGLHGFSTEFYQTYKDDL I
900	7080	A	911	22	287	RPTRPTFCTRGKPPSSNCSFFFQHQGIY GEESCKCNEFGNA/FSPKNYCLENTR VYMKIYFCRCSKYEKIFNSKLICKY QRIYSRIRY
901	7081	A	912	12	186	LWDVDVELTAYALLAQLTKP/SPESK ELAKATSIVAWLAKQRNAYGFPSTQ DTVVALQ
902	7082	A	913	311	424	LSHTKWSAWPGAVA/STLGGRRQGIT RSGVQDQPDQHGE
903	7083	A	914	2	184	LNVSRNLNAPIKRHRVTVWIKQDPMV CCLQETHLTCNGTLRLKVGWRKIY SPNKTEKSKR
904	7084	A	915	3	373	RLFDYSFYSGIGENHPVVEAKYASD DTALLLFAILKCLGKEKPKSSRAHP GTVPSLELIYDTSFTHVFLADLLPTI TVL
905	7085	A	916	1	366	PPIAPRISWAPSQPP/VLGKFKNFCKK PVSP/TPSPGGIPPGSKESPPLWPA KGWEFRGKPKPGSSSSSS
906	7086	A	917	235	386	SHFLRLILAYRKFNFSIGWGHKYS NYTPPVPPVYHEYSVPMAEM
907	7087	A	918	1	316	REYGTPOEQLNLALLTLNFI/SLPKGQ MLSAAEQHLQKPAKTEA/GRMIMWQ RDPITKIWEIGKIITWGRGYACVSPGQ NHQSVWIPSRHLKSCSHGPDAAKEEIPG

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						GS
908	7088	A	919	3	190	DGFTGEFYQ/SFKEKLHQYFKLFQKIE REGTLLNSFYEVISITLITIKDITKKEN YKPIAFMNM
909	7089	A	920	2	365	RSCRVDQDPLQPRVVTHPGPEVHVGE A/PLAGPWASALEEAWRRTVPGHKY MRI/PWASRAPGPTQRWGPVRKPVA QRLFTWEGPSWGRRTTPPPSPWGHH QAAASWHRTRRNCWVLWPSRLT
910	7090	A	921	3	1055	YASLGLLKNKHGCDICRCKKCPCLSC SKIC/LGFGQDSDHGLICKCREASAS AGPPILSGTCLTVDGHKKNEESWHD GCRECYCLNGREMCALITCPVPACGN PTIHPGCCPCSCADDFVVKPELSTPS ICHAPGGEYFVEGETWNIDSCQTCTC HSGRVLCETEVCPLLCQNPSTQDS CCPQCTDQPPRPLSRNNSVPNYCKN DEGDIFLAAESWKPDVCTSCIDSVI SCFSESCPSVSCERPVLRRQGCCPYCI EDTIPKKVVCHFSGKAYADEERWDL DSCTHCVCLQGQTLCTSTVSCPLPCV EPINVEGSCCPMCPEMYVPEPTNPIE KTNHRGEVDL
911	7091	A	922	3	721	SSGFARRPYIGSPSKELPASCSPDPEY PPGQVEQRTVPQLVMLSSYPDGCSM RSRLGLLPPPPSPMPLTGLV/SDPHA MASSTSLPAPGSRPKPLGKMADWF RQTLKKPKKRPNSPESTSSDASQPTS QDSPLPPLSSVTSPLPPTHASDSGSS RWSKDYDVCVCHSEEDLVAAQDLVS VLEGSTASLRCLQRDATPGGAIVSE LCQALSSSHCRVLLITPGLHDPWWK NRW
912	7092	A	923	1	332	THASDSGQKPYKCECGKSFSECSLI KHRRHTGERPYECKCGKTFQRSST LLHH/QRVHTGERPYECKSEYKSF ASRLVKHRRVHTGERPYECKCGKH QNVCCPRS
913	7093	A	924	463	906	MLASSEYGNFSLVYYQSWAMSKL AAAHRGAIKALQMFVTFQDRGEHP LPARCKELGSLIRQLFLCSVKLDADP SVPDVVIDILQQIEALESLLDKKLSPK KVKKCFSEIRSRFPISGQKALERWPT SPKGERRPLTAKDTHNV
914	7094	A	925	2	220	EATSQSYSRCLMLTHVARHGMPC HLMVASHNEESVRAQTKRM/WELGIP LDGTVCFGQLLMCDHVSALALGM

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,197,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
915	7095	A	926	183	633	WPLAGGPEQLSSRWLQEQEGVGGGGTSCCGSGSGGGSPMSCVFKAADCATPILPQPAEAPRRHGASIALDPGPIA/D SHL/PATAGR VQGGGGAGP/AGSAILHGAAGSQGGQEGAPSPQAPKAHHPEGHRNGAGPSYPFAQSGTEGQAEHP
916	7096	A	927	3	595	QQGLLMQLLKLTHNCLNFDHGTSTD E/SGDDLCTVQPTSWRS AFLDSSTLQ L/VFDLYHSIPSPFSLVLSCLVQIASVR RSLFNNAERAKFFSHPVGDVVKPILEPQSLSDPNYHEFCRLRLARKSNYQLGELVKVENYHEVIRLIANFTVTSLOH WEFAPNSVHYLLSLWMRLGTVTSVPY VKATEPHMLEITYTP
917	7097	A	928	1	205	SVVVCFLSPGITSHTVVPIMFKIGAK KVVHWKSLFNKSCWRNLSTCIRMK V/DPYVTPGKTINTNWI
918	7098	A	929	2	235	GEIGSNITLAGDFTNTPFSIMDRTSQGEI NK/D/TQDLNYNLDQMAITDICRIVHL IAAKHTEFSGIYRSFPRIDHWKSLN
919	7099	A	930	2	184	LNVSRNLNAPIKRHRHRTVWIKQDPMV CCLQETHLTCNGFTLRLKVKGWKRIY SPNKTEKSR
920	7100	A	931	2	375	LCLLPACADGPCCSHPNVLAQHTLE EMDFYRVIWWSAALNLDGRVKHLIQ KAEDPSQPD SAGYTYALYYASRNGHY A V/CQFLLESQANCDATHGGATGLY RASYCGHTEIARLLLSHGPHQHG
921	7101	A	933	53	396	APPFSRNAGSACPPGRSQDKHPLPTF DTGSPGEGSEGTPAGTRATQPVGGQG QESTGSASPACRPGAPHAPTNSSSAPS SRSAAGLAQRLARTRT/VSQTPHSP QS
922	7102	A	934	158	377	FPLAYSLLFPF/CSRLNRELLEAVKPE VLQDSDLRCYSTPSSCLEQDSDCLPY GSSFYALBEKHVGFSLDVGEI
923	7103	A	935	1	369	DLSAEAGGNFTTKPGELYIHNGITHI RYTDLP SRMDTQASTLYSNITKLLK AISPKDKNCFYDVKDQDFDGTMGHVI RGTVAMKDGKVIUFPAPTKNIPQGAP VKQKTVAELEAEKAAIT
924	7104	A	936	2	371	LHRDLTTQCEKMDIFFLSYLPTPE/VQL INEAYGLVVDVAVLGPVGEVGGP CTRALATLKL SIPLVSLDIPSGWD AE TASDSEDRLRPDVLVSLAAPKRCAGR FSGRHHIFLAGRFVDDVRR
925	7105	A	937	56	385	IWLILPILYSPQNLAFNCPPEASSPPQP THPSSLSASATLSFSLPLPPSP/SPKLL LPALLPPLSSWQTPTHSSCESRVTPE ENCCPPAGW/PCVPASPSVQGPSPEH P

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
926	7106	A	938	1	361	SLSSWDYRHTPSRANFVFLVEMGFL HVQGAGLELLTLGDPPAWASQSAGIT GVTSVTQPR/YTFLIRF
927	7107	A	939	232	251	IGKQKTFLSRLFRSASK/DPTVSQTFM LDRVF/NPEGKALPPMRGFKYTSWSP MGCDANGRCLLAALTMDNRLTIQAN LTSAWARLENLCKKKRKKMLVLK
928	7108	A	940	8	226	FRSSKPAWATRGNALLAKNTKIWPS SSPKAVVSAPRGGGGGKFFSPTGGGC NELRSCPLCPVWATKGDFAPN
929	7109	A	941	835	1064	WLGTGFSDEELEHHQSLKALVLPSR RPYVRIDGAVIPDHWLDPSAVVERK\ AADLSVCGMYPVGRG/LGERDRGVF
930	7110	A	942	85	344	KRKEKEPCQAPGTGGKNWFGKKRP MEPCPSGGPPPLSL/LPGNGGFPFGPS GGTGKTGFAPRGLPLEPQFGKPW EELYLAGF
931	7111	A	943	3	1160	RVDPRVRSPLPSSHFAFIEESHVPVI EESLRVQICEKAELKDIVEPKKSTLN ENQPEIKHQSLQKNVSKRDPSSHG HSNNKKNLLKVENGVTRRGRSVSPKK PASQHSSEHLDKIPSLKNNPKRRPRD QS/PAPAKGKIKVRSAPGQALDKISA EKAIEVGRPAQKKQKQIEGSKAPSNAE AKLLEGGKSRRIAAGYTGSNAEQIPDGK EKSVESSGKMQRISWKKSRTRSPEKK IKRMVEKSLPSKMTNKTTSKEVSENE KGKKVTTGETSSNDKIGENVQLSEK RLKQEPPEKVVSNTKEDHKGKELEA ADKNKETGRFKPESSSPVKKTLITGP WKVPSGNKVTGTIGMAEKQYLLYK TKKNTGVIFSLQKHFRSKS
932	7112	A	945	1	704	FFFYECGECGKFSQKSSLIQHQRHFT GKEPVGCEECGKFSFSEGLRSHQR VHAGERPFKCGECVKSFSHKRSLVH HORVHSGERPQCCEGCKSFSQKGN LVLVHQRVHTGARPY/KCGECGKFS KGHLRNHQIHTGDRLYECGECGKS FSHKGTLLHQRVHPRERSYGCCEG KSFSSIGHLRSHQRVHTGERPYECGE CGKFSHKRSLVHHQRMHTGNSTTW TMVS
933	7113	A	946	37	359	SSQMLGEVDPSPSGGECCHNACVCLPV SEMEVNGQVESVCESVSELESQA EALDLPMPGCFMRSHSYVRAIVKG CSQDDECVLSRSYSPPGTITTVRTIQS STCE
934	7114	A	947	106	468	PSLHTSHLRFFHLWADCSNTNPSQA KLRLRELSIQAERLTRYNELLK SYQWKMLNTSSLLGAETRQFNW/V SRL\ANLTQGEDQYLYLVITVSCVPA TCCGSGARAVIGSRGMCAFD

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
935	7115	A	948	81	388	FCPPFKGEGINPFGPTSSPKPKHPFVG PKPFGKKIPLSWPPGGFGFGKPPPLP NWGITQPLITRPKTCWLPLFSPEVVK TKKPWKSWGESS/PPPNYQ
936	7116	A	949	176	523	PSLRGPAPVFFLTWSVNSVHWAK GSTQALPATITLLLLTDWLLVGFPLT VIGGIFGKNNASPFDPACRTKNIAREI PPQPAWYKSTVIHMTVGGFLFRYPFF IPWLLSGS
937	7117	A	950	71	690	TLYLCCGGLFSLPGTVKEKACKSSLEAI LFGHAKLEPGRLPRPTQCRVEATVIV GTNSPLDNPLWSISWSLWQKPVGTSQ QQPLGLWTRFPLEGHLLTRNETFTE ATPLIPEIGMLSQMMSEEQNSNGDG/H AQKSSMTQWKWFIEDHATQGMQRIS FPLGLTLELCEKLLDSTVPNKQLSTD QTRASWFMDSKSAQNARKNCVSV Q
938	7118	A	951	24	365	PPFIPPLGSKRGGPPPIQGFGPPSLDP GFPPPS/PSLGAKVGSPPFKKFFSSSSSP PPLFPFPPGGASREGFLWPKQGGSLGP FLPHFLPPGGFLFSSSSPPQKQKTKQ NRTAS
939	7119	A	952	3	349	DFERLAHLTYDTLHRAYSKVTEVMHS GRRLGLTYFRVAFVQGFDEDEGKE YIYKEPKLTPLSEISQRLKLKLYSDKFG SENVKMIQDSG/KAHCFYPYVKKRIPV MYQHHTDLNPIE
940	7120	A	953	2	352	AAQMMMLNNPLFAGNPQLQEQRQ LPTFLQMQNPDLTSLAMSNPKAMQ ALLQIQQLQTLTAEPAGLIPGFTPL GALRSTGGSSGTNGSNATPSENTSPT AGTTEPHHQQFIQQM
941	7121	A	954	2	347	IFKKNDYKAPVKIVVYWHKDRQED QR/NRIESPFIYPHIEGQMIFNKGAKT TSSSSSSS/FSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSPARPETKLLGNRG KKLHDI
942	7122	A	955	609	744	NLTQISSPGKITDALSS/LAKRNSNFRAI SKKLNLCVGTGMVVRGDSG
943	7123	A	956	3	355	KHRVLKEVEAVIPDHCVFASNTSAFPI SEIAAVSKRPEKVIQGMHYFSPMDKM QLLEMITTEKTSKDTNSASAVSLKQ GKVIIVMDGPGFYTRCLAPMMSE VIRILQEGVDLEKL
944	7124	A	957	273	528	ITADNYIFMLFYLWFLMHFSHIHNRG DRVILLKRVDQNWVWKGKIPGTRNQ GIFPCSYYEVVKKNTKGAEDYDP/PI P/HSYSSDRI
945	7125	A	958	4	361	QHHLGDNFWVLPFRFCFACVVSPIR IHGSRNQIEGVVPLTCLPLNWSSTG LEGLVFTGMLPGNTRQQLNWTLR LTCCFGFPWALNQANKEGFTDSGVL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/19,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						PRGNKCCCLGAGRTV
946	7126	A	959	6	376	STVGDILGFSNPVSFPFGPEKGLHFGQ WWGGNIPPOKKGEKGGKTGAPPLEK PPSSSSGPTS/LPPGKKVPPNFFGQ/RG TPGIPPGKNSSSSSSSSPS
947	7127	A	960	1	356	RFERRMKLDLVLLSYTKSNSTYIKNIS VKPETVKLL/EQNIQKILLDVGLDK
948	7128	A	961	81	352	QPPRGLRRAKGEGGHAHGKNFFSGG FPLPGNYPPGPKPGPQGGPPFPQPDH RGLPKKVFPPSSSP/SGHPAACFPNGEK GP
949	7129	A	962	1	428	VHWGDLGSLQPPPGFKRFLCLSLLR SWDYRGLPRRPANFFLVEKGLRHV GQAGFETWPQANPAALASQSAWIT GVQ/HRA
950	7130	A	963	2	360	EGEEDEEDHEDPVRGDMFKRPSRSL PAPPRGTLRLPSGCLSYRTISCINAM LTQIN/PACTQITRELTGKSIASIPDE AFNGLPNLERLDLSKNNTSSGGPKA FKLLNYALPROK
951	7131	A	964	550	308	RINQLYEQAKWALLEIECTEEEMM MFAALQYHINKLSIMTSENHLNNSDK EVDEVDAAALDLAITLEGGKTSTILV G
952	7132	A	965	23	389	RFKMAPLWPGAMGPFCSPPLGGPG RWVPRFKNSDPSGPPGETGSSS/LPN/ QNLPGLVGGAPFSKFFGGGLKGRNGFT PEGEVSLNPNGPALQPEKKNSFFS SS
953	7133	A	966	2	387	TLYRDNAIPITPMTLFIEIKNTILKW MYWYHRRVQKAKPSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSNPQIYIKLIFNKKWQNIQFGKNS CFDKWCWVNRISTRRN
954	7134	A	967	2	382	ECTGSMPSASRIGRAGLWGRGARG SCKIKKVPKVFVIKKDEPWGHWGRS CPVWAEPAVSLRAPGLLCPASRAP HRLSLGRDCSAESPSPRFLPGSPSPSPT \PVGSGTPVLRPWFSSSLPRLPS
955	7135	A	968	2	900	FFFLRQEYSGAIIAHCSKLLGSSDSS/ SSSTS/CHHAQLIKFF
956	7136	A	969	1	332	ERASICRRTTTGDVQVLGLVHTIKLG VISDKVVVTYSKGYPCGGNKTASSVI ELTCTKTVGPRPAKFRFIDISCAYYFI WDSRAVCAVKPHEVQMANVTLNSP MNGESFOL
957	7137	A	970	1	713	RHCPTPSRILESSGVIIAHCILQFLGSS HPSCLSLPSSWNYRCVPSHIALHFSV GSYYIAQAGLKLSSSDP/PASA/FQSI

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
968	7148	A	981	3	192	AQGGDARLPAHQQQFRERLMQELL SRVQLQQTWNTAGMLNALQSEBRTLV QDLACPDVVRVT
969	7149	A	982	3	365	YIEPQLPDGATLKDVRLQIPMQIYSAD GELIAQYGEKRRIPVTLQDIPPEMEKA FIATEDSRFYEHGGVDPVGFRAASV ALFSGHAVQGARSITQQLARNFFLSP ERTLMRQIKVEFLA
970	7150	A	983	30	288	VSFTTVPPSPPTGSPYP/QSSPPYGPPA VPVPQTHPHVT/VLPIHGPPPPRALPS TSSGHLPGAPERPRTPHQEAPSLYPL KAGTP
971	7151	A	984	1	274	CCLQETHFTYKETH/YLKIKTWKKIFH ANGNQKE/AGIAMHTSDKINFKTKTIS SSSSSSSSSSSSSPQEDILLVNI
972	7152	A	985	3	383	PTGMALKVCPHLTLLAGRFDAYKEA SNHIREIFSRYTSRIEPLSLDEAYLEVT DSGHCHGSATLIAQEIRQTIFNELQLT ASAGVAPVKVLAKIASDMNKPNGQF VITPAEVSFAFLQTLPLAKIPG
973	7153	A	986	1	144	WRNGKHTDHAFLA/N/HGPVVCGES LQEAANNMEELEGAKLFIILGDR
974	7154	A	987	217	737	LAHRRPELQQLLVLYFGLGQPFQDHS QSSTACGPPSLRQETQTFQEQTSLGH P/FALGGKQSRTPPSTC/RHRSRPLSC PGRKRSEPNPVHLHSCSRSPSAVLGG RGQSRTPTCTSTRSRASSALGGRGQ SRTPLLALLQKQSVSCQVEGVSVPRT LPRGARQGVNARGSSVS
975	7155	A	988	2	348	KISVRPLCWLNPNAKLCVPQTIDAGP EGRTVFNLIRFDLAMLNFFTPTQAS GIFPGKANVAWDTTKEGLPQGSITLS GRNVQVTQTVMDAALPVAFQTLNLT AELRTTPAYL
976	7156	A	989	2	285	GGTFLGSARFPEFRNENIRAVAIKNLK KRGL/PKLLVNGGDSYMGAMRLTE MGFFPCIGMPGTIDTDIKGTDYTGFFT ALSTVVEPINR
977	7157	A	990	1	424	QKRCPPLEATACAPPHSVFVPLWPS PPFPDCKACVVRGSSSTALP/HGPIPL PPGPD
978	7158	A	991	1	76	TNAITMFEVGVKTRIQRSREVILMA
979	7159	A	992	3	164	HLKGCEPDVRIILLTRH/GNNNGSQSP WMEEQIRDAWGSMLVKNVREITDE VGKG
980	7160	A	993	3	337	LNWYDVLITNGPSTDLGELALGQKM RVAFMPWNVYNLKDSILVSEVVQF DRFTTHIQELACVSRNTKLGPEITA DIPNVGEAALSKLDESIVYIGAEVTTG APPLVAK

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981	7161	A	994	1	309	PRVACPSPPSLAICPPSPGGSPAPAS PNPT/SGPCPAAISLAPAPMSPASRLM PQTALPACAFPSCTA CLHPALSQPQI WAVNPWFSASAVQGRTEYQRTAN
982	7162	A	995	3	86	RAKAEQAGDNLSCIMETYPSTHGVY EE
983	7163	A	996	2	387	GLSGQLLELYLLVLEKEGSLLRQEES KAAPGDEAEAVH/TDFDKKTSSSSSSS S
984	7164	A	997	7	254	LRIHCPDPDIKVSVLTLTRPLMMEDT LWAASGGQVFIIIVETHAVEVSHLGG YTVWKKCISETAQLTSGAEVKASCL WLNFL
985	7165	A	998	1	80	IERYQLPQSYQRMPDIRRRFMQV/CV N
986	7166	A	999	1	99	STVSELMGLMDY/GLKEFKFPAAEAN GGVKALQ
987	7167	A	1000	3	102	MTTVFVQAIDLRSSSTA GWRNALSIV EPVCNEIF
988	7168	A	1001	1	236	CCLQEAHFTYKETH/YLKIKTWKKIF HANGNQKE/AGIAMHTSDKINFKTKT ISSSSSSSSSSSSSPQEDILVNI
989	7169	A	1002	291	671	MLEADMSSSKGRKCPYRPPISAPAT VNQSFCLYSPPIFGPATFTQFGSLSL PFVWPSTCHPSCFVYSPPTLAPANCH PSCFVYSPPTSPATV/TPSCFVYSPPI SPAIVTQASVFLVKKRCRFR
990	7170	A	1003	3	109	SERKFTFHRPLIARTL/VGYRSWGYEN RHYYRRDAGN
991	7171	A	1004	3	141	FPEYHQLWPNNKFNVTNGITPRRWIK QCNPAAQALLDKISQKEWAN
992	7172	A	1005	89	339	KVNMKNQLLSYIEAINNWNLFQNI NATAIKIPASVLTVDKRLKFLIWRG/ KRPRNTANKIGREENKVRGVTLPFTES AFLQAA
993	7173	A	1006	31	253	DLHTVLNWRFSKATLRRVGANS DGS GVLCPFASGDSMEPVPDGTAVAVDA GNKQVIGGELCAIS/QGDLRVPT
994	7174	A	1007	1	142	IFKQKQFFANVWIEYSRIKAMNLS E DGLVLMQLEQRLLIIRVRNID
995	7175	A	1008	3	116	EIMKGQRDQMKRPLEERRAMHDII ASDTPDKVKA EA
996	7176	A	1009	68	217	QIPGRDIYPISAKVFRSFNTPK/MVSA RDVAQDTISR
997	7177	A	1010	3	81	ALKGLRVLLVEGNDPQGTASMY/HG WVP
998	7178	A	1011	21	388	PLGPEIQTPSPPGTETPPFFKKPKLTGG NGRPLLFPPGRKLPENSLTPQSPGFQ FPKFPFPFPPALGPK/PRL

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999	7179	A	1012	3	385	LGGRVPLGPETPPSPGETPPFFKKPK KITGGKGRPPYPPFPGGLGPKIPLTPK AKGSVFPNSPPALPLGGPKLTPFSSSS
1000	7180	A	1013	3	663	LKGLFFWAPPLLLLLLASTGCESALF IPLTFGNHPPGALLAHTSSTLFSEEN CQLLQHIADRIAIAVGNADAWRSMIT DLQESLQQETLQLSEQLLSNLIGDII YQSQAMEDLLQQVDIVAKSDSTVLIC GETGTGKEVIARIAIHQLSPRRDKRVV KINCAIAPASLLESELFHGDHGAFTGA INTHRGRFEIADGGTLFLDEIGDPRGP SASLCQRG
1001	7181	A	1014	1	262	KGFLLSPRVGGQRGVLSQQGPFPFGL KKFSCAPPGG/RGFRGPPPPPGASSSS SSSSSSSSSPPEGFYFPAPIFCRPGPKR WGSRV
1002	7182	A	1015	3	238	RPTGRRAGPRAIPRYAASFHGSVP Y/HVRTIPVTRRSPDPLSLAPRKERP TRSPGAAVKPRPAPS VHASRWCLPE
1003	7183	A	1016	2	261	DKLMERRNRRTGRTEKARIWEVTDTR TVRTWTGEAVAAAADGVTFSPVPT PHTFRHSYAMHMLYAGIPLKGLQSL MGHKSSISTEV
1004	7184	A	1017	3	463	TERADTGRGTRDQHERRGGPAESE RTPGRSDAAGASAA/PRERAPITAG HRGGPGPPARARRRRPPGRAAPPQPP PSTSYSSSSSSSSSSSSSSSSSSSSSS
1005	7185	A	1018	217	435	VTTGAGPSWGTTRVTRQASVRPSRGP APGTPPPRRPPPA/RRRA/PGAPAVV AWRPCAFACDAAGKPRAAQSLSWG
1006	7186	A	1019	1	229	SSTPRFTPSLPRYSSPLPSPNCFSHS FPFCLPSFARQPNFYSLPIFPFPPPLY IPASLPSLLATVCFYSIAL
1007	7187	A	1020	3	402	PSPSSLPLASRSNSQGP PPPVQSRHHS QPT/SRPRPREPDTTPPSPLPAMRLPRA PRLPPMQAAQPNLPQPT/HPLPLGGTD LAPFSSSSSPVRN
1008	7188	A	1021	1	181	FALPFEPAEAEADDEEYDLWSTGRVL EHWHTGSMTRRVPELHRAFPKAVLF/ IQPLDAKAR
1009	7189	A	1022	3	248	VNFSCPMTSHAMGSDVGGQSPDMV KKYSRAV/KRGSQAQMLGKMTANIG NILQLA/LAPQGGPDGIATNSPVKSL SIFDPVV
1010	7190	A	1023	1	482	HMPSGETAPLRIVDTGTGTVAAYA PTELGLHEMHKHYMAHILESPLRFY VTTPTPVPSVAYGPGLVYGVANNTA TFTIVTEDAGEGGLDLAIEGSPKAEPP RPRLSRAPGVDGAGASPLGDIETGPG APDLQSLDRSASRPLLRPHLRFLSVG VSAVC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1011	7191	A	1024	2	249	YAIPLRADTSKPKLTQQDVTDLIAYL NKGGSVLIMESVMSNLKEESASGFVR LLDHADQSMALNTSLVNN/DCPGNP TRSVR
1012	7192	A	1025	86	657	PGFSLRFLFKSKGGERMAFPNPWPHR NFSWVLPPRVCPRIPSAMPKP/TSQ NLAGYWDMLQLSIEDVSMKFDELQR LRLNDWKMMESPERKVRASM/PGPA PSKPP
1013	7193	A	1026	2	591	PHHEGGAPPRWGRKRKNVIPPVHT RADPHLKQSSSHPLQQLLLGGRRNS EQSTIIGKTRRTQKRKGS/AVPIVGG GKRIIFPGGAPHCYPRPPSSPPPPPP PPPPPILTSSSSSSSSPLPLPLTSSSS SSSSSLLSSSSSSSSSSSS
1014	7194	A	1027	1	103	YGDGSSKAGMMNPSYPLNYMEKPLT RLM/LGRS/WW/D
1015	7195	A	1028	3	522	PMTMTTRFLRPLPGDLALKGLPVLLVE SNHPQGTASMYHGWVPDLH/ILVQNT ALLPFYLGKEDDVTYAIKPTCWFGLD IIPFCLALDRIETELAMGK/DEGKLPTD PHLMRLRLAIETVAHDYD/VIDIDSAPN LGIGTINVCAADVLIVPTPAELFDY TSALQLFDMRLDLKKNV
1016	7196	A	1029	401	649	ARELLGPSSEHLPTVTC/AAFOEERKV PPPIPKKPPK/GKFPITREKSLDLPDRQR QEGRRRLMPAKRAS/FRQDSASERA SSI
1017	7197	A	1030	215	651	ERTLPSFFLFLATPFPAPPPPTPK/PPP TPRFPFPFPFP/PPKHHPPPP/PAPAPSY PRHPPYPPPT/PPPLFS/PRGCLF/SFP/PT KSSSPKSSSSQKDS/PGKQKASRCKDS SSSSPPKKGT/SDPKDQKPKTD/SSSS SSPQKKA/SSSSP
1018	7198	A	1031	313	687	GQTPPSKGKT8FKVTLRHCNLAFAF VLT/TTWEKPGGNPLNSLGRK/SSSS PSPRNPDT/ESHSPWGP/PRQGP/PLSS SEKG/PHTGPPYP/PGIDP/PTPRP/PTT NTPPRLSFGANAP/LL
1019	7199	A	1032	103	708	TAAPPPPPSWPPGSAGPALRHRRLGA AAPGNW/AHPV/PGM/WMMW/MGHLPGPQWLLGCGPKVELD/GDVM/GAP/S LQPVGS
1020	7200	A	1033	136	410	RRFLCLRIKVKSTVEILEKSOIEAIAS SLASQNEVPAAPLEELAYRSLRVAL DVLSPGSCSQESSAGTGRDNRSLRG KPMYCD/EMVGP
1021	7201	A	1034	2	395	FVYSACTCESLDVKA/AHKRPSQR/IG S/RSLATACTMDHASHGLLERHRTNG ILDSMGRFFGDMGAPKRGSVKDSH IIPARTAHYGS/LPKQSHGRTQDENPA VHCLKNIVTPRTPPPSQGGRGLSLSR FSWR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
1022	7202	A	1035	406	13	CPRL ESTACASPSLSHAPSFPVHPWA PDPQAPSSSSSLRAQTRPVSLSPGLRS DAPPRVSSSEGPGSPAPVPKLWRPRP NPPSHTCLRTVNASPVNQFFGYTAN STATLSWVRPPTPTTRTPVT
1023	7203	A	1036	1	397	FLPSKIFSNTPPLPPLGSPVPPRGPFGT PPRAASPRGIPLPREPQGIAFLTA/PP KFPPPGTSPVEFPLLSLGRRIPLTPEK GSVSQNSALALPPGGLKLNPPFFSSSPS SSSSSSSSSSSSSSSSSSSS
1024	7204	A	1037	1	301	WVPGGGSGSPRSPPPGPGPP/PGGPQ APPPNAPPAPRGNPPSPKSKIFFSSSP RGPHSPPLGGPRQEKGLTSSSSPSLNP GPPPPSRPGGQAKPLGEK
1025	7205	A	1038	2	512	FVKRHVTCKMCAVPGEAEPIWVVL FSDLGLNNITAKALAYGDTNCCRDG RSSKHPEENHADRRVPIGVDHVRRSV MVEAEGVPRAITYSAFFCPSEVHIIS TPNKYEFQYVQRPRLRTFDDVA HNDARVALSSVPHDTARMIEILGGH QNTSRWISTSKMGEHVA
1026	7206	A	1039	20	453	GIPGSTISLFCSEKKLREVERIVKAND REYNEKFOYADNRHITSKYNILTFLPI NLFEQFORVANAYFLCLLILQLIPEISS LTWFTTIVPLVLVITMTAVKDATTDDI LQNEKWMNVKVGDIKLENNQFVAA DLLLSSEPH
1027	7207	A	1040	3	416	GVSTPPGPPGVKPPFSQNPKNSSSSSP PLVFPPPGGGGKIFPPGEGGKGGK FPPGPPGPGPRNPFSKKKKEEPHGFQ KKRGRAFSPGDFFLGTPSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS
1028	7208	A	1042	1	390	IAADKMGGKVVLAETTTAHTMAGL HYHQQDWSHAAAYVTVPPLRVDN TSSYFMSLPNDTLIIVASDRRPFTTK QKAMGKEDFTKIPHGVSGVQDRISVF WERGVVGGKMDENRNNAVITSSNAV CGR
1029	7209	A	1043	3	387	AQDAGPVVLQQLPYPAPQPCQSPGR GSASAESSGAPSAVCLQGPRIVPGA AWGPAALHLQHSQTAAWPAALPRPCC WPDGPLSPARGVDARGLGPSGAGPA GLQPCPTA/PALPGTHGCQTPAAPT K
1030	7210	A	1044	125	420	RGCALLFEGGVCGAGSCVRSGCCRG VACSR/RQRDSLVEHTGFCGLVCE HIHRLNYKERAGLQRRKRENMSDGD TSATNESGDEVPELVYTAHQHTP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1031	7211	A	1045	2	409	QGRKGTTSPFLSPHVITNEPKLRPFSTMPRLGSPPRAPSATVQRSPPKPWFQSETMGSQLGTGLSTRNLRLARPTRELPATRTSRASEQQ/PSSRPALPAPEITFEAHADQTDLLSPLEASQGPVSKHSPLPA
1032	7212	A	1046	2	414	LSLSWCHLPSHPHCICSGALRRWKENTMARVDEAKKTFQASTHYRRITCSKVRYKEAS/SVTQESWDCVLVR/DVGRGWQCRFELNKEPRKVVWTFQLQHAHKHPCGHMFSLNNSKNYAINRNITHMYCGRSRKSRRLL
1033	7213	A	1047	1	349	IELLDTVQVNFVTVD/RRTHHFQAKGDSNLDLNFEISFGGIPTGRSRAFTRKSFHGCLENLYYNGVDVTELAKKHKPKQILMMVRKPNPKGKRNILFFAFKNYSCEVSISCNILRIS
1034	7214	A	1048	41	247	LVTTPAGASRDGSDPR/TGKEGQRALTLTLLKVEDGCHRLLETGPYLYVNGDLVEYDADHMAQLQLPLP
1035	7215	A	1049	1	452	RGAAATRTQPPGGTGPAGNAGQAKRMGSGPFRIPQDEESTPFCPLPGDYGPASLPPEAGMQAPDVGSSSLGQWPVWVAPPGPGWSPPRCKVLPASGGTPEASESGFP/P/GPPVSGWDPRGRQSGC
1036	7216	A	1050	3	391	TEQQFHPPEIYKSTKCNDMQSGSCPRGPFCFAHVEQPPLSDDLQPYLSCVQPHPAGSCPVOQPSAAGDSVPVSPSSPHAPDLSALLCRNSSLGSPSNLCGSPPGSIRKPPNLEGIVFPGESGLAPGNV
1037	7217	A	1051	88	795	RREVTSLGVHCGPSSGAGPGFGPGSWASLDRALAEAAVTGVLSLARKLREFPRGAANHDLTDTRADLSRNLSEIPIEACHFVSLNENLYQNCIRYIPEALNLQALTFNLISREPNLSTLPVHLNCLPLKVLIAKNKNKLVSLPEEIGHLRHLMELDVCNEIQTIPSIQGNLEALRDLNVRNRHLVHLPEELAEPLRLDFSCNKITITPVCYRNRLHLQITITLDNNP
1038	7218	A	1052	1	315	NTCWFFKTNKIDKPLVRLIKKSEKAQITNISNEKGDIVTVHTQHRIRKRLYANEFENADKMDQLLENFILPKSTQEEKEILNSSIATKGVTA VVKTLPAITN
1039	7219	A	1053	4	445	VHIIT/EILQKILRSSQCLIAITLILIMGLI AVTATAAVAGVALHSSVQTADFVN/NWQKNSTLLWNSQTKIDQKIVNQINDLOPTVMWVGDOVASLEYGMQLKC DWNTSDFCITPPPYNELAHWEWKRIKKS IWKMDMYAAGVRSTIRITLQ

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1040	7220	A	1054	1	429	YGLSQAAAVATSREAAHGEQPF AAFSSAAPPTGGPPPSADAAASGASALCA FPLDEGDRLANRTRDACYTREGRAE DGTEVA YIEYDVNSDCAQLPEDTLDA YPCGSNHTSPMASRVPLEATPIL E/WPGIQLTA VAVTMEDG
1041	7221	A	1055	1	429	YGLIQAAAVATSMEEAHGEQPFAGF YSAAPPTGGPPPSADAGASVASALCA FPLDEVDRLANRTRDACYTREGRAE DGTEVA YIEYDVNSDCAQLPEDTLDA YPCGQ/DHTSPMASRVPLEATPIL E/WQGLANSCAATVMDDGH
1042	7222	A	1056	23	356	PDLSPAPGWYMAVGTTHRGKEASTAA LRSPTLREAASSCKLRLWYHAA SIEVHPGPPLRVGGAQEGGWAAGDKQG RSCPGTPDIADV AELRVELTHGAETL TLWQSTGPWGP
1043	7223	A	1057	5	249	NQAREDFNQDQGWCVSLITDYRVRLG T/CGCWGGVELGSRPASEDPD LGLG R/RLPGGGA YFRGPAFPVGG LGFWP GLIIS
1044	7224	A	1058	3	400	GRIGRPKKYRKIPQEDFQSKGLSAP/ DVLHHRVFTASALS
1045	7225	A	1059	1	419	PISSQFTQGDVPSQVDAGLSITHIGET PSEHGKCKKILSDVSLDLHQQLHSG KISHTCNEYRKRF CYSSALCLHQKVH MGEKRYKCDVCSKAFSONSLOLQTHQ RIHTGEKPFKEQCGKSFRRSGMYV HCKLHTMY
1046	7226	A	1060	3	304	EVIIAAWYRTFIGIMNLFGL E/TKTCW NVTRIEPLNE/ IQSCEGLGDPA CFYVG VFILNGLMMGLFFMY GAYLSGTQLG GLITVLCFFFNHGEVCFLESNF
1047	7227	A	1061	2	414	NRCFGLPPDLPA PCLPSYPTCRNT/ C SWHAPPHFTPECPPA FGPQC TASPCL GLCLCWLVP/PRVCW/PCPPRP
1048	7228	A	1062	2	374	HPNNSKDVVTLEDVIEML EDEDMPCKDSALQMGSIKEKMKAGSR TGK/PQA HLLSKPFESLKLESKKRWIMEKEIPR KTTTFDMKSISGESSSHGVI MTRLTESG HPSSDA WKGENWLYRNQNV
1049	7229	A	1063	2	426	RADLFMHQKIHAAE EPHKCDCKDG FFHISELIIIIWDRDITGEKVYKDDCG KDFSTATKLNRRHKIHTVEKPYKCYE CGKAFNWSSHLRIHMRVHTGEKPYV CSECASPFSNSSL CIHKRVHTGEK/PL YCARSGR
1050	7230	A	1064	1	388	RGGSALGGGSPWPALQG/AGLPHR/ RTSAISGSPAPCSAQPSLLGFWDILAP WPSSPARHPLCPSPHVPCPGMRSWP/ SPSRTSPGPKHDYS AFLGPSFEDPL PRGDCHRCTHSSVQAMARLPIQGGCI

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1051	7231	A	1065	119	393	YIGSVLIHLCLFLKPSCAFPVCHDTEER CRLVLSYVLEGLKSVDSISKKRKAPF QA/QLTPSTPIPLKYEDE
1052	7232	A	1066	1	428	RRNSHLVEHWRHTGQKPYKCECD KVFNRNSNLARHQRIHSGEKPHCENE CGKAFRECSGLTTHLVHTGEKPYKC NECGKNFRHKFSVANHQRSHTAEKP CECNECGTVFSLLSYLARHQIHSTEK QYCGRCG
1053	7233	A	1067	1	400	RASTIIGNGDLLQKQPIRPQSSPEDVQ VATVSSSPETKKDHPKTGAKPVCAHL RIHSLAPSDDESSWTTLYQDSASASSP DETADIWSDPSFQTDPLPWPWKRV DIAGTYSWHIPTGTQWERPVSIPACI
1054	7234	A	1068	3	399	CSEHVSRRKPGTKMTPAHASTNTSL DLDTSSVPQDAATIRSSSMQVPTVCIC LIKNDSTGPRLDKKVQHLDPHYGPA RASVVLQSQSVQACIDCAHYQKTLVFC FLKQAHGGEVQAVFDREQHTLTLPA CI
1055	7235	A	1069	154	402	PPWNRVCVCICYTCGLLAQVCVCAH VCALV/CTT/ACVCPPARCLVWRHICV WPCLDTSVCACVCAPWCTHPDRRAV CLFADGQ
1056	7236	A	1070	159	583	PGRPSATRPNTSTGNQWETSGEDNPN KYHASKGWFEENFKNRCCFATYEVVDG EEGPLNPEWVSSIP/EQLERGFVPQV FN/AKEMTHLLQCMPSYFVGKQKKS GK/GLEEAKDRISLIFCGSASGDKMIK PLLLYKDSNTPLVF
1057	7237	A	1071	2	395	VQAVLPKYDDISLPKSAIA/CYAAALL KTRSVSEKFSPETASTRGLSAAEINAV DAIHRAVEFTPHVPKYLLEMKSLLLP PEHILKRGDSEAJAYAFFHLQHWKRIE GALLTLLQCTWEGTFRMIPYLEKGL
1058	7238	A	1072	2	406	LLTPSPCPESGCVFSAEDRRKGLQPHLR QTHRAVPVPCSRFGCPLLFGSQQMG LHRQAHYPPFCHSCSFSGSNVKLFERQ HQRSHGAGTQENFLPFAHFPRSCC QLPNCLQERENLHRKQVHPCLGRQ LKRSV
1059	7239	A	1073	43	400	LFCTAEV/DLFGDA/FAASPAE/APAA SK/GAAAPATPTPVAAALDACSGNGS AEAAPELDLFAMKPPETSVPVVPTTA STAPPVPATAPSPAPVAAAAAATTA ATAATSSSSSSAATAT
1060	7240	A	1074	82	398	TVPSITDGGCCRPNGPYRR/CGSPGGE GLYPGAGASIEAAGRDRILGSDGPGET PPAGGGARAGAGGARLQGF/GPGPH RPNPFAHPPSPSEAGWARSERRGDA WAR

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1061	7241	A	1075	413	2	CCLPCLTLPHARPGGPQL/PSSGGGGG GGGGWHHGPGRCPGDEDTAAM DSPCQCPQLSQALPQLPGSSSEPLEPE PGRARMGVESYLPCLLLPSYHCPGVP SEASAGSGTPRATATSTTASPLRDGF GGQDGGGE
1062	7242	A	1076	1	398	DESYEEEEEMPDSDENGSYSTSSDP DDSKAVAIKSGELSVPEKYKSIHQ RPSCAFPVCHDTEERCRLVLSYVLEG LKFDVSSIKKRKAPFA/QLTPSTPIPL KYEDE
1063	7243	A	1077	181	418	ELLYGPNQQLGERGEHSPLERDS LMPSEASESSRQACTGSSQRSSRL EEDYADITYQDL/YQP
1064	7244	A	1078	1	504	EDSSCLPEDLSLKQ/LKTIQVKEEPVEE AEEEAPEASTAPKEAGPSKEASLWPC EKCGKMFTHVKQLERHQELCSVKP FICHVCNKAFTNFRLLWSHFQSHMSQ ASEESAHHKES EVCVPFTNSPSPPLP/P GHPTAFRSQPLEPDS/PTGLSENPTPA TEKLFVFLY
1065	7245	A	1079	3	573	HEESRTVQGGVLQGWEMRLQTSWI LQQDFLRGQTSIGIQLEGKHNGREL DCEQCGEVFSEHSCPKTHVTRQSTGN THDCNQYKDFLTLCKGTSTGEKLSE FNQSEKIFSLTPNIVYQRTSTQEKSEFC SHCGKSSINESYLQAHMRTHNGEKL EWRNYGPGFIDSTLSVLIETLNAKK PYKCKEC
1066	7246	A	1080	1	384	LHFSRPGQGRGPAGDASLFGGPSRPT DSDTLARRHTASGAPGPEATFQDRPE RSARGSRGSLPSPVHGSWAPARRSN GLMRATSSGAPTPGLPGPGHHFQGI PPQIS/PALPRKQSLVPEPPQRPRL
1067	7247	A	1081	558	850	RMAKSCGHPALPGLILFPLPLQIEFVT GTTKGGTTINATSTTTTTASTAVADAQ KRKSKWDSAPVTITIAQPTLTTATL PAVCSRSPAPG/SKTTV
1068	7248	A	1082	2	418	SLDLPDYGGGGLHPAYPPSPPLSASD AFSGALRSLSLKASSRRGGDHVALQP LRSEGGPPTPHRSIFAPHALPNRNGSL SYDSLNPSPGGGHACPAHPAVGVA GYHSPYLLHPGATDEP/PRPLPRSVLRP LWMSYLEA
1069	7249	A	1083	43	395	HQTGLLAARGSRCTLYQYLSSEFCE/R LLSLLPGQA/WHGAEPQVQV/LEE QPPGTLVGTIQTTPGFTYRLSEHALF AINSSGALYTTSTIDRESLPSDVINLV VLASAPTYPTCI

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1070	7250	A	1084	3	423	GTSRRSKSTASTSSVNGTPGSQLYIPRSGKSCQCPSPSPGSLRKQRSSQHHGGS\GTSLASAKVCSSMDENDGPGEVSEEFGFIPATIA\ERYKVGRAIGDGGCAVVKCEVERSTAREYALKIIKSKSCRGMYCGRSEVSA
1071	7251	A	1085	37	376	VSGEAPGTTQAPPEPGVPAPNPLSPCYPHTPGKIQQYTGQPAQAPDPITSPGW/DPIPTSLQFPFGSHASPGFLPTYPYCPNCIKIVSVPPCPCLCQGGCHLPLGCLSLSPCL
1072	7252	A	1086	3	409	PHRSSCFELYGFDVLIDSTLKPWLLLEVNLSPSLACDAPDLDKIKASMSIDMTFVVGFCQDPAQRASTRPIYPTFESSRRNPFQKPKRCRPLSASDAEMKNLVGSAREKPGKLGGSALGLSMEEKV/IRRVKE
1073	7253	A	1087	159	402	KGTFFPGPPGGGPGGKGNWDLWAPGRKGRKRFAPPGPTAGNKGARHPGGRIFDFLKKKGFFLCGRGGIN/GPENR
1074	7254	A	1088	3	384	LLHPPFVQGGARVPPLTPKPYF/PDFMKTWVVPFFTRGPPFTPLDPRLLPQTVFFGLAPGPGPH
1075	7255	A	1089	1	280	AITATATGYQESHLSARTKQPHDPLVPLSASIELILVEDVRVSPPEEVTIYNHPGIQAELRIREGSGYFFLNTSTADVVKVAYPGGPGVSPW
1076	7256	A	1090	3	407	SSQDGGQICSLQLQENTFVEQVVNEKVKRLGDTLKDRESHRSILKDEVITYMNNRKLTLMDAQHIKDEFFHEREDLEFRINELFLAKEBQGCVIEKLKSDLAGLNTQSCYAVHPHNREEQSLKEQCIATALDETT
1077	7257	A	1091	1	379	NTLVESWKSCHGDLFRSDGYPVLEYIPENVSSALRSVCTGSSPSKIMCVCGD/EASGSHYGVVTCGSYKVFVKRAVBGKCSWLHTYLVWAGRNDCIDKIRKHCPCACSLHKCRQDGKNLGARMALWNRPPVVGVILVGLGIALVTSPVILLAPPCHCCVCKSCRG
1078	7258	A	1092	3	494	QQVTAWRKIVAIYKPKDKQPVCKTLKEFLQISRKEGTPNLSRWAAQDMNRKFTEETHSEK/HL/RRAAQSLEIREMEMQTKRQFKAAAPTCQ/RQCGDVGRS RVC
1079	7259	A	1093	544	0	TGCGKAFKLKSGLRKHHRHTHTGEKPYKCNQCGKAFGQKSLLRGHHRIHSGEKPYKCNHCGEAFSOKSNL RVHHRTHTGEKPYQCEECGKTRFQKSNLKGHQRTHSGEKPYECNECGKAFSEKSVLRKHQRTHTRGE/HPYCNQCGEAF
1080	7260	A	1094	3	457	

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1081	7261	A	1095	3	434	KCEKAFKLKSGLRNHRHRTAGEKPY KCNQCEKAFGQKSLRGHSHIHAGE KPYKCNHCEAFSQKSNLRVHHRT HGGKPYQCECEKTFKQKSDLKRHSI LLPGEKAYECNECEQAFSEKSLIRKSK AHPSVCTILYSIQDTI
1082	7262	A	1096	233	458	VEADEQLCIPPLNSQTCLLGSEENLAP LAGEKAVPPGNDPVPSPAMVRSRNRH KD/DCHIKESMAAA
1083	7263	A	1097	89	370	EEKSDGGCCCKGWRLQVPS/HSQCLDL PAASLNDQLPQHTFRVIWTAGDVQK ECVLLKGDGTCSLHLQQPPSLFSSQ GCTLQPPITLSPGRQEGWCRDSTTDEQ CI
1084	7264	A	1098	37	397	CLPPPRQPRAGSPVLC/REGCWS/RVK SPPGDVHAARACAPGRHSGEGPPQG NLSPPSCPAEAGHGCASTGRQVGVSG AGSSPSGPAPCVKCSAWVGTCPPLSL LQAAGGPAGSPNGFCPEPWA
1085	7265	A	1099	3	363	SSHQSPINGEVPAAVAPAOEKS LGNI QAKPTSSPAKGPPQKA/GPVAVQVKV KKPMDNSQSSESSVSADSEQAPAA MTAQAQKPAKLFQSKACPKKNTNP ASAKVAPERVGTQAPRCI
1086	7266	A	1100	20	400	LQEAERKEYRVNPRESVIPLEGVCEF REYGSECMKTPSPFELLELP TSGGFLR LGRPCCYIFPGGLGDAAFFAVNGFTV LVNNGSNPKSSF WKLVRLDRVDAV LVTHPGADSLPGLNSLLRRKLA
1087	7267	A	1101	251	397	RLKKLKLLEPPHNPAPLLGIYPTNM KALHKDGTCPMVMMEHLFTIQGD
1088	7268	A	1102	11	447	WTSMPARSMI/SAAGGKAETSAAALG KPTAGTTDAGEAAKILAEKRRQARL QKEQEEQERLEKEDQRLEREELKRK AEEERLRLLEEARKQEERKRQEEK KKQEGEEKRKAGEAKRKAEEELL KEKHVCVRSRSGSFGACKCT
1089	7269	A	1103	2	407	GASNRVATIKCNQC/GLGFSHKFGL/IS HEGNHAGENPCECKE/CGKAFSRKEN RVAHQKFHTGEIPYKCNCEGKAFIQM SNVIRHHRHAGEKPYACKDCWKAFS QKSNLIEHERIRTGEKPYECKEYKESF SQKQCI
1090	7270	A	1104	1	375	GRGREPQAWGAETYHSGVTIKELDY YQAIYVWHTSECGQSDSTQGGGAGI KPLPNGLHSFQDCFTVSGVWNVTEL VRVSQTPVATASGPNFSLADESPSY YNITQVTLGRSSITSPPSITSMY

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *==Stop codon, /==possible nucleotide deletion, \==possible nucleotide insertion)
1091	7271	A	1105	2	389	CLCVFLCVFISVFSIIC/LLCLSRLVC LSCLCLMSL/CSCLCL/CHLCVSVSFC CFCVSVSFCFCVSVVYSLCLCLSL DGHGQAPVCAPPPSPFPHPVQPLSLRS PLAESWTGDDWGGGRSPSGLAQM
1092	7272	A	1106	1	551	TIMVYATITSQLLPITAKSHYTFKPEG TSPKVFIQGMMLADPAQGRRTQVQL LRLWYHENCRIVFRDRLVNEEVRSW FEQLLKL.CMEQWECDLANKVCPFPQI LYGDFMSPRIADVKSYLEITSEKMM QVIEEYIEDYQNTAKLLVLFMDA MSHMCRISTRQLQALGNALLGVGRG SGRSTR
1093	7273	A	1107	2	518	PPGKFRFSCSLSPSSWDYRCSLPRPAN FFVFLVETGFHHVGQDGLYLLT/S/GD LPGLASQSAGIPQVKHAWPLFSLWL
1094	7274	A	1108	19	405	ASRPQGLLCEFVSDRLLDKW/VELRN IDSFTPPVAHCISVSQDYIFCGADGT VRLFNPNSNLHFLSTLPRPHALGTDIAS VPEASRLFSGVANARYPDVAVTFAP TNQWLSVCYVNGHSIYVRDVRDLY
1095	7275	A	1109	1	555	KKVGNYYTPIYFRMKCHLVNYYIE MQTDPANC DYVIVSGAQRKEERWD MADNEQVLTGTGERHPLTCLGAL/DE SALGPPKPSRALIVAEHEKKQKLETD AMFRLHEGEADRSTLKKALPTLSHIQ EAQSAWKDDFALNSMLRRFRVRGA PARGORGCMVDQGP GPALPPHPSFE QATCTF
1096	7276	A	1110	78	399	FIHRPSDSGPPAERSPCGRVCISGKK HSYPSCWYPLPKHTASCPISTSILTLP LADLRPLMWKDT EYFKNGDLHRW AVFLLQLQGEHQDTMIMIVDRTLTYC I
1097	7277	A	1111	366	1	APQEPGVAPAPNPLSPCHPHTPGKIQ YTQGAQAPDPITSPGW/DPPIPTSLQF PGSHASPGFLPTPYPCNCIKIVSVPP CPCLCQGGCHLPLECQLSLSPCL
1098	7278	A	1112	2	530	RSFRRRAHLTEHLRLHSGEEPQCPE CDKSFWSWKASMKFHQRMHRDEKFFA CGQCCKTYTHQSQLEHLRLHSGEK PYQCPECEKIFRLKGNLKSLLQHS QKPFSCVMCGKSFTQ/STGTEHRS STAGEE/VPSQCECDKSYCIRGSLKV HLYKHSGERPFQCPCCGGLQ
1099	7279	A	1113	3	385	KIRGQRNLPPGL/SKDRPIPNFMQGV LAKTTAHTPGNSVVPQLQAQNVQH AGGQAGAPPNQMQVSHGAPNMMQ PSLMGIHGNMNNQSDISAGHGVN NKQNNISANKPKKKKPRKKKNSQ DLN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1100	7280	A	1114	427	0	SSSVQPEFN/WGNFGLPQSPPLKE IFFPHPPKRWDHKETPPCPANFGPPKK KGVSP/WWEGWAK
1101	7281	A	1115	281	426	YAPEGVQKILIGNKADEEQKRQVGRE QQQQLAKEYGMPLYETSACTMY
1102	7282	A	1116	3	403	PLARPSIDYS/EMECPVDDV/FYRGTA VS/PSVGSIQSSGWPN/DVAGSLGST ASALRFPSTSIQQSSPYFTQSTIRCHH HHGQDSLKEFVQVFCSDGSGQATGQ PNGSGQKGKVPGSFLLPPPPVPARPVH LPMSY
1103	7283	A	1117	1	457	GKLGITPMPGARGASQATNPGPVCNP AWALCSCPACPAHWGSAFSPPMG SLPLMIHTSPPTRALAVARGRRQGAG FPAAPMVGSGVAWGWHDHANRLALP GRCREGPGHLLSGPMSMPGPRE/PQ GPV
1104	7284	A	1118	398	2	SPSW/PDADANFEQLMVNMLDEREK LLESRESQETLAATQSRQLQDAIHERD QLQRHLNSALPQEFATLTRELSMCRE QLLEREDV
1105	7285	A	1119	1	738	GSRTPESSFHTNGQEDHPPOGMLQTE VQRSOAAGRSKSDP/LAAIATGSSGN KPLANSI/PCPGGSCDHPGSGLKMN CNNRNVSLLADLKPLKLSNVQELFLRD NKIHSIRKSHFVDYKNLILLDLGNNNI AILVENNTFKNLILLDLRWLYMDSNYL DTLSREKFAQLQNLLEYLNVEYNAILQL ILPGFTNAMPKLRILILNNNLLRSLPV GVFAGVSLALKLSLHNNYFMYLPVA GVLDQLTSIIQIDL
1106	7286	A	1120	59	426	HKQIFYLGQVLPVRRERQQEVARE SAR SSATVDCCKMDSIVRASLSPATPV GKG TENAFLSPAI/NGFGTSP/TPSV RISALNIVGDLLRKVGALSKLAACR/ NFAKARCMLRLRVSKNDCN
1107	7287	A	1121	3	413	FPLSSDIVTSRQSFYDCDSLDKGLEHN LDLLRYEKGCVRKEQSNFEGKPFYHC ASYVVT/PFKCNQCGQDFSHKFDLIRH ERIHAGENPYECKECGKAFSRKENLIT HOKIHGTGEPYKCNCEGKAFIQ/NPNS IRHR
1108	7288	A	1122	96	466	FREAPGCRRLPAVPVPGCSRVAWGHL GTDGSCGSPSRIVLRVQRGRCHWSL DLWSREVPVPGCSWASVAGAGVTLCF PLQLYLSQDGVLCMWQCDTPEGL RLKPPAGWKADL/QREEDSQE
1109	7289	A	1123	3	435	RARSTSPGTPPRGPPLPKKSSPPPPPG CQKYTA/PASPLNTPGMAPRASFSPT PRLASPTSRFDGEPE/APKTLNTVRGR ARGAACVQHSQHGTGTGASSVPQEEN VSSSSSSSSSSSSSSSSSSSSSSSSSSSS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
1110	7290	A	1124	23	475	GEDEESEKREKRAVDKEQRGGEEESRE KNEGQQQIVKGHPSPSPQSVWRILGM SSTTLLPLPPS/GSSPRSPASPDSEPCSAHVSPhAYECLRARRWLLPPTTTFGR PASQPSRSTRSPTGTSSPSPPLRPCQA GSSDEIVDPEIPGRYKGC
1111	7291	A	1125	1	414	MRVMAPQALLLLSGALSLETWTGS HSMRDFYTAVSRRPGRGEPFRFAVGVV DDTQFVRFDSDAASPRGEPRA/PWVE QEGPEYWDRETQKYKRAQADRVN LRKLGRYNNQSEAGSHTIQRMYGCD LGPDGLRLRGYN
1112	7292	A	1126	1	387	ARKHLKDDRAWNTNPFQESGLHLSPTAAEAARRRLEPCESTSARIIRWTGTG SVKSSATYEPLFACGLTGLPLHGPW ASACPELPQPGWTGGWSCHCEISPS PGEPSPCCPPGTGGI.WQDRGRETO
1113	7293	A	1127	32	439	QRLTVEDPATVEYITRF/ISSLKHYRT QSNGRRRPFGISALIVGDFDGTPTLYQ TDPSTGYHAWKANAIKRGAKSVREF LEKNYTDIAETDDLTIKLVIKALLEV VQSRGNIELAGMRRDQSLKILHPEIEI EKYV
1114	7294	A	1128	2	397	HFVQCGAIRNHL/LQGEPMVESDAM KL.VQTRSILHYVADKHTLFGNLKER TLDIMYVEGTLDLLELLMHAF.LKPD DQQKEAVNMAQKAIIRYFPVFEKILR GHGQSFLAGYQLSLADVILLQTLALE EK
1115	7295	A	1130	20	444	SFAANPSFNRAFMLLLFLFYGLCCP GENTGGKPEAWLSCGSPGPGRLQLV CHVSGFYQPQPVVWMWRGEHEQRG SHRGDVLNPADETWHLRATLDVAAG EAAGLSCWVKHSSLWGHDLIHWGG YFIFLILIRLTVKVT
1116	7296	A	1131	12	469	VDD/KLLHAAFIPLGDITDIQIPLDYET EKIRGFAPVFEFELAEADAASIDNMNE SELFGRITRVNLATPMRIKESSTPVV SDDDLWKKFSGKTLIENTEEEGSQPP KEETQGEPIAKKARSNPQVYMDIKI GNKPAGRIQMLLRDYDVTMT
1117	7297	A	1132	239	422	LPP/PEKKTGFFPSSSRGTSSSSSLFFS SSSRTSSSPFFPSSSPS/SSSSSFFFP PPPAGTSSSSSSPPPPASSSSSLFFFP PPPP
1118	7298	A	1133	3	436	IKRLLGRGGDAANNYARG/HYTIKGE IIDVLDIRKLADQCTALQGLFVHFS FGGGTGSGVTSLLMERLSVDYGGKS KLAFSIYPAPQVSTAVVEPYNSILTTH TTLEHSDCSFMVDNEAIIYDCCRNLDI ERPTYTNPDRILISQ

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/19,785	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
1119	7299	A	1134	6	423	VRTAEHQSDQLVWRTEVVFINLNPS WEFFRLCLHSLCSDVHRPLKFLVYD YDSSGKHFEHFEFTSTFQESGGRLPCR DQGMNPKIGQREYK/NSGRRLAQSR WEGATFLDYIMGGCQISFTVAIDFTA SNGDPRSSQS
1120	7300	A	1135	6	434	PAYAKLGTR/FALLQEGAHVPLQFRIV SGNSADFLHTVGAEDSGNYSYIYYE TTMSNRGAYLSMPLMIWVTDTPFKP WLFAPSSVVPMGQNVTLWCPRPGRH GVRNLALATEREATSMQLWGIPNSDG AFPTNISGTSMGALP
1121	7301	A	1136	2	409	ILGRAADIHLFANDMLKLGDWGEM KYGADGAVIDIGLTTVKGKRWDMNTI TIPTWSLVSDSKNCSGMSTFGARCIK RNIHIDATSIKSLDEDEMQRNLKAHSV QPYLTSRHHIDINEGNSQQGSRESV/N LRRM
1122	7302	A	1137	77	414	GGEKRAVNIHYGEVVGGIISRLTYH CEPKVPVPSLLKYAPNNGGLNPLFGPQ QVAMLNQLSQLNQLSQISQLORLLA/ QQQRAQSQRSPVSGNRPQDQQGRP LSVQQQMKPQF
1123	7303	A	1138	7	432	YGSLAADWKTGCYTLCSRALLVSSTS WTKVEDFSILLAALEKFEQLTLDGHN LPSSLVCVTTGKGPLREYYSRLHQKH FOHIQVCTPWLEAEDYPLLLGSADL GVCLHTSSSGLDLPKMGEDMFGCWL PVWAGNFKGLHGL
1124	7304	A	1140	21	436	RTARNPQKRVERREWSRLKAKDW GSSCGSQGREDSVLSYETGTQMEGH YARPHILGPTKDRANDLLSEFPDKF GSWVPHITRSKREYIDGRDYHFVSI REKTENDIQAHKFIEAGQYNSHLYGT SGRSVREGGK
1125	7305	A	1141	97	460	VFPSPETAPRRQRKGLAPPPQAGDPPP TPGKSSQSPV/PLPQTLPEKKWLPHGP EGPEAEAVLRHGVFPVPSHRGGQSP YLHGFVPGRPRCPVPRPCPTFKVANV FPGLPPAPEWATGE
1126	7306	A	1142	546	680	LNLFYKNGFPGWA/VVDHACHPSTLG GQGGRIITRSGVQDQPDQYGE
1127	7307	A	1143	47	468	LDRALTE/SFETASAMATLGEARLRE MEALQSLKLANEGKLLSPLQDVDIKI CLCQKAPAPMIQCELCDRAFTHTSCV AVPRISQGLRIWLCPHCRSEKPPLEK ILPLLASLQRIRVRLPEGDALPYMRE RTANWYLIAQH
1128	7308	A	1144	1	472	SELKNSWPDGLPOLELNPQGLWDIIV EFYIQLQSFQYRCKTAKKSQEEIDFL RSNPKIWNHNSVLNVLHSLVDKSNIN RQLEVYTSGGDPESVAEEHGRHSLYK MLGYFSLVGLLRLHSLLDYYYQAIKA LENIQLNKNMSYSR/VLECLGSTFY

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1129	7309	A	1145	42	501	QTTTQSWPGVGRGWPVS/QVPRRLPRG LHCSA/ARHSSEQSLVPSPEPRQRPT KALVPFEDLFGQAPGGERDKASFLQT VQKFGITTSVRNGGHIDFIYLALRKM REYQVERDLAVYNQLLNIFPKVEFRP RNIIQRIFVHYPR/QQEGCIAVLEQME
1130	7310	A	1146	15	411	LGGKQEPGWCLPCFHRVPGSPGSGSDG VTYSTECDLKKARCDSSRQLYYAAQ GACRGPTFAPLPPV/APLHCAQTPYG CCKDNITAARGVGLAGCPACQCNP HGSYGGTCDPATGQCSRCRPGVGGLR CDRCEP
1131	7311	A	1147	2	566	DFNMKKLASDAGIFFTRAVQFTEEFQ GQAEKTELDAHFENLLARADSTKNW TEKILRQTEVLQPNPSARVEEFLYEK LDRKVPSRVNTGELLAQYMDAAASE LGPTTPYGTKLIKVAEAEKQLGAER VDIHTASISFLTPLRNFLEGDWKTISK ERRLLQNRRLDLDAACKARLKKAKAA EAKATC
1132	7312	A	1148	2	459	RISWPSDWENSYYIFSPQRLSMRLK QROKARRAGNPSSLRDIGNRRSPPS LAKQKQKQAEHVPPYDGGPSMRPVG LGGPSLKGVEVTDMMQKALFDFLKH RIDGRISITRVTDLS/AKRSVLNPNP KRTIERSARSSIGFDECFPPPI
1133	7313	A	1149	88	437	FIFFIRWKLTPLSLPEKDR/CPGCFPA SPQFPICCASGRRGTPGGPAPHPTSPK GKDKASRSQGFPTFRLHPGRPNQEG PQQRVCLVLPALPFPGTGKALSGEGA NRLSAPGPPNA
1134	7314	A	1150	42	469	RRPIAHHRTHSGEKPFFCYKGGKGFTL KNSLITHEQTHTEKLYTCSECGKGF SMKHWMVHQRTHTEKPYICNERG KGFALKSPLIRHERHTHTEKPYVCTE RPKGFTMKSDDLIVHQRTHTA/EKPYIC NDCGKGFTVKS
1135	7315	A	1151	3	411	LTGVVSLGGRPVVLTVFYTPNSIPG WDVCAFDLTQVAAVFEGRFREQKSP ESIWTPVPEYQVPRPRPGCAAPGMQ YNASSALPDDILNFVKTLPLMDEAVP SLGHAPWILRITLMRQHLTRVAVDVG AGPWGNQ
1136	7316	A	1152	3	456	TSLDGPAIQPVVLVKDQDITLQKVVA PGITLPPVLPESHITAIEICPHPTDLVA FNLQDPQHDSAPAEASAL/SQEKNPRL NQLMALMLLTAQPQELVMFEEVSV CFTSEEWACLGPIQKALYLDVMLEN YGNVTSLEWETMIENEVTSKP
1137	7317	A	1153	18	323	DYNRAFRMRMRDGFPP/VISPETRTPO P/PLLLIQPERTTTPPGGPPSW/WPAA EAVHGIQVATGPHPPPSILEGPSVAD TMARVLFPTPVGLASDRSSSLH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
1138	7318	A	1154	1	145	GTRYIEVFVKSH/RTEMDWVLKHSQPN SADSANDGFVRLRGLPFQCKIFF
1139	7319	A	1155	3	412	FGRAYIGAEASLQAEIRYEGILYITDT ENSTVALAKVRSFGTEDRPTDRPIPPR DEVFEYIIFRGSDIKDLTVCEPPKQCS LPQDPAIVQSSLGSTSSFSQSMGSYGP FGRMPTYQSFPSSLVGQQFGAVGVA G
1140	7320	A	1156	169	419	FHGRTKPSGRHPLPLPGP**GCPRSA PRPPSCRHRISEPAAGTRASRRRLR RRLGVLSPPAPTATPAAPLTPHVPCAP PRH
1141	7321	A	1157	80	585	FRRGGSAKLLGHGRGSGTRGGTRPFS DSYELCPGLPGCQSLNQVPPGT*EDL GGNSLCWRVCTAPPTAFPLNQDWGK ERLIPPCGAGRECPQILHHDPIPKLEIP RLPAMEGEWGPVAPHHSGLPHSGWP GTQLFQVSGVAGDPGTPREEFPESCR LGLHSSCQAWGN
1142	7322	A	1158	3	434	GGKTIYVEDGLNSFHVKKHGADFLV TDVENGSLFTNKAGNLSGAAEHL AVSEKDIQDLKFGVQHDVDMGIATFI RKASEDHEFRKDLGEKGNINIIST* NHEGRRRNEEGLGANDGN*LRSGDG PTCIHWDPGDLALKMR
1143	7323	A	1159	3	366	LNCLRGGLITPRASYTVGSSIEQKTES ADKKQHMAREY*EKIDELTDICPDV LSLLEKFLIPNASQAESKFVYLKTKRE YYRYLAEDAAGEDNKGIVDQSQQAY PEAFEISLKEMQPTH
1144	7324	A	1160	466	742	IGFTCFEAIYKWNHGLSGFPESRSSEK KNLSAVVYLAFGSRM*VLSGTRDSH* EKSLCKGN*T*RY*KTDEQPGTVAH ACNPSTLEGQGRITRSQVHDQPDQH GETPSLLKITT*KKPGEVAGAC
1145	7325	A	1161	4	399	PPSGPOQHGVYPRQPYGTQSPQRCPM TMQGRAQRAMGGLSYTQOIPPYGOQ GPSGFGQGGQTPYYNQESPHPQQEQP PYFQQPDQTPHAQPL YQQPLSQPP QLQSYQPTYCQQPFQAPHE*TPAPYP SQE
1146	7326	A	1162	1	408	SIKSLPIKKNLPGNPGTAEFYLLFKEL MPILFIFANKTASSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSHSRDQMRFISRMQG*FK PPKSISVIYHVNRMKDKTYMII
1147	7327	A	1163	2	392	NLKHKCFRNSLENNETL*SIMNTLESE EDFRKYFYYLEGSKDALLCGFSTDG QCPEGYTCVIGKRNPDYGYTSFDTFS WAFALFRLMTQDYWENLYQQTLR AAGKTYMIFVVVFLGYFLINLILA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1148	7328	A	1164	59	328	VGFPARGGPPGGIIIGHNYNKGGI* NKGSPFLFWKGVLPNP*T*KTLLAPPFKIP GVPGGNPAPGRLGFPPFPWGPQLF FGSPKLTPPN
1149	7329	A	1165	83	377	GKKNFFNPGGDKGGKPKKRGTTPPL GLKKILAPTPTKTKGKRGSSTINFL FLKKNGV*PRGPGGP*TFDPRGTTPPLG PKKGGN*REGPPSPAKNYF
1150	7330	A	1166	2	423	SPPPP*KIFFSPKALNFLSSPPKGP KRFFFKKPPGGFFSPPLSSPPFPSSP
1151	7331	A	1167	27	144	ILGFTILDINLLKEFMTKSSKAIAATKT IDN*DLITLKS
1152	7332	A	1168	27	144	ILGFTILDINLLKEFMTKSSKAIAATKT IDN*DLITLKS
1153	7333	A	1169	73	390	ISPGAFPPKPPPEFFPGPF*PPRKGSPTL KKPGKPRPVWPPSSSQKG*EQREP GPPSWGKSPPLKPPGARVPKQKPW GGIWPEFPFGGKQVSKSSPPKGPSKF
1154	7334	A	1170	116	367	KTLSHYWTRLGCLPLPLINLGLKIL PREIRLEKEIKDFPTKCNQALFLTEK IHIEKT*SSSPLLLKILKFRKGAKYK T
1155	7335	A	1171	226	398	LMKEIEEDTKI*KDIPCSWIGSINIVKM SILPKAIYRFKEIPKLPMTPTFKIDKTI
1156	7336	A	1172	3	287	ELCFHLRRRLIFFPLPPQKSHLQKPYEI NLMEELTLKGETOYYA*GTERQKVH CLNTLFSRVRSRLLLNIISRPVKQKI SSIFPSSLYKSS
1157	7337	A	1173	166	453	LEVLAIRAQEKEIKGIQIGKEEVKLS LVSDDMTVYLENPKDSSKRLLYLE FSKVS DYKISVHKTVALL*NNQGENQ IKNSIPPTIAAKKKST
1158	7338	A	1174	20	341	RQVSLHCPGSRGCEPSSCHCTPAWE TG*HSVSKNKHAKLSYYPNENYVL TFLFLNHPCLCKYKGRDEKRTL C WIPVKRTWSIEKSWANRNRWDISVHF WLHL
1159	7339	A	1175	127	379	KGSLIFFPGGRGGGPF*TKGGPRPRGK PIFLAWALGEGGKTGPPRQIRIFGIL KKRGVPPGNPGGP*PKNLGTPLGPP KGGE
1160	7340	A	1176	3	410	APQGSKIFLPQPPKGFRRRSPPPG* YFVFLKKGVFPFGGGFGLPAPRGSS SSAPPKGGDSRG
1161	7341	A	1177	136	392	NPLMGWKTKNLPLKKHGGPKEMKG SSSPAF*THRKKNPTFPNFWEQFKTSS SSKFYPLNAPQKKEKPTQIGPLTFPFK KPKKPGP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
1162	7342	A	1178	1	282	PGAGLPAIIPAPWEGQGGGSPWGSKF *SPPGHKGEPRFFLNQKFLGYSSPR YSRFPGGGGWGIPLTPGIKLMGPGW PPGLLAWGPKGNFVS
1163	7343	A	1179	203	459	GNKLFFAPAGGEGANLGLMEPSPSG LKGFVWLNLPRWD*GTSSPCPTKFW IFLRKRGVPHGGQGCSPALGELPG LTFQRGG
1164	7344	A	1180	2	268	SAVLLNANNVQAEKHIIKNAILLKIA TPPKK*LGVCLTKVVNYLYEKNYKIPV KEIRDNSNKWKISCSWYERININEM CNEIVDPESP
1165	7345	A	1181	4	444	PWVAEIKKPLLPRDVAFFLIRPRRAQ GFNPLPGYNKNGSPLYPHPGGPRW GVPLGSGFQTPPGPKG*FPLFPKIQKL LGMGGRPRYFPLGLGLGRKIPKTLET KSSNKFNSGPPSPWGP
1166	7346	A	1182	3	214	SLNTINTKTWLFESIKMDKPLISGM GYITTSPPDIKRIMRE*FHVHKFDNLD EMVKFLERQTAKAHFK
1167	7347	A	1183	245	428	KKLQGGSSHQTFFGAFFCSPRMVNGL GNALGCVHVEEEEGD*TEDESLVENY DNIDGMWSCM
1168	7348	A	1184	171	455	KKSFFLSPGWKPRGEIVGNVTPPLQG KGDSRPQPPGKGGIKGAFTPPGQFLD F*QKRGFVGVARGLKLGRPGGEARPG PSKGVGLSGGTMGPGKK
1169	7349	A	1185	176	421	GGETPPKKNPPPGGGGPPGGVKFFS PGPPGKIFGNKNPKTPGGEGL*KNRK NPRGPLGKINPLFLTFFSNGFWGPEIQ GGE
1170	7350	A	1186	195	441	KRFLFFSPGGRKRNQF*MQSSSSL KKFWLTPPKTWYRRGTNPNGNFGF LKKTVSHHGSSSLKLLP*RDSPPLAP QRGG
1171	7351	A	1187	125	405	TSRVFKRQSFSSRCQGPDRDKIVRNE KGEKRPKERERNTSKESKTQNRKTKI QRQFKGT*QKRSRGCKQFRENPKDR NPQTAGKRQRPRDADK
1172	7352	A	1188	18	436	ATKELCDCQKSCVSKCSIIICEKQPE VCVAVWRKNDEINTLKTGCHDPKLP YHDFILEDAAAPKCMKTSPPGETFF MGS*TSEECKDNILFYEYNTSNPDL LVIFQGTGISLLPPLGVAISAIIFYCYR VNRQ
1173	7353	A	1189	1	193	RDCSELR*CHCIPAWATE*DSVSQKN KTKQKHNSLFCGLGQMLGALSTDW SLCWEPLFPPIPG
1174	7354	A	1190	1	131	QPGPEGKIRFFLKIPNLTPSGGKSLKFP LFKRVPKPNCLSLRG*GCN*PGPEGKI RFFLKIPNLTPSGGKSLKPLFKRVK ENCLSLRG

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1175	7355	A	1191	2	408	LAVFHSHLPLFQAEFLSSLSQPFVSVE EQEHILSCLSIIVLSL*LSASRGSRGPP SKGRSGFSSHQPRPLSSSSSSSSSSSS SSSSSSSS
1176	7356	A	1192	2	331	VGRQEDIFRVGWKKRFQRVVRWELS PSKAAQSTFFLLHPTNALKAAEDRVL QEGTKGQDNAESALHPQACWDPRSP SPGPFPSRAGALDGA PG*EGGLPQKY RAGRPGSTK
1177	7357	A	1193	156	457	EKGFCPCGPKGEGKGPNGAKGKPA GKKNFPAQTTPKRGKKGPTPKGREK SSSSSSSSSSRGVVRGAKGK*KNWK *RGPPRCPKKGKKKGPPRKISFF
1178	7358	A	1194	9	239	LQKLIGISFGSLHGLRTKCAVSNGLTQ QEIRLTLEVRLKV*GRTDLSGTPVKEN *QSVVIKGLSWESDLEDCTLG
1179	7359	A	1195	119	435	TFPFLKSCPPMILKGGKVKTIFYRLSP PRPWLKGPHLSPLFSPPSRGSLKIGV VSPKYVPIGPFLNTSP*NPFLTRKGP *PGRRAATKPPKVPKNNNLAGLK
1180	7360	A	1196	3	440	SSSSCSGARTELRSRTQHKSGAPGSR GGPRPRAPTSAPGPPGLFRNSGRVV SQLQGLGLSPGLSRDLHHS*RQQLP FPPHLKRSPTATCPSGGRPEKHGYN LPTREPSSSSSSKGGKFWFCPPSSSPR GGI*VNGTLGLRVN
1181	7361	A	1197	2	429	FVSGPGVCPFLWAVGRKMV*TPGGS LPYKKNWAQAFPLGKKGEFFSSSSSS SSRKERNPFSKPKLQTMWTHPESHR DWMATPGLYWICRHRA YAKLPDQ*A GSCFIGITIKPSFFLLPIKTKLLGFPR
1182	7362	A	1198	1	119	IIASCLRKEYAGKRKGCFSKRKNKIAT RNVSF CVRKGW*GKRKGCFSKRKN KIATRNVSF CVRKGW
1183	7363	A	1199	1	227	LKGWENIPINIKIE*TPFFSPYQNFNP R*VKDINIPAPNTINFLERNIGEPL*DI DMFTKISKVQKNPKIDK
1184	7364	A	1200	409	416	LADFLS*VYSLIYSR*IFS KVSKNMYL KMDTFFSKYCWGNRISICRKNLNPY ISSYTKINSRWITADAWVA
1185	7365	A	1201	2	215	ISNSLHGAALKAALNEIRVYVSLGEAQP DAYKDKARKAAIDNVHQAQ*LAIGF HRKLSPVYSVRVYHSNYQ
1186	7366	A	1202	246	414	KKNFIFAPRVEGKGKNPPSGLKEIFCL NLPKNW*KAPPPPSYFCFFNNKGV SPG
1187	7367	A	1203	263	430	HFFFFKVNIRLGA VVHTCNPSLTGGR GRRIT*SPGV*DPGQHGEPCLYLN QKN

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1188	7368	A	1204	191	394	IPIMGPLLKPPGLEKTWGYPN*YALD KEALCLSTLIRCIDPLGYVFSHEPRD HAKNALLCRSVRTGG
1189	7369	A	1205	103	354	DIISLEWELDTDLTPFKIMFLKWTDL SVK*KTIKLL*NSIGENLVDLGFNSDF LEAIPKVQPMEEID*LNFIKINFYPV TM
1190	7370	A	1206	3	480	RKFCPPGFKDFPAPTTPRSKD*RVGSS SPANFVFFYKRGFPILARGVLPNCP QGVSSSRPPKRLGFG
1191	7371	A	1207	2	289	SNIRDSLERNCEIEESVINFPKQKV PGPDGLTGEFY*TL*EEIPIYNLFQK RETEDILPNSFYEAISITPNLFYEASIT LTRHHQKERLQ
1192	7372	A	1208	220	462	EKRSTFFPQKPGGPNWG*LDPCPPG WGEFFAPPPPNKGAPLHSPVIF*NFKK EQGFPMGAGGLIPGH*KPPNPPQR GG
1193	7373	A	1209	3	260	PLLRVPVPPQGPETKIIFFPQTPR*VWA PVATSSSPKIFIGFKKRVPICPGNPQ PFKPKGFPFPAFSAKGNSSYSPSPAP FK
1194	7374	A	1210	1	182	VCVEFEKAGGLDDEEAELVPS*VL MHQAIHTIEFCLGCVSNTASYLRLWA LSLAHARE
1195	7375	A	1211	2	93	KECWHRPGVVVAHCNSSLGGPRGR ITRSGF*DQHVRT
1196	7376	A	1212	107	299	SRPLLTDQS*DILGNRCIGNHCTEFM GSRNLNWKLGVVVAHCNPSLGG*GG RMSSGVRDQPGQ
1197	7377	A	1213	231	448	EREPPFAPQAE*GPNLTSKALPGL TPSSCLSLQRS*N*GPRPPGRVIFGFL RKNGVSLFNPGGVKPPD
1198	7378	A	1214	314	427	RQMFIDKGTKAICRMDSLFNKW*RS N*ISMCEKNKY
1199	7379	A	1215	3	390	SAVEFAPRGKTIALPNTAGHLDPGN LTRPPRPFGLFSVPLGGGGGRQVGP TGLVVRQEKGRKGRPOLGPVWVP PDAPDSE*SRAGPRGSPASRARGVLS RAVQGLGGRGHAATWPGQGLRGA
1200	7380	A	1216	27	301	PGHCFYNFNLFYFIFFQNLVANS SLFLYQTLILSFNIFYLYLIQISIVFQ SVIL*HFSNSYSWWYGFWMVCMITFEG KKQCAHV
1201	7381	A	1217	2	440	SGGIPCSCLWYFLFPNCLLSAYPVP MWPHLALGPPSGLCLMVSVPFR*IA VSSYVFIQVCSLAASSSSRRSFSF CPPGGGAGPNFGLLAPSPGLKEIFGL HLPRRGE*GTSSSPINFCCFKKKG VYPGGAGGVKIPNL

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1202	7382	A	1218	12	437	GHKAYAKLPDQWTGSCVIGTIKPSFF LLSIKTGELRGFPVYASRSSSSRRNR TIPLGN*KKDKGPPSSSLIH*GPPI*K QKG*GGYGTPIYMLKQIKR*QAV*KII TKKTG*PLTVLARQETQIKKAFYQKK LAFDYILE
1203	7383	A	1219	251	465	IQESIRVI*WVCIRLLHSTAAEYTFFL NLH*TKDKHILGHKKYLNKQFI*IID SMLLDHTELN*KEFHH
1204	7384	A	1220	236	432	IQESIRVI*WVCIRLLHSTAAEYTFFL NLH*TKDKHILGHKKYLNKQFI*IID SMLLDHTELN
1205	7385	A	1221	373	474	MELIDIYRAFHIMAE*TFSSAHGSP SRIDCV
1206	7386	A	1222	1	291	LPKKLKPPLAIFPPPLGKKPPPKKFPF FTKSPFPSPQIYFKIKFQTKAFDFFP KIT*WPGGVSSSLYTPPLEQGNGSP* VPKFGPPPTMLNP
1207	7387	A	1223	138	368	GGPLKRPNFKSRGRERKNFLKGAPK* KSGAGF*KRGRGKNPGVPKLKPLEK DPPSEKKRIHYCDYPGCTKVYTKSS
1208	7388	A	1224	51	406	KVAAMKLPSPRPPCSTATPHCWVRL PRQQOEGPDGATLSTGQTRPTVTLPS DPPRPPLPHSHFLRLHPKRPALTSSGV LNI*QEQTAKGTRSSSSSSSSSSSSSS SSSSSSSS
1209	7389	A	1225	1	284	FMFPARFMRPGHHPPS*RAKYGYPPH PITPPLLRIPLPQREGVSPMLHPGFI PSPIKFQYPPPPPSAFALFLYPELEVYF LIYIIEYQQRHN
1210	7390	A	1226	356	491	LVTCKRS*IRLSANFL*TEARRQWA DIFKVLKNNKAGAWTTGF
1211	7391	A	1227	1	342	EYWDYESHAEW*IHDDYHLVQK*G AGKYREVFEAINTYNEQDVAILKPV KKKKITREIKILENRGGPNITLADIV KDPVSRTPALVFEHVNNITDFKV*YIT NCFGLVGF
1212	7392	A	1228	250	417	CKTONLQKNRENKHICFPQ*ISPEDIV FMITYHHKAKSDRIWGEHEICYLLV RKNVSLNPDPSSETSLSSSSHSSWD R
1213	7393	A	1229	122	400	YGGQLQYSGG*DVGPASSSSSSSSSS SSSSSSSSSSSPGQPGRLRTGKNSRW LRGRSLMTCGLVLGAKSPNGSGG *PSGGKGFGKKIP
1214	7394	A	1230	2	254	SPQRGDKVGITGPCTLGPPGVKVPPP LAPQEIAGPGPPPNQGNLGGFGIKGA GGGF*PRSGGNFAPARPPKPPS*GIR GKPL
1215	7395	A	1231	20	279	GRMSKFTANPGAQKNQPSVSGDRR E*SPPHPSPOGIPRRQRPGGCSQA *RLGTQNVPPTRWGGPVTPPPAAS RCTQKPHR

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1216	7396	A	1232	114	383	YITLGLYFLFNIIICV GIFAHLCLM* ¹ E YNLYDKEKVIFLYSNNEQVEFKIKNT VSFKLAPK*YLSINLVNVSLEHENCRI LMKEIQER
1217	7397	A	1233	3	243	CTGRPTRPLVYL*SIRKPSPEPRAQMR RAASSDQLRDNSPPPAFKPEPPKVRG WEAQDQKEEADASEASWTAREEHA H
1218	7398	A	1234	2	440	IYFFYF*RWGDSSVS QAGVQWCYHSS L* ² P*TPGLKSPPTSAFQSPGIIGMSNHA WLAFFILKYL
1219	7399	A	1235	1	448	RGQPNVY* ³ RFAVQSLPKTPQSGVFST KTCWEVLSSSSSPDSSKFIILVSWWIIQ DLNRPDPTIKILGAIPLDVRQDKEFVT KCSKANTAKPKTSSSSSSSSSSSSSS PINSQSTAWEKIYAYYASYKGLISRIC EELTQLNRTRGSTR
1220	7400	A	1236	3	270	KLLELINKSKKVAGY* ⁴ NIQKSVFLYT NSKLSEKDNQONYPISIF**NTKYFGIN LIKEVKDLIYILNYQLVKEAGWAGR GGWLDTV A
1221	7401	A	1237	3	301	HSAARRPSSRRSSPRPETSATPSTPA GTRTPRTSSASRSMATAGSTRYR* ⁵ GL HAAPSPPHRRRSPPPGAE* ⁶ AGGRD P* ⁷ NGEAPRAILQKQKQCVDA
1222	7402	A	1238	2	270	ARPGRIFGTDPRVIFAAGVTLH* ⁸ SK ELSRKQSQHL* ⁹ LLESELRKEIRDGSAE LQMDKLDVDSFGTATFLDY* ¹⁰ HYAL RTTFPEAKEH
1223	7403	A	1239	3	380	VCTCVLV* ¹¹ LCLCVYTSVCLHVCVCA YTH* ¹² CACLCCLCHWSSLLWRPAYSTS SQGPGLRLTPALTGCGHAAHSDPPVL LACFHLELLFVPKHTGNCGLSRSRIQ SSKFLARKPLDCAVDRDPICN
1224	7404	A	1240	1	169	WPIQGTPTRPEDDTNDENFNVEIRQ LSSC* ¹³ RRFSKVSEMWKHITESL WEDL PLAR
1225	7405	A	1241	26	293	GGVWPIMLGGAAGGPGLRITPCADV DECSEEDLCQSGICTNTDGSF* ¹⁴ CMCPP GHRAGPDLASCLDVDECRERGPSLCG SHR* ¹⁵ ENSPGCV
1226	7406	A	1242	38	385	QKTDYTYGWW* ¹⁶ TVVYYFEMESRSVA * ¹⁷ AGVEWHDLGSLQPPPRFKRFSCLT FLSGWHYRCAHHHARLIFVL* ¹⁸ RWGF TMLVKLVLS* ¹⁹ P* ²⁰ MIHLPRPPSVGITG VSHCARPKFPL
1227	7407	A	1243	1	280	CSQQLSRYLHSDYDCLLDDPFAHDW PALPOLPGLHYSMNEQCRDFGLGY MMSTAIRTFDPCKQLWSSHPDNPYFC KTKKGPPLDGTG* ²¹ APGK
1228	7408	A	1244	3	188	AGLSMLGQANFRRLKPLPDFATPPPP GSFNQFFWGPPHFVKVSPGG* ²² PWAPGP KETRPPPRD

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1229	7409	A	1245	147	403	TEWEKCNTHITDKGLEYIKSREIV*IG KEKICNPVKTMGMK*LNHGTHKENKY TASSSSSSSSSS
1230	7410	A	1246	1	323	LVGICGGVGNVTVTLSLSCIKLIKLAG HGGACL*SQLGRLRLNENHLNPGDG GCSEQRHQCTPDWATRQDSVSIETK KQNLHMCISLQDSVLFLLSTVCIFIL LQ
1231	7411	A	1247	389	0	SSSSSSSSSSSSSSSSSSSSSSSSSR GGRFRGSRFTSAGLQGNIFMGPPKL NSWPAF*QRREGKTPGVPLNPLWK AFSFPSTR
1232	7412	A	1248	37	401	PGGDFFFPQKPLSGPRLFFL*VEGGFIP SQGFSPPFPFPWF* KPPGIFA*GVLP PKGGVPFSPGFPSSSPGGP
1233	7413	A	1249	2	388	VDFFFLRLRLSVSAQAQGVQRNLG SLQAPPPGFTFSCSLSPSSWDYRCPP SRPANFFLYF**RRGFTVLARMVVIS* PRDPPASASQSGITSVTPRARPRICLI QILPNKQILYVWKYVHVHSL
1234	7414	A	1250	163	370	SKLDDRFRIVHNTITLENKTRGKDSIK RGKRQATKWEKIFITHITNKALGYSM QTELL*INHKNKNYTL
1235	7415	A	1251	48	507	AGVP*QDPSSLHPQTHGLK*FSCFSLP SSWDYRDGSRCLCYLSWSAVAIPSTIIV HYSLOQLLGGSGAPCASAS*IAGITGVSH CMWLLSVFYASLFFPLPSFGLFDYCL VFNFNLSIDYFIISLCVVFSSGGSKNYS MYTKLFTFCLLELIYHL
1236	7416	A	1252	2	347	VDPVRFRSIVEAKQPVNLC*FSPCMN EGSCVLQNGSYRCCKRHGWEGPHCE NREWSSCSVCSQGWYCESWQVPQT QLKAGSKTFVQWKLFSLRPTKHLV STSCIPGIVLSAGT
1237	7417	A	1253	79	371	PR*FVNSNL*DLNVRTKIILIKV*NIP ENVYDLG*DNFNFLNITTKAEVIEKR GKLDFIKIKNCTSKNTATSRK
1238	7418	A	1254	1	419	LPPTERAGGHPPPKYYKWRKIF*NRK GINPRPARKGKNFQRPNPPPFSGKGF WAQRPLGPPPGSPRGAPPPSSSSPPG ANWPGTPPREG
1239	7419	A	1255	3	410	RGRFWAPSTPRFQGSKIFPPPPP*IGG PTSSSQGGGSSSIKKGSGPGGVPVGF QTPATKGSPPLPPKGGETRGNSSYS SSPLP*KPAPPGGPPGSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSS
1240	7420	A	1256	3	283	FFLRWSDLGLSQLPPPGGLKQFFCLSL PEVAEDHRYVSPCANFFFCIFS*RWG FTMLVRLVLNS*PHDPPTILASQSAGT TGVSHRAWPFCLCS

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1241	7421	A	1257	283	372	FFKIFGNGIWFCCPGG*EGP*ELS*PV PHFISPGI*GLGLLLSSSSSPGAGPLGIL APRGKKQGENRG*GPPGPPG*KKPG LTPQGGGQGGCPSRVIF*FWGKRN LVLLPGGAKNSGPKGTTPRH
1242	7422	A	1258	28	185	YDKPRPVGKEKIGKLDCKMT*NFCAS KNTIKEMKRQRTVWEKIFAHYISERK
1243	7423	A	1259	2	393	VNLRPESIKLLEENIREVLQDIVLSKD FFSRAPKAQASKAKTDK*NHTKLRLT CRPKEKVYKSSSSSSSSSSSSSSSL GITRSSN
1244	7424	A	1260	75	345	HNKAKKVGAVVLISDKVFRARKIIR DKEG*SIMIKRSVLHKNRKILSVYGV AVLICGLLPPPNHYRRLISLMSFRST GCLLSLPVGV
1245	7425	A	1261	100	306	LIKAKKVGAVVLVSDKVDFRARKIIR DKEG*SIMIKRSVLHKNRKILKCLWC GSSYLWSPPTPKPLPQN
1246	7426	A	1262	339	1	SE*SLGEIWDYVNCNPLQIIGTPERDR EEENHLENIFEKIIQENFNLAKEDIQ V*EIQSTC
1247	7427	A	1263	2	359	LFEQLGQEYKLQNALLVLYTKKGPOV STPTLVEVSRNLGKVVSK*WTHPEAK RMPCAEDYLSVVLNQCVDLHEKTPL SDRVTKCCTESLENRRPCFSALEDDE TYVSKFNAETFTTHAE
1248	7428	A	1264	1	369	SVEMHHEALSEALPGDNVGFNVN SVTDVRRGNVAGDSKNPPMEAAAGF TAHVILNHPQGISAGYAPVLDCHTA HIVCKFAELKEKIDRRSG*KLEDGPKF LKS GDAAGDMVPGKPMCD
1249	7429	A	1265	10	371	NCILTTQTTLEHSDCAFMGHEAIYDI CRRNLIERPTYTNLNLISQTAASIT ASLTFEGALNVDLTEFQTNLEPYPRIH FSLATYAPSI CAEKA YHEQLSVAEMT NACFEP*NCILTTQTTLEHSDCAFMG HHEAIYDICRRNLIERPTYTNLNLRI SQTAASITASLTFEGALNVDLTEFQTN LEPYPRIHFSLATYAPSI CAEKA YHEQ LSVAEMTNACFEPGNQMVKC
1250	7430	A	1266	3	212	CLANFFICRNGVSPCCPGWSLIPGLK QSTSLSLPCFWDYRHHETATGPAFFV *NQCCQKSLCFLSLF
1251	7431	A	1267	3	360	VIGLKEEVEKEI*LERLFKRIITQNL LGGKIDI*VOEGYRTPSRFNPKKPTPR HLIILPKVKSKEKILKATROKKIHY SATHLAADFSVDTLQATKE*HDIRKE LWGGKKNG
1252	7432	A	1268	48	467	HPANFCIFSRDGFPPCFSGWSQTPDLR *YAHLLGPKCWDYRH*ANHSQPNFF VFLVEMWFRHV*AGLELLTSSNPPA SASQASGITGMGHHTRP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
1253	7433	A	1269	1	348	GGRATGNEWGAAAPPTSPRNSHGP APASAGGDHSPAPASTGNSHGPAPAS TGDDHGPAPARGRPALQFQWGS CGY *GTQPAGCSERGS*GVAHWGPRGG GGWRGQHWCGPGMSF
1254	7434	A	1270	2	391	WTFRKIKNFCAVNKTIKKVRRQSTE* EKISANYLSDKGFASTRIGKELL*VNNK KISS
1255	7435	A	1271	147	480	ASYLIVSFTTLPFLGVPIVYYCQLYL HEYTLISDSKHAVFRFLQYEATVTKT A*F*CKNRYIDQWNRIENPEIKPHAYR QLVFDKVGKSKR*GKNSPFSK*CWDT WLAIC
1256	7436	A	1272	1	347	SSPTHSQRISQDSLQETIKSLTLQSQID SLAVVNIQNRQGLDLTLAEKGRLCTF LGEDCCFYTNHSGIVQDAAQQLQEK ASEIRQCLSNSYTNL*SWATWFLPFLR PMTAILVL
1257	7437	A	1273	123	324	ETRPSSPQAEQGQKDG*RKCPWPPG LRGFOAPTTPRSGDTGRAPPNTNFV NFKKKGGLAWWEKLA
1258	7438	A	1274	2	184	RIVRKYEYHLNKNFNIDEIDKSFERH KLPLKTQEEVDDLNSPISVKEVETV* KHVTKI
1259	7439	A	1275	324	470	ISNNSTQTLPLPNKGNRKNKTSWLQ AGHACNPNTVGG*GGRITRSVG
1260	7440	A	1276	1	401	PPGGSPPGKLPFTFLSAPFRVRVGGKI PRPQTQRQGGFPQPTTGSWGARSPTF EPALKFPTPFPSFQKNGGAPP*KAPP SSSSSR
1261	7441	A	1277	8	270	GGLPOGCPSPRYTRGTWVNS*MKIASR SFQILGKIYSVLSDREQRAVYDEQGS VDEDSPLVTQDTRWEAYWRLLFKNI SLEDIQAEVQ
1262	7442	A	1278	21	434	DPLQRPPVPARPASSFCPAQQPRPV APSPSYGQGRILPAHPGERAQDFVSK PYKRYEARHFTKAEDS*SPRJLEPQG TCDQNPICANQSAKGAPSKVRRLWPP GTGNLHSAQPPRGSPPNPCRAGASF TFDFA
1263	7443	A	1279	3	237	QILPSLPARTQSAPLPEIMMYLIYQHR SPNVTSQDEIHFMKVTVMQ*THNNEI HWPYNIHSEAAAGVIE**KGTL
1264	7444	A	1280	2	238	IQILPSLPARTQSAPLPEIMMYLIYQHR ISHNVTSDQEIHFMTVMQ*THNNEI HWPYNIHSEAAAGVIE**KGTL
1265	7445	A	1281	1	570	DKTCSGWRRTSGQGRAPLEGSQTPH *SGGAWMETLYCPQRWLFPRQPNSS VGQSHQFOKENQ*ANDHFHPSPPPY TGEPTSGSLPPRQI.PPPLGQ*MG*LC LPLHHGAVPLPAEEGKPIILGERTEVA MSRG*LRAGALPVPSGEVPRLISSP* AGTLVPP*LCPLKGGQHQVPTGTVC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						LSCLSV
1266	7446	A	1282	1	326	TGHHGPGCKLPFFSTRCLKPKNRLNPPGGGCN*PKLVFCPPAWARKPGFVSQKGLKKPRPIPRPKPSWRGLFLPFPFSKRAKPKISRWFALLKYLNSFFGGFLYKTRGPP
1267	7447	A	1283	3	259	RVLKNTI*IIINEAKS*FFEKINEVGKPLVR*IKKNREKTQINIRNGK*GNAKENS KIRKIWEYTKDNFMPKCSNLYCL*KYIKK
1268	7448	A	1284	372	53	VGVKGLSSSRALLSSRRGGPLWGPARPPRGTTPPPPKPAKLPRPGARGPLFPWPWGPKGFAQNILCPRGGAGKARGGPPPSPRGAPPGFFSSSSSSPS*CGFRGRGGTPWGPGGAPKGTTP
1269	7449	A	1285	1	171	GLAPSPRLECNGAVITHRSCLKPPGPNDDPPAPASQSTGITGMSHC*HIMALLSYQPM
1270	7450	A	1286	3	128	WNLSHKHIWKMLNKLILAN*IQ*HFKRIHLDQMNLPPGVQS
1271	7451	A	1287	3	382	VFWFGGPPPGGFFPPPLKK*RGNGFPPSSSSSPRGFPGEFFSSSPVNLIRAGLITRSSSSQFVGFGPWPRGVSNSTKGPPLSGFPKGGGFGPGPRSSSSSSSR
1272	7452	A	1288	145	378	TGPKVVKVRGVMGDGSRGQGGQSRSDGGWKQSRSEE*WGMEAEVVRGVMGDGSRGQGGRRSDGDESRGQGGRRSDGGWKQ
1273	7453	A	1289	386	1	QTPKACTSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSTPGPKVVKVRGVMGDGSRGQGGQSRSDGGWKQSRSEE*WGMEAEVVRGVMGDGSRGQGGRRSDGDESRGQGGRRSDGGWKQ
1274	7454	A	1290	117	288	DGILLLLPRLECNGTISAHRLRLPGSSDPPAPAS*SGITGLRHCAQPRVSFI LRE
1275	7455	A	1291	165	369	APMFGFAFVPEKPIITERAKINGPPYKSGERKOPTPRGQKIAFV*GRLRGRIIRPLPSEA*MAASEAAA
1276	7456	A	1292	413	3	RLSSSLRI*RDNLKTLNDF*KLLGDINWHIPITLGMPTYTMSHLFSTLQGDNSLNSKCSLFKEALEELPSIEEKIQQAQVDRLNIQLQLFLVFTOK
1277	7457	A	1293	1	168	VMDFTIKKNFSTNDTIKKIKRQATV*EKICKSYF**NT*VQNTYKDLLQCCKIP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1292	7472	A	1308	2	349	QLTVFFTLFSCHVIDRNPVAPADPRL PPQSCLLLPPTVRGGQKAVVSRKT MHIFIESGLRVRLNLMRLATFRESAP FSLLLNF*YCSLPLEMPYCKYILNSS STGALALL
1293	7473	A	1309	1	421	IGDIWPSRSRTSARGIAGYPNEEGMF ASQHHRGSSSSSSQHHNHQ**QH ALETNWHLPMQSSPPSAARHRLCLQP DFGGPELGSSPPVLCSSSSLSGNT TGAACA PGDYGRLSAPAEKRSG GKRKSDSSN
1294	7474	A	1310	3	42	LDYLTPHTQNLKID*NVRAKTVKLL EENTEERLLDIGLSNDVMDMTPKAQ ATKRKINKWDCIRLIHCTAKKSINRV KRQLIEWEKIFANHMPDKRLISKIYK QLLQLNS*KINSK
1295	7475	A	1311	1	388	AYYVIAWLFYVLPITVVAIGGFVH* FLLSGYTPNLT*VKIYFTHFVGD
1296	7476	A	1312	309	421	VFGEQVVFYGYNKFFGGNF*DFSIPITL SSVHCTQGV
1297	7477	A	1313	318	446	TVFFSCVCETESHVSQTARA**W*DQG SLQPQPSGLRQSSYLKP
1298	7478	A	1314	123	367	YFLLGKISTKYRPLTPPMKLTKEERR AEYNELVARVRLSDFTPERAIKVT* WPGAVAHACNPNTLEGQQGQTRSG ATC
1299	7479	A	1315	57	356	EGLFSQEHRPPVFLMHTDAKILQKTF K*TLQRRRIYHAQVWFMPGIQGRFNI EISVDQSATVIHQTSNLKDKTISTDAE KRYDKIQHPFLTFFKKILSKL
1300	7480	A	1316	3	249	HASESYCSKQKSPGPDGFLGEFYQTF Q*EIPIYNLFQIEAKDILTNAFGEAV MKLILKSDKSIIRKENRPLVCFVF
1301	7481	A	1317	22	281	THASAHASESYCSKQKSPGPDGFLGE FYQTVQ*EIPIYNLFQIEAKDILTNA FGEAVMKLILKSDKSIIRKENRPLVC FFVF
1302	7482	A	1318	3	158	GGRFKGSKFTYAGLQGGIFIGPPKSN SWAGV*QRRDGKNGPVTQLNPLVEK
1303	7483	A	1319	2	406	PRVRALGHPYLTALSLTAGWVLRPE QLAHVLGH*GSLVILQCVVTRISYT HWYQKGGQVPEALHQLAMSKLDVQ WDSILKADKIAKDGSSSILAVLKLET GIEGMNYCTTWAIRSLACCPSPQTQKD SSRSN
1304	7484	A	1320	9	274	FPIHFEATILIPKGGRIITRKENYRPLY LMNILINILKILESKVQ*IIYFRNARF WLNITKSVFSTHTSGFIFNKLSGTTGY PHAK
1305	7485	A	1321	3	172	EKGSNLENVFEDVHRSFNPFPREAN I*IQEMQRILVRYITRQSSLKHIHLRFP KS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
1306	7486	A	1322	2	392	IYAPNTGTGPRFIK*VLRVQSGSHITIVG DFNTPLVIDRSSR*KINNDIQALNPTF HRMSLIDYRTLHPKTTAYTFSSPHG TCSKIAHIM
1307	7487	A	1323	2	268	SAVLLNANNVQAEKHIIKNAILLKIAT PPKK*LGVCITKVNVNLYEKNYKIPV KEIRDNSNKWKSISCSWVERINEM CNEIVDPESP
1308	7488	A	1324	2	392	DCVQNVTVSTDLGHLKPWLLERWA AMCFPKALSDDMNNLKGRMHIAIER FYDNMPNAES*RLVMSSPAELEDDE KEGYLDTAAAYEEQHPELTPLEKE RDGLRCRGNRSPVPAEDSATDEPGE SFW
1309	7489	A	1325	229	420	SIRLSEVSQQNIAYFLKQSLFLPGFLIF YLL*KYGDIPKKCFPESYTTETRRM N
1310	7490	A	1326	3	416	PGPGGLPFNPPLHGG*APGMP*TPSK PPRGANPPSPKPKIFPGGGPGFLGPPS LKG*GGGLVLPFGAKPPCAVFPPSSS PGHKIWPP
1311	7491	A	1327	168	411	KEGLK*SLFTEDNFICRQLRLHF*KT IGTKNEFSKIPRYKVNTPQSKLAFI*TN SQQAEQKIRKTIPTMSKHQTE*YLGIN
1312	7492	A	1328	59	374	KTGLPNPKLRGS*PKGGKIPLGPNP* RGKKGEKRNSSSSPRVGFPPPKKIGK GGNPNPVPEPKTOGFPPPRKNQLISK KGTLNWANWGGFPILLTPPLYFFYPT
1313	7493	A	1329	2	344	POGWPLVVGKGMPSIPILKKRGRSNG SPPLF*PLWRPKPGGSPRARGLNPPW POGGTFFLQKPKISSSSPPPLFPLPW RVKPNLSL*PGGPNFH*PKLGPPSSW GAKPNFL
1314	7494	A	1330	3	213	QVLVRNRYRVDFFVIPPNSLLKPIS*FS KVARYRVNMQKSVAFNMNNRSE KEIKKTSFTIAPTIRITY
1315	7495	A	1331	2	228	TSTWILLWILLNLNRLCPDGPGLLD VQYSRKRNQSKLHLRTQIRMFSTAS YIIASNWNQGPSP*WESWSTLSC
1316	7496	A	1332	138	423	FFPGPAPGFMP*TPTEWGAQAGFFG AQILKPPRPTGEKKPPFFQKNKDLR GGAPPFNPLGGVGFPEPNLNGGKG WKDPGTTPGPPWRQK
1317	7497	A	1333	14	312	GPCCIPPLVGEADSSPFVKKSSPPLP RGNPLFV*QILPRRQKKAPQFNSSSS PMPLIPFSGGVL*PKFNPGGPRVQLT PGLPLPPPWGAKTGLPS
1318	7498	A	1334	67	377	NIKSLFRFRPVTKVKKNLLWCDFFSS WEARLVCLVEAEDEKYLNLMRHK RVSSITSARHIEECQCD*WLEQGST GL*VTVWEVFWFHGTIQTHTPEKNPV Q

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1319	7499	A	1336	3	385	RIITEILTKILSRSRKFIVALLFAIIGLTA VTTTAAVASVALHSSVQTVKFDKW KKNSMKLWSSQAQTDQNIWSPINDLS QTVIWMGDCIISI*ARTPMQCEWNA C EIDVPPLSRRTTEQ*SWTGLL
1320	7500	A	1337	1	386	FRLTPLPHRGLSCQRPGRAGPAPKP CSLQPPQRPVSSHFPSSSS*SE*SSSA LGAASTPSPITQM*G*TMRSQAEPQPA PPSPVPVSPPI.LHTHGC*EPCSPASAP RPLSTLLPGTQLPRSLCSDM
1321	7501	A	1338	2	253	SLLGSLHPPPSRFKGFSAVPFPGSGGS GPSSSSRSSSSSSSPKTRVFPGGPGGF QTPVFKGSPPLGPPKF*DSLKFPAPPP
1322	7502	A	1339	2	405	GGPAR*FPFPGSPRGGAQRAQRFFN PPGHPA VKENPPAPFHRKQKSPFFSS SSSSPSSSSSSS
1323	7503	A	1340	74	446	FSPLYGVRTREKYTEVL*FNPSS*DTE GQLTLSGITLGLSHNICLCVHFPMG VYRTLGVGKKSFRDLRHSHPSLYQSL KYLLECGSVYHYMKISLHSHDTLC GHPVV*DLEEYDNLPLT
1324	7504	A	1341	3	316	FSRGEHTLYCIAATWRSDASCCGR EWNTTNNGGPARARRPKTHAHSHER VHRLGAQTLPSDPQSLADPGETKTCT AKETINRLKRQPIE*EKVFANYSSDR G
1325	7505	A	1342	3	320	POGMGSKGRSSAEVGGSGPGPPASR ERE*PSVSGLRGAGAILSHVPSLWLP A DF*IFGRGGILLCCPGWSRTCGLKRSY LLGLPKCGDYRQSHCARPWSALKAG
1326	7506	A	1343	196	484	VALMDQNVAAQAQLPVISKMQTOPT VHYHIPAMTTANMKRSRHTKCW*EC RKTGNHMRQQHDGKLFPL*RTGCQ FLAKLKMDSIFSAILLWLC
1327	7507	A	1344	2	375	LEMYHPRITLRFQLARYNSPAQKCH LWLTHVPTHSGNVASARACFFSLR QSAQNFTYGCNSRKA*PKRRDRGGG RGRGGGREEEAQDDKGRKEMKKR KKRRRRRERNKRGTRGRGHHKREP
1328	7508	A	1345	148	146	NYRKEKPODFPSVCVCAVYCMFMCI CVYVHVCA CSPAYMCACVCICMCVR TCVHA*ACVCA*V
1329	7509	A	1346	3	310	WVVGFLMSQCLELLVPFIFYFFSILCM QAYCVSFLFYVCMYIFGWYIFFFISF *FNFFLFTNYSFSCFPYIFCSNFIIIFST FFSNFHSDFYYWYLDYL
1330	7510	A	1347	1	228	TFGKGIFGIENVTNRNDRIFYNAKWST HOENILIVKICAPKNRAPKCIK*KLSR MKGKIDSSITGVEDCNPI.SFFL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,785	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1331	7511	A	1348	1	228	TFGKIGFKIENVTRNRDIFYNAKWST HQENILIVKICAPKNRAPKCIK*KLSR MKGKIDSSITIGVEDCNIPISFFL
1332	7512	A	1349	1	230	TRPGGGRL*QTLLRRFKQGNLSKRS EGCTELKSCLCPSGWGAKQNSLSSSS PKTHKHRLGKV*KQMLRV*SGPDF
1333	7513	A	1350	2	339	IITPSLARGAPLPASPRPATSGASRELD ARSSKAALGAPSGPGADAWRLREP APFQAPLAPVVSQMETLKPPQQAASAP PSD*KSWHWAPVLSLTQLPGCPTGPA PLGRDET
1334	7514	A	1351	1	140	IPFCSHCPEKARA*TAECVCVTHKSQ VPRVESPAQPRPRVRSSNW
1335	7515	A	1352	1	140	IPFCSHCPEKARA*TAECVCVTHKSQ VPRVESPAQPRPRVRSSNW
1336	7516	A	1353	2	132	FFFETESHVTRLCESGTISAYCNLCL PGSSDSPASAS*AAIG
1337	7517	A	1354	16	391	QRFAFFCPGGGPGGYFGAPQPFAPRV KQIFPPNPPKKWG*RGPPPKPGKFWF FSGVSPFGAGF*IPAPWSRPGRVPK SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS
1338	7518	A	1355	264	626	DMARCGECSAAPMVLGSAAGVCSKG LQRKOPCERRRLKATVSEQLSQDLLR LLREEFHDTVTFVSGCTLFKAHKAVL LTRVPDFNFHTIGQTSNS*TNQPIAV LNVEPL*LRLFLQILYS
1339	7519	A	1356	3	391	KRSLWVEADLLIERSQDDMLINRAEA VKHFEELSRTNTSTDFYQALQNSLG GEDSHARAADATWYYSLEHSTDDY ASFRALENANRNYFIICPINMTSVW S*RTR*NTFMYPAPENYEHGSELLL
1340	7520	A	1357	202	200	FFKKNQILAKEPLKPLGLSGRELTSSS FTKGNKRLMVARGASTTRNKPLDKV YGEMEKN*FLAWGD
1341	7521	A	1358	3	283	MLGYDASFGYIFAI*LAQQGNLLEYR VGMYVF*DFAFMLSLKFHLLY*MN DGMIVYCS*NTVL*FLKL*KITLQKVK AIYRKSVFLMHISIWS
1342	7522	A	1359	1	376	RNGDQWHEISLG*LPRIHVLAQEFTE LLRVMHPPDPQRRPSAMALVKHSLLL SASKKSABQLPIELNAQKFRNSLLQH ELNTAQMAKAAAEERALFTDRMATR STTQRNTLSRLGKKMIRSVS
1343	7523	A	1360	13	195	YNPEDKAQSQWL*RGSGGAIKAKA DGSKAKVMATVFRDAEGILLVDFLE GORMPTSAyce
1344	7524	A	1361	2	327	ITQLREISFLDFLSFPLPGCGCVIHLISH PLVAQIPHSQR*YVFFPLDPHVEPPSS SPQKIYPGCGKAPFPFHWGVERNF LLPPRPRGPGFLPLPPQLGAQNTSLF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, /+possible nucleotide insertion)
1345	7525	A	1362	3	214	SLNTINITKTWLFSEISKMDKPLISGMR GYITTGSPDIKRIMRE*FHVHKFDNLD EMVKFLERQTAKAHFK
1346	7526	A	1363	1	291	LLTSRLTLLSHEFNLYLLNNSTLQPITS LPINIRQYQDQLTKKKETKDLNK*G NIPCLGIGRINIVKMSLLSKLIYKFKA MPVKIPGELFLRNQQA
1347	7527	A	1364	3	594	SGIVATGFGATGFLGR CVVNH LGRV GSQVIIPYRCDTCDIMHLRPMGDLGW LLFLEWDARDKDSI*RVVEHSNVVIN LVGRDWETKNFDFEDVFVKIPQATIAQ VSKAEAVGKFIHV AHLNVNKKSSRY LRKKAVGEKAVRDTFSEAIIVKLLDIF GREDRLNYFANMCWVGAIPLVSLG WKAVKQPVYVVYASQG
1348	7528	A	1365	1	220	NFYKCEE*ATTLSH*SSDNTHKJIHT GKKLHKPERCNAFDNTSSFSNHKK NHIGES*KCEECDKVFKWLS
1349	7529	A	1366	2	166	FFLDSTLKA*AIKAKINKWNDVKLKS FFKTKETINKM*QPMVWENIFANHLS DKG
1350	7530	A	1367	61	247	MASPOIEKKGKDVVSQHSKATVIMS MSYWGRDRHMDQ*KNKLNPKHFK GRLTFYRGVRAIQ
1351	7531	A	1368	15	308	SLNLAEQ*QSLDVCCFTLITVELHLS CFPSFL*A*EISHNLGVCIYLYLQFNK AQDQLHNALNLRHDLTYIMLGKIH LLEGDLDAIEVYKKAWE
1352	7532	A	1369	1	218	FPSPAPILFPFLKKRSPSPAPARNSK FFRPGKGGSPVDPPL*GGGGFFGSP GQRFAGAPLPRAKPGFF
1353	7533	A	1370	28	185	YDPKRPVGEKEIGKLDCKMT*NFCAS KNTIKEMKRQRTVWEKIFAHISERK
1354	7534	A	1371	114	277	LGWSPVESLCLVLAKVAFLSKPLL LDTVAHCNPSLGDGRGRWIT*GHEF KT
1355	7535	A	1372	1	89	VPRF*SLVGTPYWMGPFLISRLPYGPE VD
1356	7536	A	1373	132	358	KKRPLFVLKLGARGOGLFPVSPFFW GARGAKSFDPEI*NPPGPPGETPSTK NPKFIALYCAPVSPGPRGGQG
1357	7537	A	1374	2	393	TALFIDSSESSLFNSVS*SVTVSTAVC SGVSSITSTFKSVSYNYSSTSNYSAT PSCVISSPARAKFAAVHC*SGASYSTG ESSIPSTSSFPCTHWPSSTVCLGIPR PADCLSITPAIFPAVLFNHSH
1358	7538	A	1375	97	219	IYIFLLRDFI*ADRVLLGGPGSFYWQG RLIFFKLQVLTMC
1359	7539	A	1376	2	349	FEIEDTLETTCHVLDPTPA*CSVRQ LKEHAVEGDGCDQLKLKLDGKFSVY AKCDSSPDSSDVRKVCQDCPLLAPL NDTRVVHAAKAALAFYAQNNGSN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						FQLEESISRAQLVVK
1360	7540	A	1377	90	378	ERESCSTNPLGNHSAAGNSMVQTTDGT PTSVQEVAPHHTGRLPANHPADILAKS PQSTRAVAPQKCFLQIKGMTASCVS NIERNLQKEAG*ERESCSTNPLGNHSA AGNSMVQTTDGTPTSVQEVAPHHTGR LPANHPADILAKSPQSTRAVAPQKCF LQIKGMTASCVSNIERNLQKEAGVLS VLVA
1361	7541	A	1378	153	359	PGALKFFFPFPRQQAAPFGAGKTTILRL LFRFYNISFGCIRIKGRDF*QGTAQFF GFNIGVGPQDVTFLFK
1362	7542	A	1379	23	693	GPAARQCGVNRGGGWWGGAGRSLA TWIAAQGGPGRPLGVPRCPGAPSGAP CNSQRRLLASGASGQTPVVRGDGRCAP LSPRREAVCTWKPPQWQKVDERTGS PTPSLPSTGPRSPSEAGVGSQSRYLST LRHLLHSFSKQSKSNK*GNSVVVHTR GRGTRAPDGHSLSPQCGGGGAVREAR KGHRGRRADSGGGECPRAPQHASVT GPPQDRAARGCEPLERIPPH
1363	7543	A	1380	1	198	NIDK*NRIENPEIKPHMYSHLIFKIKINK NKQ*GKDFLFNK*YRDSWLVICRRM KPDFYLLPYNEIH
1364	7544	A	1381	1	372	HNRLKVLVYSQKGTGPGSSRKTCTRYIPS LPDRMLDAPEIRKDYLYNLVDWSSG NVLAVALDNSAYLWSASSGDILQL*Q MEQPGVEYSSVAWIKKGNLYAVGPNLS AEVQLWDVQQHKRLRNMNRHS
1365	7545	A	1382	136	377	LTDGIGVKRDYKQALKYFNLSAQGG HILAFYNLAQMHARGTGVMRSCHTA GEVRSFLPACV*GVLDLPSRKVCAPNS GFFG
1366	7546	A	1383	1	373	NWKINNSDLGGMLQDKRMEID*HS LHIGDYHRTARKGPGSRPQISKESMS ERTPYFDKNGPPSMIGGGNTATQPRG MQNSPSQPLSSF*PNLRAQAPPLLSP QVPASLLKYAPHNGGLNSLF
1367	7547	A	1384	317	552	APLQTAAVTFWVLTGWCSFRKAIL TREATGHFQESEPSPHIDPEESEETRL NIL*LIFKGNHFPSSDNK*HMSTG
1368	7548	A	1385	21	418	GTERPNNLPSQPWDSGPGSVSPATLP CYLDTFF*TRGSSLSCLDTVFSHPWC QNEVQNIKFNSSGQCEVPLVRTDNPK SWYEDVEGCGIQCNPLFTEAEHQD MHSYIAAFGAVTGLCTLFTLATFVAD WRN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1369	7549	A	1386	1	366	TTSTQFYKLSQEQINGDMEQVTDLSV TLQDQLNSLA A VVLQNNRRLDLLTA KRGGTCLFLGEECWYVYNQSRIVTE KVKRIDRIPCRAEELQNTHEWGLLS QWMPWWLPFL*PLAALILL
1370	7550	A	1387	2	304	FLGETGFPHVQGAGLELLISGYPPGFS LSKCWDYKCEPPAPRP*SQPFLYL LG *GPTFWHPNNKSSRDFFYYSNMCAS QLRCNCVLSVHHSYFPPIISFL
1371	7551	A	1388	59	288	GLSADLGLWPWEIWTGCCPICDALKE RGIIPSQEAPERAPWGWQASVRPQ*DP VAVPPSPPTLP SH*LP.LAAQRMNQ R L
1372	7552	A	1389	2	360	SVVQSGFPKPLTALPFTTGSQEVSNF SPSISKAQPGAPPSSRLGLNFYLPSPQS SLPPLYLGNPQGPQIPQPGYKP*RHTPG RRRANFYIAPPQLQSQSTPGSAHTPP SGPPV*MYQT
1373	7553	A	1390	1	119	RTRGFASLTLLNLKQAEAAKTADTAIP FHCKCLPILIRYT*LIRYT
1374	7554	A	1391	3	349	KAKPLPPPGKNL**KKAPPPPPGFGGR ENKIGLGGSRSP*WWFTQRGLPR GRGFSSSKQKRG*VFKGGRGKGPKE RMKGGGGQKPIMEGPPGSSSSSPKTI AKK*KEKIK
1375	7555	A	1392	23	328	YRALWLLIFLSLVTFVPLFFHYCLSYC *IDIL*CTILTPMFL*LYFLCFLVVAL GIKTNLTYSNLLVSVGSKNFI*YGFV PFPLIFAIIVMQIPLIYM
1376	7556	A	1393	2	200	VKDPOGPHG*TPFFLEKOKITQGGGG RPLSPFIKRVQENLFTLEGEYSIKPN CAPALQAGKKNSL
1377	7557	A	1394	158	364	KFLKPLDFKTLGDNKFGDPETENLGV GGLPKG*KASSN*KNPPASKGLQTK NFLPKNFKGTRVFAKKG
1378	7558	A	1395	3	375	PAFKATVTQGVSVQLGIQYHSHCAW RPQSSGKVEKMNKTLLK*HLKKLQET RLAWPALLIALLRIRNSPQAGLSPY KMLYGRPFLTNELGLDRETANLVADI ISLAKYQQVLKTLQACQPE
1379	7559	A	1396	150	399	PSPSLGYLVGTRGTALRL*DARAAMR PFDPTLLPTCWDYWTYAGSLTTPPL TESVTWIIQKEPVEVAPSQLSAFRITLL FSAL
1380	7560	A	1397	2	157	KIQQCMSLPSL*GTSRPSHYHVLWDD NCFTADELQLLTYQLCHTYVRCTRVS
1381	7561	A	1398	1	378	SSWTRTDR*AWVGELRTHRWKSYSD TDRSMKPWTQGTIFYDQLGETLQHIF WVYRSCFTRDVKEFAKMLR*YYPLE LQVYAGCEGHPGNASNNFFHVAFCG KEILSFQGTSEWPTHEAPLVVNLGIH

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1382	7562	A	1399	47	200	VKELRRDLRIMSQELEVNNAPYD* LKKMVKDQHEAEQKKVWGQGLACK D
1383	7563	A	1400	241	280	TWKSITKKQWEIHKHVEINTL* TTLT* ETYRKLQSTLA**IFCSSV* GTFSRIDH LSGHTPILKNIKILSIFSNHNGMNL EINNKKTVGNS
1384	7564	A	1401	3	211	SRKSIAEQTSCHIIRL* KGPMKEIHKSE REKHLVTYKGIPIRLIDL SAETLKPKE* DAIFKELKENV
1385	7565	A	1402	5	372	ADVMTAVGVGPTLLVCLNCVPVPE TPPPQVAQFGPSGVSLIPCPHALPVR QQAQMALPPG* VLTFSELLLPTPTPAS LSRPRTRPSW* SSPSSPDLNAVLPPY HPSRPPSSAVTAGLLR
1386	7566	A	1403	2	354	SHGIREGICGKKHSEQVPDILQLNAIF NMLNTKNCPSLKDCKPVIIQACRGD SPGVVWFKDSGRVSGNLSLPT* FE DDAINKAHIEKDFMAFW SSTPDNGS WRHPTMGSVFIGR
1387	7567	A	1404	3	344	KTWEGLLPRYEHAIFPSC TPDRIWVF GGANQSGNRNCLQVLN SETRTWTTP *VTSPPPPRPTFHTSSA AIGNQLVYFG GGERGAHPVQDMKLVV FDTSMDWR EPLSWSGPLNS
1388	7568	A	1405	1	383	VECYKKTKEAVLLMLK LKAWNIDIK VYASHRMIAG* GQMRNRCRIQRRGP SIINYEDNGIKAF TNIPGITLNFVSKLN ILKLAPGGHYGRFC IWTDSAFRKLHE LYGTWRNSRFLKRN YNLPMHKM
1389	7569	A	1406	2	181	YIAAVIKIV* YW* RNRHRHQWNRIEN PEIDPHKYQLIFGKDAI WGNVNEKK AFFWGVG
1390	7570	A	1407	273	394	NIDK* NRLENPEIKPHMYSH LIFKKINK NKQ* GKDFIFNK
1391	7571	A	1408	75	354	RLVFV* KDWNRNPLGAPRGVSK FLR DQLEKRRPPFSSSNP FFGLKFGEDL KKALEKASNL* EEKAHLKQENKGF KEVGGE* WDLRGGRG
1392	7572	A	1409	88	482	NLFLLLILLKDSLLSS LDGVRASGNR DVCAMTPTTHKGQR WGLLTPVDE EV* SLHLKFLATPPNGN FADAVFRFN ANISYKGVLIH AVTDGLFSENKELI NNAITALLSQEGD VVASNAELESQFQ AV
1393	7573	A	1410	7	349	LNHEYIK* VDAEQSYAMAVEAGHSR SMPLLRKPRVTHA VLDQADVYTHVL SAFAEKKEMPHKFV IAALMEYIRSLN QFQIAVQRYLHEL VIKTLVQHNLFYIL HQVLQYHVLSE
1394	7574	A	1411	1	190	FFFFLNSLFFLMRHN SHTHKIHPKVVY NFSPOAVAHACNPST LGGQGGWITTS GD* DHPWLTR

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1410	7590	A	1427	60	347	ARHNVAKLPNPPL*RPSPSRSTPHVP AAVECLSLPLCDTTSPLPSPPDWP GAAAACSEPPSHCPPGRPPQPRVAGR ASLSCGRGDTQDPVKW
1411	7591	A	1428	53	722	VRMAACGTSLSALOKLQTRHEILQHE GPGHRRLAGERGQQHPRAAADGGTA PDSSAGQKHRSSQKPRGA*GSSDTQ EAP*PILGATPOPGSQNADVPSTGERL GWTPGRLPKHFLHNGFLCLCTGEM TPHDQDQSGPEMRPHGQDQSGPEMT PHETKSAGGRDDATRPRLLEGDDDS TQPRPEPGRDDSTRPRPEPGRDDSTR RPEPGGDDTTGPHWCG
1412	7592	A	1429	114	386	FLKWPWPQPKPKNGQVFLDKRKKIG GTLGFKLI*QA*ITKTGIFWAKNQPLT PWDQRGPKTKRALYRGLIF*KGPRKF FWGKKNFFNKRGW
1413	7593	A	1430	2	373	RTLTLNTRRDAGVYQCESWNSATS SISNPILIKVIYVGPDPMPVNPDEVT AGAAALTSFCFADSNPPAQYHWEMDR RPGPATQHLVISEVTLDO*GRYTCEA SNSITHLCSVNGKIWILEV
1414	7594	A	1431	44	257	GQITKNALSFSSDFSLNHHMYTYFKK HENYNASKGGPTVVVHACNPNTLGG QDGRNA*SQGVQDQPGPT
1415	7595	A	1432	1	397	DVTLRNLRSQIDNIA*STRDSISKLKA SIDSLANVVMNRLALDYLLAEQGG VCAVISKSCCIYVNNSGAIEEDIKKIY DEVTVLHNFHGKGSAGSIWEAVKSA LPSLTWVFVLLGPAALNSLSPLWPLP L
1416	7596	A	1433	49	351	IPVDQFKPSDVEIQACFRHENIAELYG ALLWGETVHLFMEAGGGFVLQKLD SS*PLREFEIIWVTKFVLRGLDFLHKS RVIHDDTSRAFFWVTYTLFARD
1417	7597	A	1434	280	347	RCTVIWKQKSILLQNYLV*RAQSMPIV FKEVKVHLLEDAIEKDAVQTETRIIS PSGIDSATTVAATAAATAAPLIKIV HSDLEAKVNSVTELLSKLQET
1418	7598	A	1435	298	405	IIIFYCYHNTAAVAAATL*EVVM*IQ EMQRTLVRYYVRQPSRPHTVIRFSKV DVKEKIV*VTRERRPVYKGNISRHSS PFRK*LVMLSWPQGPIN
1419	7599	A	1436	25	358	TTRARESSGCAASREMRICSTPPAAC TPASTTSCNRPAAARTPCSPRTSGA QWASASMDTPPTWRASSR*RCTITTA RSSSTRSARPTTPPTAQMPARSTLVPR KTPRKK
1420	7600	A	1437	96	283	KDWKNPFGAPSRVSKFLRDQLEKWK PPGSSSPNPFRLNFRQNKKPLERA PNLSEDKKPHLNQETKGFQEVGGEK* NLWKGLPTSRQKSLT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1421	7601	A	1438	2	340	EGAGAGSGFRKELVSRLLHLHFKDD KTKVSGDALQLMVELLKVFVG*AQG PRSLRAQHPEFCVFPAGKPRRVFPFPT RA*TWVS*ACLSEAAVRGVRAQAE DALRVDVDQLE
1422	7602	A	1439	1	209	LRKSNYSQSLSDKANKNKIWGKGITL FNTWCWDNWQATCRRMKLDPHLS *TKINSRWKEAGHGGSRL
1423	7603	A	1440	3	171	GILNHSSGSPDSNQRKGPEALGKV SLPLDFDKR*VLPNCNGESLWTHLHIR IG
1424	7604	A	1441	319	391	SSTEKGLIVGSLAKAQGWV*LSAH LQVGNHGSNEAALILHRKGFDCRFSS KGTGLVCSTTQ
1425	7605	A	1442	3	392	LFLLQHQHVGFIFRGEKCVHHQPRM ISKRNKDCSAACSRPVTOHEFDNNC LVLLRAPAVYSSKIRSFHGQCQLDL CRHEVRYGCIREDCECFYASHVELKV WIMQNTGRFEC*EVCLLKSRQIE
1426	7606	A	1443	232	630	APVLPVIVCFMPVLY*HAVLMGQRT YYGYNTGMKTHMTMGRTOGAQKIQT HQQLFDKGANITQWGKDDLLNKCC WENWIFACRRMKLDIPYFYS*RKMRP GAVAHLRSVG
1427	7607	A	1444	6	333	KHHLNAGHEHQPPGRPGGRAGRMES ESEARGQEKPSSEDESAQGTGTGPGRA EGGGGPQEGRLQLCWECPHHPDRE A*QDFTPQSPRLTPQSPVPLTPPQET GRPCQ
1428	7608	A	1445	3	268	NYSMEWYELFQLGNCTEPHLRPEMD APLWCNQGDACFFEGIDDVHWKENG TLVQVATISGKL*KYSNI*SLHQNPN RDCYTSIETFO
1429	7609	A	1446	181	224	SISTLLCTKKVP*ILCFAALGGPQPC DVWSIGCILIEYVLGTFVFPVRDNDLF QPCFAQRKCLFI
1430	7610	A	1447	3	388	NQGRALFPPPKFPPGVNNPWGFKPC *GG*GLGGFLGAKNGGPPGPGFSRKL FWGLTVKPPPGGF*KPGPFVFGPK GNKTWPPGPF*PCPSSRS*KPGSFK RVVPSPTPSKNQPKKETVELSTK
1431	7611	A	1448	1	359	VKIYSDFAITGQREVTTERRDGKKKSA VFDVVMV*SGHHVYPNLPKESPSGL NHFKGKCFHSRDYKEPGVFNGKRVL VVLGNSACDIATELNRTAEQVMISS RNGSVWMSRYWDKWSYL
1432	7612	A	1449	347	0	SGGKGILI*GNPGPRGQGFPTPLP GGGNGKPPPGPKIFGFLRKGGVPPG QKGSKRGALESSSRGPPRGGETG
1433	7613	A	1450	162	366	GIFRAGLTPRGRENKAPQGGGVNFF GFLKKNGVQRGNPGGRPPDGTGG PGPKKGGE*RGGTPTPG

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1434	7614	A	1451	2	387	FVGGKPKIHVGVSNCNPKLGKNGKGRFP PS*TPKNKKKPPPKPKPFSGPGAQK KRSPGAPPRGPRGNLDPFFPHFFPGG PFPPIQKEVPRKPEIFPREIKGSSSS
1435	7615	A	1452	28	392	LPGLDGLCCSLPLCLVPGAPALTSTRQF REDDFRRVDFIDEGVNIGLEVSKT GE*ARRSPGPASSHLSAPSP*SHCLP *SSDHLFPHPISLAKIQDFKSLKDS ETSQRLANLRQRV
1436	7616	A	1453	42	363	STPLPSLSDAVFLILYKELYRHHYAK VSVSI*VSQSSSRFCFFNSVL
1437	7617	A	1454	2	120	QHNH*TLNDIKGKLLDILHKDSSLG YVILFLFWAKYLL
1438	7618	A	1455	90	232	LLGNFIANLKEALGHQVIRINYLGDW GMQFGKYT*DFHFIVKFNH
1439	7619	A	1456	212	498	RVVFFSLNVVYVPGPENSSFFSLFFG DRGLVMAPRAGVHGLILDLS*PRLK RSSHLSLSSWGLOQCVSIAHFSISF VETGFHHVAQAGLKI
1440	7620	A	1457	3	256	SPPLGRPRPADSSRLGPGPGP*GEPP SFL*IPKIALSSSSSP*FPLGLGPGNP FDLEGGVWSGPMALAPCPGWGPGPP SV
1441	7621	A	1458	164	370	VANLKICIISCCSCVQKKTKVILKI*ES WPGTVAHTCNSRTLGGRGG*IMRSG V*DQPDQYGETPSLLK
1442	7622	A	1459	3	493	RRRYPPYLSIDITAFSPQVLAAVIFY FAALSPAITFGGLGQCQYLSP*LPL TLWASVSAPTSGLCLDPPGLASA*P* LALWAPGK*SPDLDPITVISPQGAkd PGTRWGVFGAA*FTSGSGRGIFLSAL LGAQPLLVGFGSPLLVFEEAFFSVV LSLP
1443	7623	A	1460	273	397	NIDQ*NRIENPEIKPHMYSHLIFKINK NKQ*GKDFLFIN
1444	7624	A	1461	5	355	DSLAVLPRLECSGAILAHCNRLLLGS CNSPASAS*EAETGVCNHAWLIFFFF VLLVETGFRHVDQAGLKLLTSSDPPA LASQQLALQGVSHRRLSYVNFKTH TQTHIHTHTLL
1445	7625	A	1462	3	372	NAYIDITKSRRREGIFVLRA*PISIMSSS SSSPKTPGAPPPKEKGAPTPGNRGNIP PQPPKERGKIATSSSRGQK*KPFWGE GGYPRRPGGVKKRRRAPGLAPQK AGKTGQNPQGPPOKS
1446	7626	A	1463	97	219	IYIFLLGDFI*ADRVLLGGPGSFYWQG RLIFFKLQLVTMCR
1447	7627	A	1464	132	348	FGPPGGGEGAQPRPMEVQPPGGLGD LLP*PPQKLGP*RVGPPSAKFLF FLEKKGPTGVQVGLNPWA

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1448	7628	A	1465	1	413	GQEFGRTRNLRINTADSWQVNSNAG KNRSAAWATKSSLLALRGQCT*PLVNL FTKEMESVSKFRVPYVSPSSSSSEKKF PFVPQVGGQGGNLG*WPPPLGLRNF *ALTLPGSWNNKLAPPVRVNFIFRKK GFTLVARE
1449	7629	A	1466	39	371	MWWKKLPMLVDPQRTNRPTSSIPQK PQSCGKIA*KKYGGVNGQASPRSGTQ SDKSHPSRAPKDCVEAAKRIQEIHD PGRHLGARGGVLTQWPLTEAVYEC SLHPVGR
1450	7630	A	1467	3	262	EYDYRPFVDIPDIPSRIVKNPWPVGK AREHLFGKVA*IKING*IFLMLGGDHR SC*ITVSMGSSRRSGYQGMKRENHL LLSEEH
1451	7631	A	1468	87	368	KDPERGGKGKTAATSPITCVCFPPPI LPTPPAHAAWDLKSVAEGPSLHNFK NNQPPSLPKPKFTHPAFTFLNPLRTF FCDPPP*MEELGGEM
1452	7632	A	1469	25	228	VLHINIYISPP*LDDEFESTGVKRVQA LNANVWSNVMMKNGK*LGTVIFFL LFLVSFKLLRYMWNH
1453	7633	A	1470	1	385	IWNICYCRKNLELWAWGFTTDPNKR WELCEIPRCTTPPPSSGAYQCLKGTG ENYRGVNAVTVDGHTCQHWASQTP HTHNGTP*NFPCELDENYCRDPDGK RAPWCHTINSQVRWEHCKKPYCDFP P
1454	7634	A	1471	42	379	GAPPGIPPFQVEVEGGSPGPE*NTPGA PRGKPLP*NPKNPPGLGPIPLNPPRKI P*NSSSSLPRK*NGSSSSPPGESSSP
1455	7635	A	1472	123	222	TVNSYYS*VDVLNQVDWNAWLYSA GLPPIKPK
1456	7636	A	1473	2	296	SEIQSKILDLNKQTQEFQPSLETWTEF QQGLESNP*TYVKHHLNVFRLGT MLLCLCLFIVCKTGWTNWQLKVA QPGITFIQLMQKHKGDDVGH
1457	7637	A	1474	15	264	NNKLF*YKHKHKLKKNIDKLDFTF M*NFCAKNTKIKV*PPSA*EKIFAN HRANKRLVFIYKEISQQRPPN*KWT NYP
1458	7638	A	1475	51	256	FSVSQSPTGTDSDSLGGLQAANQTSQ LIIQLSSVPMNLNCFNKLFSMLQVHH VQV*LQEKWCIFTYYC
1459	7639	A	1476	3	388	VATFTSSATDNS*NRKATILAGTANV KVRSTTIPLEASHPIENSSVPRSSQFV GTRKSEPDDELFPNFLNRSQKEPTGR VEIKKEKGKTPVFHSSWTSSVSFVNP SITTI*TEEKSEFGKCIHKCLH

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1460	7640	A	1477	143	947	ATCREPEGPNEEYPYCSLSFEMLCRKR EVSLAFARNQSGTGK VASNRVLQME KGNQAYLNLLEWET**EFESA WVL TN ASGNSLQTRIVIQAGAVPIEILLNSEF EDVQEQA V WALGNIAGDSTMCRDY VLDCNLPPLLQLFSKQNR LMTRNA VWALS NLCRGKSPPEFAKVSPLNV LSWLLFVSDTDLADACWALS YLSD GPNDKIQAVIDAGVCRRLVELLMHN DYKVVSPALRAVGNIVTGDDIQTQVI LNC SALSLL
1461	7641	A	1478	2	344	TWSGAQYLTHSS*VPCNGFSDIENLE GPEIFFEDELVCILNMEGR*AIYSGLIK ANKSLLKLWLTFPLVLYGTFVHPQK KSLVLQGSQCH
1462	7642	A	1479	32	358	LIIHLIFTRGSIPLMYETFILEIFYKNCFF IIFLSFLSLSHNIFS*QNRVVGAMQLY SVDRKVSQPIEGHAAFAEFKMEGN AKPATLFCFAVRNPTGKGVRSTLLSS P
1463	7643	A	1480	3	212	VPIFYEFTGEGPQKKEGKA*DLGQC PVRINQAVRTSKHMQAGRGWRWEW GIKQAGKNGWQVQGVPLEP
1464	7644	A	1481	152	371	RRIFPCSNPERTAGLPLTDIPIPSLKDS S*PSPITESMPL*HLCYHPGPMFLGTN LSTVPGRTCPALSSITPP
1465	7645	A	1482	3	348	GRVPPPPFPFLGPHPGFPFGGFFFP APIV*TPSSSQNKISPSSSSPFPPL GGVPENFFFPSSSFYTPFFFPFP
1466	7646	A	1483	2	341	NTCCPSYEKGGGYRSGILIERLPDPQ RTHVMWATIKDFMGPLRFGLTYLPQ YQDVATAEASLCRYHRLNLGVDDQ MALLLRHRDEENEDHILPHSL**LKV LKILTTSRGAQD
1467	7647	A	1484	23	522	VSRDLVCFQLQDHVNYYGQDYRNN YKAPTDYCLVLKHPQIQKKSQYIRYV CCDDVRTLHQVWNGIRIAKYGKQLY MNYQEALKRTEAYDWTLSSSSIKS GSSSSIPESQSNHNSQSDGSVSDTQP SRDTSVPQSIGELPYSSSEAPNEALSW KSPAR*QASF
1468	7648	A	1485	2	364	LEFLQLSPQTLFMQGCVFCSVHFLK TRVSRGRGLSLRSEACWCRGASKPY LLGTPACMCSGTERVEQSVSTHNAH QTWDVAGSFPRTRKDIHSGTTV*LPH YDPPVCPHRSGLPFSLPEK
1469	7649	A	1486	2	327	IITNLLKAGAESNRTGSTLSISPLMLA AMNGHDPAILLLYMGSDINAQV*T NRNTALTACFCQGRA*PKRLLDRKA NDEHMAKTGLTPLMEASGGYAEV GRVLL
1470	7650	A	1487	1	119	RTRGFASLLNLKQAEAKTADTAIP FHCKCLPILIRYT*LIRYT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1471	7651	A	1488	72	228	WTHLYGANLRFKDCFFAILLHKKDKLRFALCAFC*KGPASHYQWVKVLPHG N
1472	7652	A	1489	2	38	AQIFISKCVSPAEGKQGVYVNIKLWKNGFSVNDDFRSYSDGASQQLNSIKR G*VSR
1473	7653	A	1490	3	421	ALVPSLGLPLEGLPSSL*SLGRRSVVDFAKRFSPGQACQDDTNMNPDLGLR SQARGRQQWLHRDPRTPSRSSSGSPPGSGRIPPSRGRTLLDRHGREKAGKRLCRGEGSPLSPQAALGPHLALSTALPSGPRLAS
1474	7654	A	1491	10	387	ISKIQVYTKPQADIQTPGGQYAPGGQHTPEQQATVWHQGPKNKALGDYQAIGSH*SPAGQ*SLGGYLGPRTWLDPRLKQKPSKKIKPQVDNQLGKYTNLKLTPGPWTPKQPMDFRPQVNTLE
1475	7655	A	1492	1	162	YLIPTADLKPGEPLLEVGNNWVVLPEMSIHISVSSGDVLPK*APPSIGIKTDS
1476	7656	A	1493	2	364	PFPSPRRVPPPTPKNVRRKKPSTPRFGNPLGKPPFWERPRGLSPNFGVLRNKGFRPTPGLGP*SK*HRAQSVPRQDPAVHRPOPLSCDKKTEPSTASD*PRPSPLOHLIGHRSILHRE
1477	7657	A	1494	16	225	SSSHIGTTRPGARTVLRHF*LNFPFNP GIVLLGVYTKELKTCVHTNTCIEMFT FIAAKTWKQPGCLSVGE
1478	7658	A	1495	1	162	YLIPTADLKPGEPLLEVGNNWVVLPEMSIHISVSSGDVLP*APPSIGIKTDS
1479	7659	A	1496	2	176	QSHSL*IALSSRVSEWDSVEMIGDVFVASVIKLGHLDVHGALHAPVLSLLRLMFCF
1480	7660	A	1497	2	347	PLAQFIFLKLWGVALFVRRIPGRFSA LM*IVLSLTVSCRYIWWRYTYTLNW DNPVSLVCGLFMLFAETYAWIVLVLGYFQVWVPLNRQVPPLPKDMSLWPSVNIFVPTYNHPPT
1481	7661	A	1498	16	225	SSSYIGSTRPGARTVLRHF*LNFPFNP GIVLLGVYTKELKTCVHTNTCIEMFT FIAAKTWKQPGCLSVGE
1482	7662	A	1499	45	256	SCSYIGTTRPGARTVLRHF*LNFPFNP GIVLLGVYTKELKTCVHTNTCIEMFT FIAAKTWKQPGCLSVGE
1483	7663	A	1500	2	163	YLIPTADLKPGEPLLEVGNNWVVLPEMAIHISVSSGDVLP*APPSLGLKTD S
1484	7664	A	1501	1	418	TLITVRPDNV*VGKRRCNRIIGGLPTET QEDVLSISGGFDSGVSSYMLMRRGC REHYCFNLLGGAHEHIGVRQVAHYL WNRFGSSHRVRFVAINFEPRVGEILE KIDDGQMGVILKRMVMRAASKVAERYGVQALGHPG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1485	7665	A	1502	6	292	LRTRGPPAETLTGTPGPAETLTGLGPPAKTLTGTGPPAQTLTGTGPPAETLTGT* AAGNPSRVQLLRFQGGNGMDISTSHKTSVRFLIPFLCLRKN
1486	7666	A	1503	100	345	ALRRKLSPASSRWLSQPGCCARSWGRCSCQHGQTEGSLAPGPVVGELFARS*RQVAQNLAWSGNGWNGWETGQTAGVFSL
1487	7667	A	1504	6	338	AGHGLYLYSAAETLG*AT*DIYQKMLDGRMKNSIFNYPTLSWADIGVIGWLEDGAPIVNHVALCRTSYGPYARAMVKICKEESFHQRQGFACMALAQGSEA QKQMLQDA
1488	7668	A	1505	89	285	NNLDPLTHDWT*GLQRLIKKEDERRAADCCRIQLQLPGKQDKLVVALKR NLLGQCWGENGSL
1489	7669	A	1506	1	82	NMMEQVLDIPSL*VISKDNANVTIDPA
1490	7670	A	1507	3	133	DDRYDLRFSAWVTYPKGEWGKGTVQLVDIPAD*IRYHLVVSCQ
1491	7671	A	1508	41	526	SANNVAIPQLICLGPQQLRTRLSSGSHHRVRSRAAGHQRADSVAVALAVSACPLPNA*GLPS*SVHHEHHTRTASHPRLPQPSITCNA GPPSPGGSPAPSPNPTWDHVLPPFPWPLHPCPLPPARCRRQPCPARFRPAQPVYILLFLNYRFLGL
1492	7672	A	1509	415	339	KF*IECAAYNPEPYLNNEQSPDSFSTA HGFLWVRVCVYLVLVQVHRESTFMVGVMRD
1493	7673	A	1510	16	255	SSSHIGTRTPGARTVLRHF*LNFPPNGIVLLGVYTKELKTCVHTNTCIEMFT FIAKPPWKQPGCLSVGE*IVKPHLHPS
1494	7674	A	1511	22	311	TALSVRKRSKSTAQVQVELLVPVHL SVLELQQAQVQLALAAQAHPAQWRLPAQVVPDAYGERTLVQTAGPSVLHAAWAACNRLGVL*VPKWE GPPTLGYMLPKLHEEPMALPSEQEFARHKRPEPALATFAMPDVPPAPTPAEPAPV VAPAPKGAPATPAAPAQGILLSRFFGALKALFSGGEET
1495	7675	A	1512	1	200	MITDSLSVPVQRCDWENPGATQLTGLATQILSISFANHNEHPSSETSLPGVRR* NSYLHPQQTTPVHL
1496	7676	A	1513	101	352	ALRRKLSPASSRWLSQPGCCARSWGRCSCQHGQTEGSLAPGPVVGELFARS*RQVAQNLAWSGNGWNGWETGETGGVCSLCL
1497	7677	A	1514	3	82	GIALWFPGISFTGKNV*DVKGHGV
1498	7678	A	1515	2	174	QKIFNYIQLTPVRKEGIVGYAAKPGADRSLFDASGFKEG*VAIALSHSLADLRVGR

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1499	7679	A	1516	3	199	CVGCGCCPACPYRVRFIHPVTKTAD KCDFCRKPTLQAGKLPACEE*PTKA QTFANLDDLVRVAP
1500	7680	A	1517	7	167	LKDCGQKKK*HTTDWQKIFAKHLSN RRLAFRIYKQLLKLTSRKTNNRI*QLA K
1501	7681	A	1518	657	817	YFLFSPE*VGCSYRKITPGAMAHTCH PSTLGGQGRQTMRSRDRDQPDQHG E TP
1502	7682	A	1519	3	134	AQLWQ*PVTAGLSLPGTIFVVRDIAH AKLKELIDAGKEVPQSIK
1503	7683	A	1520	12	368	LRIPVTRRSNRM*YGCGRQIYWHNF ASDQDPSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSPVNKSANYGVLD KLARGYA
1504	7684	A	1521	1	213	QGGGAGSKNSPLGPTHITPPPGPKTP PGEGPFKIRPQAVNSPNPCDPV*NPP PQS*NPGPSGGLPPVFL
1505	7685	A	1522	3	315	QQERVAAWNLRAE*DLA AFQTSPKQ AYQDEKARDRLCDNLEPIRRSGLQ DGMTVISIRHAFRGDDQTVNMVMHVI AKMGFKNLTLASSLSAACHAPLLPHI RQ
1506	7686	A	1523	1	319	LLFFGGAAGKGFSPRPGKQIFYSPP FSPRGGKKGGPPFSSSSSSGPP*NPP QFHGNGPTTP*KPPW*FKPLRPKKKFS FEPIGQKPRSPFWGIFPPGFKGP
1507	7687	A	1524	1	135	KYIDRALNFMIGTINV*CAADVLIQPT PAELFDYTSALQFFDMLR
1508	7688	A	1525	91	354	KKMSLLYPQGGGQGGNFGKRKPPPG G*NAFCGPNPPKKGN*GGPPSGENF GFLKKRGFYPNPGGLKTPGLRDTAP LAPRGGIKRG
1509	7689	A	1526	32	420	VSGERISVGAAGSFGDEQRTKWPA HRMAPCVGWGVTNNRRLRRHERAIA EQM*RNARKSAKKGPGVGHDAEFTM MDLYMAYADYKDVMLPESLFRTL AQDILGKTEVTYGDVTLDFGKPFELT MRE
1510	7690	A	1527	3	397	VFLYRSPIGGRALPDGPYSRTIRAVVR AKMRHTPSS*VAADKFTEVDSVGK EVYSIIRLDPAAVKMVRVQAEKNR YRAEELAEERILDVLIPAKNSWGQT EQQQEPSAARQAFRKKLREGQLDDK EI
1511	7691	A	1528	45	251	GIVLGSNTMTTPPLWEPLISPKAPATP TDSLLCPQCIPMKIPT*KPSLPGSPL SPGTPAKRLLWL
1512	7692	A	1529	1	213	QGGGAGSKNSPLGPTHITPPPGPKTP PGEGPFKIRPQAVNSPNPCDPV*NPP PQS*NPGPSGGLPPVFL

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1513	7693	A	1530	31	611	GALKILLQPSSGTHCGLWKL*NETYS FVSDLLFFIETFGIFFDILEFHCLQWVS FPSILLDTL*ALST*ELSSILFILPLNIF FSIFILCSWNSIICTFSLF*IPLLTFNPF FYTFSLFLPLG*VASSLIWLWAAFG LIMFPYFNYFGC*FTLLPCFMSLVSA FISFENGKLEKILGASGLKLLTGGG
1514	7694	A	1531	303	537	YDCRCRCRGICRHP*GDRPLIGAPAP GNTPNKKGVLSFPNPGPTGEKNPQL GPWALPGPNLPLCPPGRPFTPGKKAR
1515	7695	A	1532	48	633	IWSFRGAGGYPYGNPPWGGRGGTTP* SGVFNHPAHKGETPSLKKTKQKFPALG PGQNPPLSSSSSGKKGLTPGGGGPR DQISALPLVGGGQKWNFGSSSSSER
1516	7696	A	1533	3	621	STQDDRPRTNQEDGSPGQSNQKITE QSTSHQHRSKCLCTCFVKISYSPNPTS FKKFLGGVLDFTTFPNKPGRVPDPAL KSPNPSQQCTLGLIEIFRLKGG*VWVP TPPRLGAPRVSAGRDVLGGGASA QRPLPQVSSARGGPQKGRCSGRGLGS ARRTLPKGRSSSEPGA GSA GRIQMLGA GRALGLPSDPSRSEKPGSAGQ
1517	7697	A	1534	1	213	QGGRAGSKNSPLGPTHTTTPPGGPKTP PGEGPFKIRQA VNSPNPNCDPV*NPP PQS*NPGPSGGLPPVFPL
1518	7698	A	1535	4	643	IPLTKKKVGDHARRLSPNYKDGKGP PLCGRGWSALSTTHGERRGPTSYSS MAKTPHLGAPPSSSSSSSSSSLLGP GGPPPLIPSGGARGGNSRGPQGNF QDFNIPFPFPPGGPKRGPPLSSSSSSG SPQNGPPQFNGNWAPGS*KIPW*KPK LRPKKKGSLKPKKKPRAPNFWGKF PPGFGSSSSSSSSSSSSSP
1519	7699	A	1536	3	127	SGGGRDPNSPYRGNNNSWAGV*QR GDGKNPGVTQFNRLCK
1520	7700	A	1537	16	225	SSSHIGTRTPGARTVLRHF*LNFPFN GIVLLGVYIKELKTCVHTNTCIEMFT FIAKTWKQPGCLSVGE
1521	7701	A	1538	16	225	SSSHIGTRTPGARTVLRHF*LNFPFN GIVLLGVYIKELKTCVHTNTCIEMFT FIAKTWKQPGCLSVGE
1522	7702	A	1539	3	636	GVLWKGFSHCFNPHGSRGLPIFFQQ NFLFLGPQKFIFFAGGPVFSSSSRAP AFPLFSWGPPTLIPPLFLGPGRKGVK KFEASSSSSPKGGFLFFPYSSSORGV FSSGHPFPFGFKFFAFTPPVNGG*RA PQPQRKFLGLKKGFSPPNPEVFLF PPPNFAPPGPQKGGVPGLGSSSSGFF PPSSSSSEASSS

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1523	7703	A	1540	2	445	DRPVKNSRADDFVEKRPNLITGLHGR EGSPPPSGRARSPWVVGALPKLLGG CCHFSPSPPCPTHRCNTFPSSQGERSPS NLGDPPTPFMFLLGQDASPPPTPLHPL SWELPTPRLFPF*GEASCCPLEIHRH TFFLSPHSLPPFS
1524	7704	A	1541	1	411	FVQSKAASDWLIASVEGRTELCEGD LPTIAIVGHYDAFGVAPWLSLGADSN GSGVSVLLELARLFCLRYTY*RTHAG YNLLFFASGGGKFNYQGT*RWLEDN LDHTDSSL*DNVAFLLCLYTVRRRS
1525	7705	A	1542	1	443	IFQSWLCRTQTAIAS*DMPYTMTEAE KLLTQHETIKNEIVNYEEDYQKMRY MGEMVTQGGQTDQYMFRLQRQLQAL DTGWNELHKMWESRQNLSSQSHAY QQFLRDTKQAEAFLTNQEYVLAHTE MPTTLEGAEAAARNRRRGRSRTVV
1526	7706	A	1543	2	400	LLSFL*HEEEFARLARGRPWCRCRH LGRRWQGS LGGAARTCAGARGGWR CNRRAAPRSSWTRRSRWPRAPWPA PRGSRTAACGRT*ARCGS*LRPRWTN HPPGRQAPGAR*APAAAAAVDGTGP PAAPLCTK
1527	7707	A	1544	108	397	LSWDPPDFIDRETTPRMPWRDVGVV VHGLPARDLARHFQIRWNFTKVFIPS DRGWR*GGSQRLAPPADSAIPPRQT TKAKYKTPTYPYLLPKSTS
1528	7708	A	1545	1	408	FRGEHHAWFGFAVTSGYLSPQVLWK DPYRKPDVLWACGVILYLRGGYPFF WDEQDHLRYQHIAAAAYDFSPPEWY TVTPEAKDLINKMLTINPCERTAAEA LRHPWISHRYTVAYCMHRQETVD*L NKLMPRRN
1529	7709	A	1546	163	484	KVNTMQNYTQSEKINFTRDHFALVTT LKSSSSNVGNETHSSCKMLTADSSGI PTSWTRELI*EMSPPCSPTESSSTDSS SSMDSSSSMDSSSMGRVETATCAMI
1530	7710	A	1547	389	1	SSSSSSSSSSSSSSSSSPRESSNSV DLGQRLPIGSSKLDDYEDLDGTHA* TSM*SRKTQPMFEPSTPLANPRPRP GHPPSCPLPHSSPSRGPHFPFPFPPIPR SRRTPPSSRAVSHTPQTK
1531	7711	A	1548	2	422	FRWHRLFEFGTTGE*PLAVAADGHFLC LALTTQYMIHNYSSGGFHDLSYCSE ERPPIVKRIGRQEFLLAGPGLGMFAT VAGISHRAPVHWLENVIGAGVSFFYV IALDDEFTIVHSMLD*LQKQTLPFKEG HILHDFEG
1532	7712	A	1549	340	432	ACESWVHVSPSFLCLNVV*VSTCVT RTAQCSICDCRYP*LV*QC*K*CEKG YVSQCVSAGGCNCRGVTVSLCTGAC VCQDMCEPVSRCMCRHHFSV*MC MCMPLOCAHLCDSD

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1533	7713	A	1550	2	259	KKNNGFGPGGAPPLNPPPLGAQGGGFGPGSGN*PPPGPSSSPPLFLKKPKKPGFGGGPPFSPPLGGLTPKKGLTPGGOPPNNPKF
1534	7714	A	1551	2	419	FVKSNIDISSGF*YEEPKRPMRKQSDSSTYDCEAITQHHAFLSSIHSSVLKDESETPAAGGQQLPEVSLGRDFDVSDFFLFGSPLGLVLAMRRRTVLPGLDGFQV RPACSQVYSFFHCADSPSRLEPLLEPKIHLVP
1535	7715	A	1552	59	391	VTFCCKAEAPVGAGAVGVRIRGPAGYKQQIPPSVLALTSPPGKAPLHLAELEK RAGSHLYLSRGEGTARALAPIISALRS APRTPALSLTPSLTPRP**PASLPPSSASPVTK
1536	7716	A	1553	1	496	TDVPVRCRVDHFVLSRSRNSSGEAPRLGDRRAHCSPLPPL*PQPLPPPGERQPIVFLRGEGEELSRLGPRGSPGSR TNGTTEEVTSKEDEEEEMDEDIEDLDHYEMKEEPISEKKLEDEGTEKENWAI LEKIMKTERQGHNLVLTIVLCTVIFRSYKAI
1537	7717	A	1554	2	420	TQLPDLNSRDDDAEFQEPVPASIPFY YKIIKKPMDLSTEKKKLOKKHSQHYQIPDDFVADVRSIFKNCERFNEMMKVV QDYADTQENLNADSEVAHARKAAA LYFEDKLTETYSDRTPALP*FEQEQD DGEVTDSS
1538	7718	A	1555	33	460	DDIVRMSLRGKAEVFLGNNTMMRKAIRGHLENNP*PLEKLLSHIRGNVGFALT KEDLTEIRDMMLANKGPAAARAGAIA PCEGTEPTQNTGLGPEKTSFFQALGIT TKISRGTEIILSDALLIKTGDKV*ATEA PLLNMLNIS
1539	7719	A	1556	404	2	PPKRGEQRTSSPGAGDSSSSSGG*KKRGVQGNQRGSEPPPLLPQVGPPEGGGIRGDPGGAPEKNF
1540	7720	A	1557	132	424	NSPVAFYSSWNRTPALTLAPKVLDPDIPALPSHP*LFPRSPLLSPWLTLQAHP*PFSPQTQKFPQPDMSMLALHKMPGVF SHIRSQLSCHHFKGQFLR
1541	7721	A	1558	21	296	REAHRAQKGVSRGPVPTPPVPSPWLCCRYSPHQDADPLKPREPAIRIIFAIYKNQDHGAWLRGGDVWLDSCR*VRAACGFGTKGAWRVFP
1542	7722	A	1560	367	554	NKGHPRPRTAGAPRQEDMLRKPFHGRARSHACNPALGGRGGWITRSGV*DQPDQHGTEPS
1543	7723	A	1561	417	27	SSSSSPVQTEVGEDMFCLDNTFTSTSEKVIFSELILDNMGEQAQDQEDWC*YISGTDILDMLKLEDILESINSIKSRVSKSGHIQTLRLAFAEARDRNIQESNFDVRNF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,919,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
1544	7724	A	1562	2	434	SRAAAIHGLSLFSEHTPSPGSQNSDCA VVSSSSARHTSARGRGLPRPPSRPASP AAYSPHAPAPGPLAPFRSPRFHNLRL RASGAARNGT*SYKENTAGSSGGCN GDPKAP*PTTITAPQLPPTSLPCPYST QNRSGSSSDE
1545	7725	A	1563	256	488	INPMMQHASPAPALTMATQNVPP PYQDSPQMNGTAQPPSKAQACHISGP SAAASTPVPS*GPSQRPRDHPNSPPCE SIP*CNMPQPPL*R*WPRRMSRPHPT RTAHR*TAPPSHPRPRLATSLAPOLL PAHLCPVPSTPRPSWRLTSELY
1546	7726	A	1564	3	446	RFAFLDREEGCHQLCGFGFLARKCKN RPVPRGGGRIGQSRQRSEMITSPPLGLC GIHRCLPHSTALLRPPDADGARHPHG PPGKGHDSASLSGSSVP*CSPPQKKGS PSGEARAPPSQTPEAPSKKNCNAAST RPPPTTISPR
1547	7727	A	1565	1	435	PPGLKGPFPYPPGPPTIAPQEGGPRGG PCPPQVF*PEGPPHQGGPQWQGN*DS SSSSP
1548	7728	A	1566	39	423	VCGKLVPAAPSSCFEV*VRGKHPAPAS ACREV*VCGKHPAPASARPEVSMRG KLVPAPASAREV*VRGKHPAPASAC REV*VPGKHPAPASACREV*VPGKH MPASSARPEVSMRGKHPAPASAHHE V
1549	7729	A	1567	1	405	FRPHPRPSPATGH*VQPLGQR*GTRL PACQGRAYDTPLA VVPGRSAVPDPE RPLGFPVRPSEATPRKGKHHL*TLGA ALPRTREPRVRWQTPPASPARVSPV ESSSPLRGSHRSPDVAQPCRQGWGHP SLSWT
1550	7730	A	1568	3	386	YTGCVWVVGFCDPVLEKGLSLRPGI SCLVGDGDGAGGGKGGGHQSPSSSG LGASSGSSSSKYLSSSRATMSRLSKS GLSSTVL*SKSPSLPSTKRWCMLVN SSRRISLSSESQTQASESLDLS
1551	7731	A	1569	3	403	KNSNKEKEKEKTRPRCSRSRKSRRT RCRSPSHTRHRRHRHSRSYSPPRRRP SPRRRPSPPRRTPPRMPPPPRHRRSR SPAR*RRRSSASLSGSSSSSSSRSP PKPKQKR TSSPPQCI AALRLNITS
1552	7732	A	1570	1	92	SEA WQGCVCCTACACVCPYCVGM YLCVCL*VCM*ACMHVVCVQVLYP WAHVNICVGGCVCMCVYECMPMDV CAHVSGVILRLRGAQEAILLPVCLTL TNKP*CVCACTACVCPYVCVGMV CVCL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1553	7733	A	1571	199	375	RDHLEYILCMIAVTPNTKACIKAPIS MVQMEKIFSA*IPAL*FTMSSFTSVGF GTVSANTFAEKIFSICTMLIGALMHAL VFGNVTAIIQRMYSRWSLYHTRTKDL KDFIRVHHLPPQLKQRMLEYFQTTW SVNNGIDSNEVMFISHVVFRRQKAHL R
1554	7734	A	1572	44	409	PPASPLALPTSSSIFLPTPTGVFRRL DKKTTTEH*SYHKL YPFTSPPLSLFLV PPNMGVSPFWLPPPPSSVA*ALSNPLR SSFFPHLSAQMALSETTHKPLMPNLT LVCVCPSHIDHPMY
1555	7735	A	1573	123	448	GEKKGRQIKHEEASTSWGKQDRSC SWGQGSIMRHFFPSSSRKGSFFKFT GVHGPDLGSPKSRPPR*NKFFCLTLQS SGNNRFAPPARANLCCF*KRGFHFVG KSWP
1556	7736	A	1574	85	446	MSTLLKEVDKFNAISIKVPCHFLQKN TNICINHIRHQIAKVIWS*IGKIIIV*MS TLLKEVDKFNAISIKVPCHFLQKN CINHIRHQIAKVIWSKKNKS
1557	7737	A	1575	11	451	LLNNFCTISGKRSTRNFRWSWAFSR SMS*TLGKCRKKKKKQEQATEAQEN KRYENEYERARREALERMKAEEERR QLEDKLQAEALLQQMELKLKEVEA TKLKKEQENLLFIFLQLFDSPLSSTFI THAFCCVPHFRCFVMVK
1558	7738	A	1576	3	422	LSLGSEFSSSELVESACEEKTNFIQSOP PEEEVDGFEADDDAFKDSPPNPSEHG HSDQRTSGIRTSDDSSSEDFPYNMTDV VTPSPASDSTVLLAPSVQDSGLHNSS SGESTYCMPPQNAAGDLP*TDGDYDYD QDCMRPV
1559	7739	A	1577	1	404	WAPLAVCRDNRNRRSGGSTCCSRGGD PETRSLGAGPRARQSTRSLARSHPPQ SPPRACPNPOAGRPRSGKQPLSPRATP GWQPSADNVQSTTS*TCLPVGVAVE ALKKYRCPSSTAPPQRLKCDWSGR GTGHL
1560	7740	A	1578	2	401	STNKEIPPACDN*PSLASFLQLGLP*P ATGPA*SSHSP*HSLWFPWVRVAVGA APSSLPPLPTMPPLPMCLVSQPPCSL VAPALAMISHVPVFPHP*MLLPCLLSA LPGLRNEVFRPCSSPVLSDFTVY
1561	7741	A	1579	1	404	VRVSSKQYQNILMSGSLYRLTVQNS WKAFTVLSRAYLMAFQPAKIDEDPL LSYNVHVCLSVQMDILDGCD*CFVI FPQNVLRRAETRQRAQEWMEALTI AANVARSEQNQVTLRNKRKQDM GGHELKNV

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1562	7742	A	1580	77	146	LREVP EHTS VSTPGP*S*LREVP EHTS VSTPGP*S*VQQAPEHTSVSTPSP*S*V VQQAPEHTSVSTPSP*S*VQQAPEHTSV STPSP*S*VQQAPEHTSVSTPSP*S*VQ QPVEHTSGSTSPS*SAAGA
1563	7743	A	1581	2	405	IHRRCSSPPITPRTGAPRV*EQHSNNPT VFMSPGRAPCLEATTAPSALP*QPASP VFMSPPGSSGT*PEAPHQSTLLSLP SPSKIPTRAQLSPRSPGFSLTVPGVQQ EGSHLTPACGPWHHPPLPSVSRRPG
1564	7744	A	1582	44	402	LSLAFLVPCGLGEVLGGRRVPSSWS GREEMCPKEGWQRPLRPFPPTPGS SSDSVLGTLSCPSEASEASRALPFI*PH PSPHVRKPVSPGASCHRGSPVESQG STRPHGVSSLQPG
1565	7745	A	1583	218	400	WDGVRYALKRLLEGPA*AHCVLKPP QVHSLGLKSGIYADMGNFKMKMGYPG TCTIAAALGF
1566	7746	A	1584	3	403	TLASSLRGPLIPNPQTQRRTLHPSNF PSP*LVQIRNGSTSFSPWPRLGFGPGQ PTHPLPLLPPPRPWVTAPLRPALTA ASKCAQLTVLPYQQAAPSVS SHRLS AS*IPP*VPCPLPQRLP*SENPTPC
1567	7747	A	1585	2	409	PTLSFRHKGLMCPDHK*EVTHYCKTC QRLVQCLCRVRRTHSGHKIPTVLSAY QALKDLTKSLTYILGTQDTVQTQC ELEEA VRHTEVSGQAKKEVSQLVR GLGAVLEEKRASLLQAIIECQQLRLA RLSARCI
1568	7748	A	1586	3	412	SEYDQVRVYSLSAQVLRGEYLISAGTK TFRLFIRDASPYYLLWS*QTPDAHEAD LGIKSEEARKFFISCLDDMAQVMNTS DLKGSDMLVEAVARRFEIDLKKML SIDSVKRFSPVGSLNHPFVTMSLFDFE PHSMY
1569	7749	A	1587	87	425	LSPOQSGRRGKTPWTDCSCSPHPGKT LDPRQTEKFQKLQEPLNELDKRKREV LDASKALLGRLTTLIELLLPKLEEFKA PQQAACIRAHINRGLEQLEPL YRSAG RF
1570	7750	A	1588	34	386	RDEGQQGRERGSSSDGELGRGGGIW SQDRQSSVVLGGQGEAAADKESRGR TTAGGDLGSGAKEWGQGSQETKKG FNRESRDKGRKRQK*MEIGDNQKTE ERGIRGETSCKNNGTEHV
1571	7751	A	1589	3	419	PDPLLATLEKEEIEQLLSNIFHHKEKNE SAIVSAIQILLTLETRPTFEGHIEICP PGMHSHACS NVKS VLEAIRGLRGSFH ELLLEPPKKSVMKTTWGVLDPPVGN TRLNVRIKI*SLLTNTNTSSVCGRSVPIA GOP

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1572	7752	A	1590	1	407	AFYHHQCSLMKPAWSDAAHGDVEVP YVFGVRMVGPTDLPCNFMSKNDVML STVVMTYWTNFAKTGDPNKPVPQDT KFIHTKAIRFEEVAWSYNNPRDQLYL HIGLKPRVPHHSRATK VAF* KHLVPH A VLRPLWRR
1573	7753	A	1591	3	388	SQS*PFYFCMNGDRMNSVLESDRHH THIMDVMDQLFSGASSIDELFQDRFF AREPQDTHYVVPFSLRHGRLLRFFVPK SRIVRSLMPFSPYEPVNFRAFMPFHE MIREGQQAMDHFHSFPAFQPPV
1574	7754	A	1592	295	427	VGEFEMVALADEGLAHARGNAILNF LMIWHPLPIARLYWLG*YSKPVPS GDGERVPYHKEVQDIAPCMCKALI GKGHHEFFSNQQDAQEFLLRLINMV ERNCRSSNENLNEVFRFLVEEKI*CLA A*KVKYIQRVVYIMHLPVPMDAALN KEELLEYEEKRQAEEEKKALPELVR AMYWG
1575	7755	A	1593	3	387	HFYLEGTVLKPSMVTPGHACTQKFSH EEIAMASVTAMRRTPVPAVTGITFLS GAQSEEEASINLNAINKCPLLKPWAL TFSYGRALQASALKA WGGKKTLLTA AQEEYVKRALANSLA*QGGKYTPSHV
1576	7756	A	1594	3	402	WRVPVRKARKAKNPQPSNNLPKSS *SQISSPATSHGDPVVGKGGQDRPPL GPTVPYTEALQVFHHPVAQTPLEKHP YLPVPVSLFSFQHLVQHEPGQSPEFFS TQAMSSLLSSPYSMPLPPLSLFQAPVY
1577	7757	A	1595	2	252	GPPPPGFKVFQPHRRSGMEGCPPPS GPF*SFKNRGPHGYGGF*TPAPRGS PPLGPGVPPFPQSFVPVGGNPFAPW NLW
1578	7758	A	1596	3	110	FSFKTEEKDGLLLHAEQAQGNVYTL LEGAHLLHMSLGELGDHVRGCANP *SSWRGHTCCCT
1579	7759	A	1597	2	218	PQTSARIL*SGRNTPCAACVVCART VCVHVVCACVCIVCACVCAHACAC VCISIMLRGFSYIKIKTFGY
1580	7760	A	1598	23	425	TERPQYSGTLEFFIVILPGAPIWVKLR SLRRSSPTLALAEQGRVGA GLKAHP AALPPAPRPCPLRLGPPPLPRKRLAG SRWSAARPRAPPLR*IAPCSHSLAPA ALPAPPSTWPRPY*SAPWPA GD TAPF
1581	7761	A	1599	2	103	TGEKVVPGEVNPNGVGDPLSLLFG DVTSLKSFDSLTCGCDIAEQDDMSM TDSMASGQRANRDGTRSSCLVTY QGGGEEMALPDDDDDEEEEEEEVELE EEEEVEKEEEDDDLEVI*EGSTRRG KPTQWPCGGPTEPLVWGDIDPEKL

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1582	7762	A	1600	32	395	SGGHQGPSAAEPTA WCRD TYWENPT PQASVPSTAKGRHWAGWLQEGFFEE GTFGLRPTGGLGAGQVEDERA VFQA EQTARGRSTWSG*GTAPAERWRQGS RGQQQLPGA WGLYPNPSSGSV
1583	7763	A	1601	17	431	VSFEPIERPQYMG P*D*PPCILRIISIQG GGFRIHV LQVARPEPGSPPGELRGRD LSQWPPQQA* RQI*PQFRYSLKRVPY AGLLHRPPREEHSPRPPRLAPQDAT DCPFPFSGGHSPPWPA PSETASWAR GTTP
1584	7764	A	1602	4	412	SCQDIIEFGPCPENKSKGLLGIDGFT NYTRSPAGDIFNPEHHVHDMQTPL SHYFTISSHNITYL VGDQLMSQSRVDM YAWWLQAGCRCVEVDCWDGPDGEPV VHHGYTLT SKILFKDVIENK*AFIKN EYPV
1585	7765	A	1603	2	385	SWATLEVPVPAGQPERVSRGKSGSPK RSQHLGPSDIYLDLPSLSENAALYF POSDSGLGARRWSEPSQKSLRDPNP EHEPEPTLDTVDITL SLCGLADSRD ISLDQFNQHSVS*QDITKNPECI
1586	7766	A	1604	3	433	MLGSSSSAAAIHCOGGLSSIFARPWG DAGQSCPCGPRNPGVGESGMVPELP NHPAQDVRSSPERPEPGCGGAGTV GPACPADRRQPADARVGGARALRVS PS*DSSRAGTTPHGRMGSHMVPRTPD* GLQQTRHSKRSGGL
1587	7767	A	1605	3	427	QVCGQSTDQGGGLEKGGQTRLRVRFT SLTSLCSLQESILAQQVRVKGVSVA LKEQQA VTTSSIMQTMRSAAGTPVPS AHLDCQAQAHILQLLQQGHINQAC QQVR*ALGPLRVTCLLTNTNHTMY STHCICPL
1588	7768	A	1606	1	166	WEEEPS*VRRCTWFKGAADSRFIPY TEEFSEKLEVRVLYFSMSFFKCRSYI HW
1589	7769	A	1607	2	524	GSSDSPASASRVAGITGGGHHTRLIFV FLVETGFHHIAQAGKL LLA*SDPPASA S*SAGITGLTYHTWLIFCFISRDGVSP SWPGWSQTPDLK*SACLGPPKCWDY RSEPLCPASNL I*VSFVFSSPYMC*QL FQHKLHYNL YPFKARVYITPLRVENG NITLCLCHWAPFQA
1590	7770	A	1608	2	450	LALLLLNPDGSGCLWGRPGHRRALAA PLASAPCQEHPIPLLRQSKVSPMLM SQARPISSEHQKLALLAEPREVTPPPH PGVGSSSQCRDTHNTAASAS*GSGK GSRAPGAPGAGGPPDARALMLPKGR PLAGSSLTGILGEPSPHTV
1591	7771	A	1609	262	457	ACSCSLQKFLWFNIGSVDFERNLES AQGELGIEPHNQAVVVYTESD G*AR MAKRLWRILAGV

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1592	7772	A	1610	418	12	ARITLGRITLQSSRN TALAGAPSPFPGS GSGPVL PWL*GALCPQNVRLLRQPQG AGGTPHRSPGRGPHLP TILRTCLAWP GDVEGPHANEVAPPTQGTNAGAPSS GGATRGPSMCVWGGGASSRPGGQPL PPET
1593	7773	A	1611	1	397	LTEAHAAVAQREPEAE GSCQFARGA PADREGEGAHCSGQQRSPHLLGS*AP EAVGGHPGHPEHCEGAADMPAGPGA RSSREGGGLPHSPAAA GVHAAALGT GA*GHTGLTGQEKPAFSQLPRLASHG SAEWR
1594	7774	A	1612	1	381	PSGRKSASTTTRSCPRSSGSSFP SLW TSNPTMGLGRSCP*KRCSSV*SSPPR PRNTDSN*PASLRSTGASSCLAGL*AS THPWSCP TTRSSLPPRPYTPPWLQCT SSILT*A*DQKTPSPACI
1595	7775	A	1613	3	349	PHHAPGREPQLGEPAQLHGG*GGED QT*AGGTARGEPRGPQCPGHQCEPAA VHRADLGSRAQEAGTLHK*VQEARR GEETGERAHGAQGGRTQGCTPVTPA QPSTNQPCPGSPSS
1596	7776	A	1614	82	410	AVGACSLPHPTLPILPSTALTTPALGP AIGCPLRLLLQLHPPRGHLLVPLSP YYPALLSQHPQGPCCGASAPPSALL QRAPPPGT*APPDAAGTFSPVITFNF PC
1597	7777	A	1615	3	367	YTSLIPTQRFSATGHFPQLLVCLAPSQ LPPPPYVPACPPVCTGQSSWA*PLCT HSWGPSPPLSLPAPHSPRTPQIQPV LRIKLPPAHRVPTDGIPGWQLRW TET LESSLRSSFWDLGR
1598	7778	A	1616	1	361	IGPSLFFICCTHEIFQAYQISDDDVIE TCVSTSQLVRPQAGCVAEPLLLALV EEELRARTPGLGVDVSP TLVATVGFQ SLVGPEFGEPRIAAEPVYHAAIDL V QDLAHTYTRPELWTGLDRP*LRARV CVCQVLHEVNSGVS VVHRLCDSWFS KFRANKGLKTNCCDQC GAYITYTKSG SPGPPELLFHGGQKRCNTTCLRAYK NLAGGYTGLCYIIITYLVCLKYFVCT TYKK
1599	7779	A	1617	41	284	RYSNRCIEMQYPFSP L LFRFSQLKGLN L SHNKRGLFPILLCEIS TMTELNSCN GFHDLPSQIGNLLK*VTFIRLFLSLAE
1600	7780	A	1618	1	373	LISEERENQSLAFHGRGWWPQGVLC DGPSLRTAQGFWM TLTPFPKPVPK AGTPSGGTGPGVWPTSVSQAPAEGR HCVPGASWPPPKTEQSGDTPP*RTPF FAHPVAPGDRHPYAESLLAS
1601	7781	A	1619	144	401	NLEKKFYFFPQGGGQGENLGSLEFWP PGLKEFFWLNLP RRGD*RGPLPRGN FWF*KQRGFPHFGPAGGKLLALGNLP PLTSL LKF

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1602	7782	A	1620	96	404	NLEINGKRRKGKFTNMWKLNNLTLLN NQ*VKEDIKRIKIRKYLETSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSASSSSSSSSSSS
1603	7783	A	1622	3	427	FSGIVKGARDFYAVGSLVCLSGGRGQ TYMEDALRGDGPLPVFH*APPRGRRR CTPSTGGFCGKETPSEDDRSQSREHM GESLSLKAGGGDLLLPSPKVEKKDP SRKKEWWENAGNKIYTMAADKTISK LMTEYKKRKQRV
1604	7784	A	1623	48	213	QCTFCTTGANLKVISTMSVGDHLAL DEIKKR*QLQGIWRGPRERGGYERKK SC
1605	7785	A	1624	3	413	VPFHGEGGQDAEAGACAPSGPGPRS CAAGGHS LWVAAHGCPRSPETPGSE TGWEQSHGDDQPHPSNGVILKALG APHAACPFLLGSFGCH*GLASQGGG NFTHRVVGKGRNHHSLGEVDGLLRH GGRRRLPSTED
1606	7786	A	1625	3	413	RGEKRGGRVVSASGGVDQRFRAGKKP YGDNECGEAFRCCKSILT*HERHTHTGA KPYKCNCECGKTFHCKSLTLHHRTHS GEKPYQCSECGKTFQSQSYLAHHRT HTGKPYACDHCEEAFFSHKSRLTVH QRTHTGDCL
1607	7787	A	1626	88	300	LAGFWPESPPLGPASA*CPWPA*CTW TATRGSVPRWPPASGTRSRCSACL HT*PSGRPPGGSRAPRRWG
1608	7788	A	1627	2	391	VIHYAGC*GOEKIVLWLYQFMQEQGI SLDEVDDQDGN SAVHVASQHG YL GCI QTLVEYGANVTMQRNAGKKPSQSAE ROGRITLCSRYLVVVETCMASLQSVV KLTKQLKEQTVERVALQNQLQQFLE AQCI
1609	7789	A	1628	25	541	EPLRRVRSRGLPSPHTKPHRRERPSA GEVCGVRFTRKVKVILMRKHAGER PYS*PRCSARFLHRCDLKNRMHLHTG DRPYECHLCHKAF KEVLLQRHLKG QNCLVVRTRRRRKDDAPPHYPPSTA AASPAGLDLSNGHI.DTFRSLARFWE QSDPTGPPVSTPGPPDD
1610	7790	A	1629	2	400	PSRAFL*ASRVMGETQEREWVLT.VS RRSCQCSPDNSTSDGIHAFPCALMM FSQSLHGHNIGKKMSCQQF GIL AQM NDGGQVCAKDLLSILYNSIKNEKLEWA IDEDEL.RKSLSELVDDKLGTAKKVT RCI
1611	7791	A	1630	2	367	VQPPSKPA*SVASQPASIPNSIPALFP CQKTRDLISLPCSQALGQPPKNRPAT RPPSHIHLAGLFSKRFRKHLRQPLTP LPQALGQPPRQSPADPAFQVSKRIS QTISFQITNLPCSQR

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1612	7792	A	1631	2	172	NSKSSSTGVAARPGRFYSIYVL*GLNPR HQGHVYMGFTVSPACQVQQHNGDH TKGRA
1613	7793	A	1632	2	393	TPAPGSPTFPRLPPSPGRRRRSVG TMQG*AGKICLHCKCQPEHMMVTVM PLEMEKTISKLMFDSQRNSTDSDSC CALEEYAVWPPGLRPEQVHQYYSCL PEEKVPYVNSPGEKLRIRQLLHQVAS HN
1614	7794	A	1633	3	438	ISPFML*SARRAQAALSQLRVFL*GEL EGICGAGAW*SERVITSRQGPRIHV D GVSGGNAPFRESFDLSRACAGMEV LEEGVGGSYTLISYCSPSHLGRLYGF LILTLAWLNPFDGRRRFAQQENPHFL SGSFVKVSTNCCCT
1615	7795	A	1634	554	1007	HKDLWKLLDVLNKIKIWERIKRHLEG HSTNLFLDMAKLKEQKYKASQAHLT LMPGTGVLKGAADKLAASNPLEWIK TLGSSVISMMIVLLIGIVCLCIVRCGI LTPVRK*LTVSKAAFAFISFAYRTGG HVGAQAPPKI
1616	7796	A	1635	56	430	ARAGSSTVATPLIQGTSPSPHPHTRTG PCWRKISPPFAGAESQGFDSHRVWNV P K*RSVPVWSPHQPQGAHP*KGVPAAPPM PAPPDPVTRPNPQIPGLPTGTPKADPP LLKKNPNTNALPASVLRPL
1617	7797	A	1636	283	448	SSQAPSPCLP*GSAPSPWPA GYSPLA PA*SSQAPSPCLP*GLSGLVS*WVPT SGSCSPAPGAGCWNSSARESIQAP
1618	7798	A	1637	119	420	KGSLAWSRRGGRRGGTPAQGTGLGP G*GDPSSPPQKGGIKGWPHGANKIL DFQEKRVWPRRASNPGRKGTGPPNPT KGGGPRVGPPAPGLKLIFKJKA W
1619	7799	A	1638	162	445	HLYAHRLENLK*MNTFLETYKLPRLS QGEIESLDRPIKSSKIKSVIKSLPTIKDP GQE*FTAKFHQMHEK*LVFF*LKLLQ KIEEEELLSN*FY
1620	7800	A	1639	2	172	IHTWLSHRKQGKAGLTLPQARYSPSG RAGSRLSTAYRGRSPSSCRIRYTSLLS P*LPLPAILFGGDRREVYRILQEEGI DLPRYAVLNRDPAPEGEYLA*GQVL TLRPGRFIVEHSISRQINTLFLQDPVHL PPVTPK
1621	7801	A	1640	1	391	KTLPTVPLTTGALTGALCTQAPIQVL GPPSHGHLESVTPASTHQGRRLPAR* GKRPQPSTQGLPGGAGCSPRLGT*P TGTQPGRGQAGT*PGQRTTAGPRES RGRSTRSRG*RGSATCRHLGALGS
1622	7802	A	1641	1	374	PSQHCLSLGSPMSILGLAVGGWEQW NSRCHFVQGVTSCHLSVPLP*QPPEI IKALSWNROAQHILSSAHPSGKAVV WDLRKNEPIKVSDHSNRMHCSGKA WHPDIATLYCGRYRGYSNTTRA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1623	7803	A	1642	1	337	MCKFCGKKYTRKDDQLEYHIRGHTDD KPFRCCEICGKCFPFQGTNLNHLKRNH PGVAEVRSRISPERTDVVVEQKLEN DASASEMGLDSRMEIHTVSDAPD*DG KEVHPNKAH
1624	7804	A	1643	1	535	SKRPCENGIGCFLLDGHPCTCDCSTAG YGGKLCSEEDVSQDPGLSLRLMMSDQA REENVA TFRGSEYLCYDLSQSPQSSS DGVALSFKTWQRNGLIMHTGKSAGY VNLAMKDGPSLVVNLGSGAFEAI EPVNE*FIVNA WHDKVVRNLRQMAI SVDGFLTSTGYTQEDLWSDSSRMS
1625	7805	A	1644	26	359	KLSPPTTSTSNQASQGGRAIRRARPO LPMPPGGPPLCGPPVVVALRPRQRAT GLPVAPGFLCAA VCLLSRPLSSAKR PCPTWPLGPVTFPSPCGK*GSAGPTFP VLMPA
1626	7806	A	1645	357	0	PPPKLGLFTPVPPP*KKPPSSSRGGVF LAPSNPPLQNF*ITFGPPSPNRSSSP APSSPQRLSSSSSSPP
1627	7807	A	1646	16	436	LPGTTHAAADIAEVQDNFF*LKRSL NPAERKMEGQNSHSPQCFKTCSEQN GYVLTLSNAQPVLQYDGDAGAFYPD EIQRPPVRVPSWGLEDNVCSQPARN FIRPDGLEDSIEDENVPVTPDPSL HLRGHGTGFC
1628	7808	A	1647	1	351	QPKILRDGDHDLKRCQ*VTEKVLAA VYKALSAPRIYLEGSLKPNMVPVPGH ACTQKFSHEEIAMATVTA LRRTVPVA VTGISFLSGAPRRRPLQEWEGAGPG VLGAATDPLRLIGV
1629	7809	A	1648	1	255	GHTYAHTSHIPAHHAHTSQQLLTYHS HAHASSFTPH*HLLTHISPLTAPHTC SRMHHS AHAYPLACLRACSHSASQS LLGTGQ
1630	7810	A	1649	2	463	RETAPEVSSRATRPECADKMHMVL ALVQNSEQLLRTL*GTVSQAHDIVV QMADLVTTTKSLHHEVKRLNEDNQ LRAEQQLASSAPQGSQEQGEESLPS VPELQQLLCTTRQEARLQAQEHG AERLRIEIVTLREALEEETVARASLE
1631	7811	A	1650	2	410	LPEGAKNIEDISFYEISRAPDELHYTY LDTFGRNVIVA YKKNLVEQHIDIVV HYTENKVLMLQEPLLVAAFYLIFFT VIHYVRLDFSITKDPAAEARMKVACIT EQVLTLVNKRIGLYRHPD*TRYKYN* FRDI
1632	7812	A	1651	1	411	VTKEVVTS EDGSDCEAMDGLTSLGI GTLDGFRHRHPDEAAFFDTASTGKTF PGFFSPMLGEFVSETNSRSGKSGIFTN TESSSHHPAIAEFPRGRSCSYRNRNS TI*PEYHTGYSRFVR*RYKPAYDGV DSPLP

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1633	7813	A	1652	2	402	AYDG*DYLTLDNEDLRSWTDAVTAQ IYQQLHDFAFEAEHQRAYLKDTCVE WLHKNL*KGKETMLLLEPPKTHVTH HPISDHDAITLRCSLGFYPAETITLW QLDGEHGHDTDELVETKPAAGDGTFFQ KRAPVVV
1634	7814	A	1653	10	377	LDKSQIHIDIGLGGGSTRIPKIQKLLQD. FFNGKELNKSINPDEAGAYGA AVQA AILSGDKSENGQELLLDGTPLSLGIE TAGGVMTGPIKRNTHPTKQTQTFTT YSDNPA*LDKSQIHIDIGLGGGSTRIPKI QKLLQDFFNGKELNKSINPDEAGAYG AAVQAAILSGDKSENGQELLLDGTPL LSLGIETAGGVMTGPIKRNTHPTKQT QTFTTYSDNPAGVPIPGYGER
1635	7815	A	1654	18	478	APQHPKIRLYNAEQVLSWDPEALNS TRPVGYRVQFKYTDSTWFTADIMSIG VNSTQITATECDFTA VSPSAGPFMDF NVTLRLRAELGALHSAWVTMPCFQH YRNVTLVLPENIEVTPRERSLIIRFSSL FDIADTYTGFCYCYVHY*EKGG
1636	7816	A	1655	1	446	FVVHSGGILALERTKLETHIDHLYLF FAKRSAPFNWMEGAMEDLHDTFIV HTIEDIQGLTTAHDQNKATLPDADKE RLAILGIHNEASKIVQTYH*NMAGTN PYTTITPHEINGKWDHVRQLAPWMD QALTEEHARQOHNEKLPKQ
1637	7817	A	1656	1	211	EEVPAEEHDPSPPEAADSAGAPNDFQ NNAQVKVIRSPADLILFI*ELKGGTKK GKPNIGQEQSVDAAEV
1638	7818	A	1657	3	229	VPSECG*IPCECPWKLPLSADQQLPEA PGHLGSP*KNVSVTSGLPGESEPPMP GQAKPQRPSPPPQVRALPAA
1639	7819	A	1658	52	448	HPIVGLRRMGDFKACQFQEGGRSV GGVSRSP*WPSLRASPLSTSSDISPSG HPAPPTPPQPTQLSEANSQSEGLS LERRFPVT*PWGTSLPFLSPPTSAVL IARTLAYTKDGGCGCGAELVLTPIK
1640	7820	A	1659	98	427	ALSQLGAGPFFHCPSTFRACMGESG TL*SQLEATKRKHQEIARMRSQLTKEI DLGAAMEEALILDNKYTGHRVTGLA QQWDQLDQLGMRMHNLQEQIQAT NTTPGVTGA
1641	7821	A	1660	3	216	EGINNMQLQDQTKKEARKEKEIYEQE ANASTFHRRTPLDKDLINTGICESSG KQCLPLVQLIQQLR*ITCCNRYIKKK KHGRKKKFMNRKQMPQHFIIEGLH WIKTLIRGSVSLANSVCLWFSYNS FLGKSY

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1642	7822	A	1661	9	417	QNNWGKNCIAKVAAYVNSPPLSPDPT TPDYLTSLACGLDQVTGSGHCPYST AQKAEDTDNFTLPEIGVNGIEERMTV VWDKAVATROMDENQFVAVTSTNA AKIFNLVPRQGR LAVGSDADVDCDP D*FETITAK
1643	7823	A	1662	1	429	RPDTQAWTTRVPMMLTSGRPWPS WNMRHSGTRPWPTSTRPAC*RRWPIS TEPPRMGSPMTWEAVHRAAVPKLSP RSPMSMTFHQPPMCTRSNPSGWELV SPKAPARSRRPRN*WRLGSGSKPPS PSGEASMSPRAGPVAIPG
1644	7824	A	1663	39	454	ISPTKYMVSVSHRR*CLTSYVCLSIQSS RCLRLTIRIFMPDSSLKWLCLTSYVCL SIQSSRCLKLTIRIFMPDSSLKWLCLTS YVCLSISSRCLKLTIRIFMADSSLK SCLTSYVCLLIQSSRCLKLTIRIFMPL VPRLA
1645	7825	A	1664	2	403	SRKCLREEIHKDLLVTGAYEISDQSG GAGGLRSHLKITDSAGHILYSQYDAS KGKLPFTTQNYHVFCFESKGTGRI PDQLVILNMKGHEVAKN*EIAKVEK LKPLEVELRRLDLSIESVND*FAYMK KREE
1646	7826	A	1665	477	19	SSLNSNWTNLNAKCKTIKLLDNIGE NLDDFESINGFLNMTPKPQSMKE*ID KLGFIIKKNFCSGKTLVTSLA
1647	7827	A	1666	106	403	EEALEGRDGGAGCKGTALGTAGAG NHCGTLRLYRGSHPAIQAPSGLAAS SQSGGAGSQVLAATIPGTCPPQPYM VTLTHFTGHRTELGEGRVARL*APSG IELSHNSTTDSSEATGGA*AKKTLA *EEALEGRDGGAGCKGTALGTAGAG GNHCGTLRLYRGSHPAIQAPSGLAAS SQSGGAGSQVLAATIPGTCPPQPY MVTLTHFTGHRTELGEGRVARL
1648	7828	A	1667	15	482	HAYAKLGTGRPRANLGRMIHTOGFL QVGDEILEVNGTHVTNHSVDHLHKA MKETKGMISLKVIPNQSRPALQMF MRAQVDYDPKKDNLIPCKEAGLKIA TGDIIQINKDDSIWWQGRVEGSSKES AGLIPSPQLQEWVRSMD*SAPEAPS W
1649	7829	A	1668	242	398	QMYSESFPQTIPKLTFPGGLIG*SPA FMNAPKIKGTHITAMKSGILAPQSI
1650	7830	A	1669	5	444	RRHAKLGTGRGKHPRAVFDLEPTVI DEVRTGTYRQLFHPQLITGKEDAA NYARGHYTIGKEIIDLVLDRIKLA DQCTGLQGFLVFHSGFGGSGFTSLLM ERLSVDYGNKSKLEFSIYPPGQAF TAVDEA*ISILNHHITL

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1651	7831	A	1670	104	442	DLLLGPLPGVSLSGVSGSRPSDRVRES MSPLRAWQASPSAAPRSSLPGEACA RGASGCPAGCQRL*PSPSSWPPALG AGASPRARSLLLGQRSFQLLPSPPTC ASVQAGC
1652	7832	A	1671	194	427	ICQPLSLSTTANHPLVLCFCTHKNLHI FIAALFIIAKSWKQP*CTSLDEWIWLG LAPLYLTREEWDCVCVTVYWDLL
1653	7833	A	1672	88	311	GHCISPASEWVHWSWGFRPSLGGAG*G HGSSPSPSEWVHWSWGFRPSLGGAGYG HGSSPSPSEWVHWSWGFRPFLGAG*GH GSSRPSEWVHSRGFRPSLG*STPGGF SAA LQMTCTHT*TPRI*GRH*SSPSE WVHWSWGFRPSLGGAGYGHGSSPSE WVHWSWGFRPFLGAG
1654	7834	A	1673	2	433	IQDSDHRRDWNENKGGGPGGQGFY PYKAVFSTQGPPLASLQDSHFLTDAD MVMSFVNLEEHDKELFHPRYHREIR VDLSKIPEGEAVTAAEFRIYKDYIRER LDYETFRIAAY*VHHEHLCWGLDFLL VDKPEPSVRLVGGQ
1655	7835	A	1674	16	476	TTTRENSLDSLHRMWSQPDLKYNIPP TQLSLKPNRQSLRSGNWS*RKSHRLP RLPKRHSHDDMLLLAHLSPSPSSL NEDSLSTTSELLSSRRARRIPKLVRQI NSIYDATRGKKRLKKVSMSSIETASL RDENSESESDSYDRFKAHTQAP
1656	7836	A	1675	17	481	ARHEEMDIESQPEACAYDHL*VFDGRD AKAPVLGRFCGSKKPEPVLATGSRMF LRFYSDNSVQRKGQASHATECGGQ VRADVKTKDL YSHAQFGDN NYPGG VDCEWVIVAEEGYGVLEVFQTFVEVE ETDCGYDYMELFDGYDSTAPRLGRY CGS
1657	7837	A	1676	2	299	VDPKLVLFKFTWKGRPRIAGTILKE KKVRRLLLPNFKTHYKATVIKIGW*W *NNRHHNWNQIGSEPIAPHKYSQLIFD KEANAQWRKDSLGLWGSWSC
1658	7838	A	1677	215	420	LLKSSACFCGHFLSTHENTQRIVIFLL KNGLLS*VVQATGGPELARSRLSPLL NKDTIEFLN*TVKV
1659	7839	A	1678	2	441	YDTHSWPGDCQETVLIGWRREGI*FL RNELFLDVLSEVNLLMSPQGQVLSAH VSARVVMKSYLSGMPEQFGMNDKI VIEKQGGTADETSKSGKQSIADDCT FHQCVRLSKVDSESRISFIPDGELEL MKYRTTKDILPFRV
1660	7840	A	1679	64	430	SNFRVEPATGTGLVRAA RLGPRLW LSLEAPGSTSSQGGGQGRGP*SPAQS ERNSWENEAAGPPLSPGAG*AEDQG QRAPRGEEAAGSGESSPGAGAAGAA AGEGEDQRRHPACQAPRRG

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1661	7841	A	1680	2	461	TMHYGITGRTGLQKQGQIVSHARVP KRISLNALVASLAEPDFVETDFAKVS RPAQVHIGLQALHQICA*HGRPPWTR NEEDA AKLVALAQAVNARALPAEHQ NNLDEDLIRKLAYVAAGDLAPINAFI GGDLAQEDMKACSGKIMPIMQWLYF
1662	7842	A	1681	1	485	PAFSYDHHYCLSWHHGSGSTEKSSIH RNEIEKSNKRSRSGSGGITDSVEKSK KREHSPSIEKSRKRSISKERSHKRDHS DSKDQSDKDHRRRSQSIEQESQEQKH KNKDETV*KYFVKVDHIESYK*LNLL FSPTLRCLSSSHSSSPCLRHFFHFLFRV G
1663	7843	A	1682	16	401	RDLGEQLHRRRPQSITTSIPRVHEIKF ELIETDNLEGGPGPESGLSRERPSGGE RKSTPDRPRDKQGDNSKRSKDLGFK SPTSCKDDKRTGKNKSKVHTNKAHPD NKAEPFPSYLLGGRS*RDLGEQLHRRR PQSITTSIPRVHEIKFELIETDNLEGGP GPESGLSRERPSGGERKSTPDRPRDKQ GDNSKRSKDLGFKSPTSCKDDKRTG NKS KVHTNKAHPDNKAEPFPSYLLGG RSGALKNFVIP
1664	7844	A	1683	82	441	PPPLS*AGLHYDLGLRQKSI*PEEA VR TQRLQLSQSRG*LQPGESGGSTAGG GTEEGLGGAWSRPPSPAPPPTVLCPY LSCSLSVGSPCLCPFFLSFRLCHFLLPL SPSLSLYLALQSL
1665	7845	A	1684	113	404	ASF GHDFSKKSFNDELFTILGSALDKI TASLCDLKSRLDSRTGVAPDVFAEN MKLTEDTHLGNKIKCSLS*PICRSII KDATYVIRISRLYSLI
1666	7846	A	1685	11	406	AIRDEEKQEGMANLAQLEALYQSS WDSQFVSGGEDCFINQS*EVGKDEQ DEKENTYTSYLDKLFRRKEDTEMLT EPVEDGKLGGERGHEEGFLTYSVELVY NKQLESIGLPQVPSPHDPLKSVTCPF FP
1667	7847	A	1686	2	441	GIRIEICSLYSTTYITCPADHKKTGLK LPFLDMIMTNLKKYFTF*AOVLDDKK VRSRFRSSNYQSTTRAKPHICTMPMR LDDGWNQIQFNLLDLTRRAYGTNYIE TLTVQIHANCRMRRVYLDRLYS*DE LPAEFILYLPVQNK
1668	7848	A	1687	3	427	FAWRCAIAKAESLYKLLGGLAVRR ACYGVLRFMDSGAKGCEVVVSGKL RGQRAKSMKLV DGLMIHSGDPVNY VDTAVRVHLLRQDVLGKVKIMLP*D PTGKIGPKKPLPDHVSIAEPIDEILPTT PISQQKGVKPEP

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1669	7849	A	1688	3	424	QSNPEASADDRLVLSSPNSILL* LQYMAFHLQASEIEKARAVAEALRTIS FREEQEKLNEWALLSLENNYGSQEP LTKVFERAAQDNEPLKGLHLADIYA KSQKQFEAGELYNRMLKRVYQEKAG WIRYGAFLLR
1670	7850	A	1689	3	425	AAIRHEEPSKKNVWEQICTEYEDHP PFPGKYTVAEQPVITVAPL*EMLFHV SAEHYFPVSHFTMISRTPCAQDKSETI NPKTCSPEKYLETFIFVLLPGTASLL DQAKNE*CLERKAKFIGCDFLTEWL YNHHPQKA
1671	7851	A	1690	1	466	IRQAWHEGVSTPTESGVPSAEVEFGS SQPERISPEGLAKAMLTIAITATPSLT VDEKEELLTSTNFQVIEETITTKGFL KYMDNQSFATESQEGVGLGHSPSSY VNTKEMLTTNPKTEKFEADTDHRTTS FPGAESTAGSEPGSLTPDKEK
1672	7852	A	1691	14	591	MHLHYASLARGPDGQMPSPDKTIGGG DDSFNTFFSETGAGKHVPRAVFDLE PTVIDEVRTGTYRQLFHPEQLITGKE AANNYARGHYTGKEIIDLVLDRIKRL ADQCTGLQGFLVFHSGGGTSGSFTS LLMERLSVDYGGKSKLEFSIYAPQV STAVPEPNSILTTHTTLEHSDCAFM VDNEAIYDI
1673	7853	A	1692	3	1049	TRDELDQFLDKMDDPDYWRVTQDP MTGRDLRLTDEQVALVRLQSGQFG DVGFNYPYPAVDFFSGDVMHVPVNR PADKRSFIPSLVEKEKVSVMVHAIKM GWIQPRRPDRDTPSFYDLWAQEDPNA VLGRIKMHVPAKPLAPGHAESYNP PPEYLLSEERLAWEQQEPGERKLSF LPRKFPSLRAVPA YGRFIQERFERCLD LYLCPRQRKMRVNVDPEDLIPKLPR RDLQPFPTCQALVYRGHSDLVRLSV SPGGQWLVSIGDDGSLRLWEVATAR CVRTVPVGGVVKSAWNPNAVCLV AAAVEDSVLLLNPFLGDRLVAGSTD QLLSAFVPPPEPPLQPA
1674	7854	A	1693	3	451	NASLDEAFFSETGAGKHVPRAVFDL EPTVIEEVGTGT YRQLFHPEQLITGKE DAANNYARGHYTGKEIIDLVLDRIKRL KLADQCTGLQGFLVFHSGGGTSGSFTS TSLLMERLSVDYGGKSKLEFSIYAP QVFTAVPEPNSILTTHT
1675	7855	A	1694	182	450	TFFSIFMMGLYNRNFFQNDKLSIFFP TQLFLKYLYFLYLKCSENATMTLPGL HPPTLNQVRLFFYFDLVLGKICEKKM YRSAPAFQS
1676	7856	A	1695	2	182	KKHKHMLPSGFRKFLVHNVKELEVL LMCNKYCAEIAHNVFSKNRKAIVE RAAQLAIST

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1677	7857	A	1697	10	205	LHPTITGEFLVEIGYGYVAQAGLKL GSSDLPASASQSDGITGVNHCAQPYF LTFKMGISTALIG
1678	7858	A	1698	91	222	FSKQKRKGGRNFQSAAPRRNMLKGPH EKEAAVRKRKQEEQMEPEQ
1679	7859	A	1699	2	388	FGRPRGEAPRGTDFKPPGPGPPGNPF KKIQKLPSSSPGAPFFFPKSLKQKKG FTPEGGSGKNPKLAPPNSPGSSSSPP PSSSPKPKERTSSPKG
1680	7860	A	1700	1	202	FPPGKTKDFFPNFRGFFRPVGLVPPP CWVLVCPSPGRAPFPKPKNCQPPGV FFWGGVVFLNENQK
1681	7861	A	1701	3	392	FPEVLGQGRREVRVTEREAGSSKGRV CLCTKDPDPPCSAPGPSLPHPLSSPGLR EGRPSRLQTQPHGAGEGAGIGGATH CTASHTKKSITQNYVQYFFFLRQSFD LVSAQLGWHLNLSLQPPPPGKRF
1682	7862	A	1702	16	134	VEMGFHHVQGAGLKLNSDLPAS SQSAGITGSPNVFM
1683	7863	A	1703	1	233	TRSEFFGRREAGGPDQHALYEKYHLT SQHGPLGLALLLGGGSAYMALIIAFS QGVSEGSF WASRLGPNLQGAIFS
1684	7864	A	1704	2	314	EAGGEKDRERQKEKELEKEKEQK REMTSSSSSSSSSLERQKEKEKEQK MKEQEKECELEKEREKLEKEIEPREP NLEPMVEKQESSENSCNKGLIVFIFL
1685	7865	A	1705	1	239	GGRRRLQPEHGRGGGRPKGEVCW VHGGQAPAGRQVQRAADEAGPPARC QNTVTPGEEELAQGGGRDLAEVALT TOPPS
1686	7866	A	1706	219	476	KRCQAWHPPLPSRGSSELCCCLLL LPALASSFVDRDLQASRLGCVGPDHS WQLSPQLNFDLDRGVFPVVIQAVVD EGDGEVLF
1687	7867	A	1707	95	393	DRESAEQVQRCDETRVRGRRHSWRS RQSRQTKEFIFSELLSNLYSRGNLQTL VEALAEQADQGVHLLRADVQPVLA WEREDTRGGVGRAGRPMRSSYS
1688	7868	A	1708	194	428	LLGKGSSTFVAHPGQGGNLSRLNPP PGLKEFSLCLPKTWNNRGQRGPP PPNFILRKKGVFESGPGWSETDPL
1689	7869	A	1709	2	336	RNSRVDGRQEKEKDRERQKEKEKE EKEQEKEQREMTSSSSSSSLERQKE KEKEQKMKQEKEKEKEKEKEKE EKIEPREPNLEPMVEKQESSENSCNK GLIVFIFL
1690	7870	A	1710	3	204	ELERQKEKEKEQKMKQEKEKECELE KEREKEKEIEPREPNLEPMVEKQES NSCNKGLIVFIFL

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1691	7871	A	1711	277	406	IMNDGPGTVAHISNPSTLRGRGRLT RSGDRDHPGYHG
1692	7872	A	1712	156	462	IHHQSHQSVHHQSVHHQSHHSVDHQ SHHSVHHQSHQS VYHQSHQSVHRQS VHHQSHQSVHHQSHQSVHHQSHQSV HHQSRHSVHHQSRHSVHHQSVHHQS HH
1693	7873	A	1713	2	273	FFFEFMEFHSSLDGDRMLHLKQNKNT NEREGSGLLMTKVVWNPCCSVGE WRKKMWYMYTMKCHSALKNKVLL FATFMNLKQMLSKPST
1694	7874	A	1714	17	458	RWSTISCRFESAKSIEERKEQTRNARA EVLRAQAKANFEKEERKELKRLRGE DTWMLPDVNERIEQFSQEHVSKKKK KKDKHPSSSSSSSPKSKKQKYEKN ESSDSSSSSEDEWVEAVPSQTPDKEK AWKVKDEKSGKDDTQIK
1695	7875	A	1715	146	478	RMHMGCTEEDAHGRMHMSTCEW MSPYKQETPSCHNLRPPLPTARDPL FLSQPETPSSCHGPRPPLPVTAGDPLF QSRPETPSSCHGPRPPLPVTAQDTKSS NREFRPST
1696	7876	A	1716	33	259	ASILKEWNRKYMTRKPKFTCIWCSE QLLPFMQLGSLRELMFYDLKQTDND VLLTFEALKVKFLKILGHRGFFK
1697	7877	A	1717	31	302	LMSSMVGDPGPSSPGSPLPGVISPSS KGSHSPPLPLLFLRLRDERPAERDLE RRRHRGRWRMLGARESPGRSPGHGR SGSGDEIVDPG
1698	7878	A	1718	3	169	NRVGFHRVAQAAGLEPLGSNDSPASAS QSTGITGVSYQARPGQSLKCFPCQT VTL
1699	7879	A	1719	223	358	SELSPPMLIEHPLRCLVLCAQVHAGM WRRNGFSLVNGVSVF
1700	7880	A	1720	24	273	KPVRVRQVLLRLINFPFSRQETKEAQ LYAAQAHKLKGEVSVESGNAFSLYS PTLFSSLVPLIDSLPNLIFKIGLCSL
1701	7881	A	1721	1	158	HREKMLNSDIFWKQAEAVQGEPLNP PVHICGPPSPSPPGFCCSWLEPGTVI
1702	7882	A	1722	2	317	FVDSPREFATIDEVETDVVEIAKLDK LVKLCSGMVEAGKAYVSTSRFLVSG VRDLSQQCGDITVISECLQRFADSLQ EVVNYHMILFDQAQRSVRQQLQSFV KE
1703	7883	A	1723	248	365	LNRFLQALPSRLVKAQPEADGGKCD CAPFRHGPVHVE
1704	7884	A	1725	187	407	WGILHPYGCCKIHLGAKGIGAMFLA VNGHPWPVGAHAACNPSTLGGQDG RITRSGDRDHPGNGETLSLLKI
1705	7885	A	1726	188	452	LVSNVLIFSCTNIVGVCTHYPAEVSQR QAFQETRECIQARLHSQRENOQQERL LLSVLPRHVAMEMKADINAKQEDM

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						MFHKIYIQKHD
1706	7886	A	1727	1	600	MFDPRVRGRVGVRLPSGRLDNQEMT NQESAVHVKMMPEFQKSSVRIKNT RVVEIICGLIKGGAALKQUITDFDMLT RFSYKGRKRCPTCHNIIDNCKLVTDEC RKKLQLKEKYAIEVDPLVTEEKY PYMVEWYTKSHGLLVQALPKAKL KEIVAESDVMLKEGYENFFDKLQQHS IPVFIFSAGIGDVLEEVIRQ
1707	7887	A	1728	1	123	FFKETGSPYVAQAAGLELLASSDPPAS ASQTAGIAGMSHHHT
1708	7888	A	1729	1	164	RKCGGIYCKNTAIVMTVGYWWMER HINQWKTIEDPEIPHAIQWRKDSFVN KWY
1709	7889	A	1730	72	287	TPQIIPFNWPHHLPRSGAGLKKRGVA RTRGPPPAAPAGPKLWVPWARPLSRG PLGPPCLGKIFPAPPLKISL
1710	7890	A	1731	177	426	TNPHLPLGSRFFAQTPGRAGNKGAPP SPPLIFGLKKNKAVPGQGGLLEIPNP RETPLPGQGGGGNGGSPQSPGSPSL NRG
1711	7891	A	1732	1	105	TPAGVPDSTTRPQCLFRQKGSMTMSI QWKTRQLQS
1712	7892	A	1733	285	389	KGGRGKPNPWAWETPLPGPPNGGKK GEEPRAPP
1713	7893	A	1734	189	370	DFTEDVNCAFEFLKLTPLLDKADQR CDCDCTNFLQECGKHGLLSEASVN NLMAKRKAD
1714	7894	A	1735	113	359	ALPGGHTSGPRAAPLNSPPHPSQDLL KHTPVDHTDYPLLQDALRISQNFLSSI NEDIDPRRTAVITPKGEVSEPGTAPH PG
1715	7895	A	1736	125	346	AKENLEGRGVCLLHCLGFHTPATGT ASQCFSKACTLVRGNAEGFFKNIHR NNVSMRPVASHTRGPEQQGKGQ
1716	7896	A	1737	302	431	ALGFFKFMRLFILFSPGLAWTHRQQQ QHNNNNNNNNNNNNNNNNNN
1717	7897	A	1738	103	416	GKWWGFRGPRASFFLKKPPLPFLKNP SSSSFRSSSPNSSSSKKGGPGPNIG GSSSSAPKPPFANPGPPGPPVLKK KGANPPLNNRGGFLKSPKGGVKPK
1718	7898	A	1739	115	238	LVTMTLNSNYMFPQNSECEINIEITG EESVKKPQTLMEVS
1719	7899	A	1740	184	460	TYLSLKDPHDAVRVSWADNSVPKNQ KTSEVRLYTVRWRTSFSSSSSSSSSS SSSSSSSS
1720	7900	A	1741	228	415	AYHFLSGEDIGLLTHNGAGKSTSIKM MAGDTKPSARHVLKGGSGGEPLIFM GYCPKDNASA

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1721	7901	A	1742	1	311	SPVFEFGKCGLEIFDPPPEELERK V WEL ARLVWQSSSVVFHTGAGISTASGIPDF RSVIVQGKSRQGLPGCQRLPCEPHIS GNENTSICFPFGCVLGTPTFKMCP
1722	7902	A	1743	30	321	KICPARVWHPFSPPI.WGPRGADSPRS GVSGPPGPPCLTPSSSQPKNLPPSSSP PRFSHFLGGLNQKPLTLEGAPINKN SPSPFPPLKNQTPF
1723	7903	A	1744	331	412	CTVLPFSSRYLVTFSP.LMDTQDDPQAI
1724	7904	A	1745	180	409	PTRRVPQASPLGGLPLPVKTPTPOV LKALLPLRALKNRGEPA GTLLIKTHQ ALNRRDLTFGAGPFYYKLGAVDQN
1725	7905	A	1746	2	133	ETGFHRVDRAGLELLTHLGLPKCWD YRRDDFLNIHEEQITIDHN
1726	7906	A	1747	2	353	RDRFTAMVWVAITFPVGFFFCIIWS LVFHFETVATDCGVSSAPSGSGP GQEVAVRVELDSGEEVEDQREGKGQ GDGGRVVGKSESQIHHGRLRENITAL PELEDDDRNAREM
1727	7907	A	1748	79	201	GERQVVEVASGVWSKDDQYHHHHHH HHHHHHAPALASIGLVR
1728	7908	A	1749	1	312	KLRKSES KSSISSKRSSVRSDAAMSRI SSSDANSTISFGDVDCDFCPVEDHVD ATTETETYMGEWKNDKRNFGFVSERS NGMKYEGEWANNKRHYGCTVFDP GS
1729	7909	A	1750	231	480	PSYLVWSQVHQEDIYALNQYPTYGM VCPITRIHRSONQGVVGVAPLTVIPT DTLAKFKLPVPTILCYIGLEGPDA WV DPRDS
1730	7910	A	1751	119	392	RYTGFSLNKKQVPLNKEYSLETTGKA LSPAEAAGLRDQGSWARRASGAW RGGAPITPLQRQSRGTRRSASGPCYIQ SSDPGSAPEGAERK
1731	7911	A	1752	18	701	CSGIPFRDQSSTRAACFFPAWTRMR AFPSMDRAAVARVGA VASAVCALV AGVVLQAQYIFTLKRKTGRKTKIEMM PEFOKSSVRINKPTRVEEIIIGLIKOGA AKLQITDFDMLTSRFSYKGRKPTC HNIIDNCKLVITDECRKLLQLKEKYY AIEVDPLVTVEEKYPYMVEWYTKSH GLLVQQAALPKAKLKEIVAESDVMLK EGYENFFDKLQQHSIPVFIFA
1732	7912	A	1753	3	170	DAWDQVPLTIPLKPSHSYPAQCQYPI QQALRGLKPVITHLL.QHGFLPINSY N
1733	7913	A	1754	3	207	RAAAILSRDRLLPRPGPYLGDQALAL WNQVGILLPLQMGILLWWDEQVL SPPSISYTLHSLSELE
1734	7914	A	1755	277	418	THLKVDGICISRSSTGRSHLDNNKLTR VPGGLAEHKYIQVYVYLNHNNI

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1735	7915	A	1756	126	397	PLTEDGSPGPPPEGFKDLNRQRPPTH GPWRGPGSPGPPRSGQVPDNSTRCFL SDFWSPQGDQRPCSPYTGARPRQGA AQHLRCPSSRRR
1736	7916	A	1757	121	392	PLTEDGSPGPPPEGFKDLNRQRPPTH GPWRGPGSPGPPRSGQVPDNSTRCFL SDFWSPQGDQRPCSPYTGARPRQGA AQHLRCPSSRRR
1737	7917	A	1758	60	414	QSRSEFIKCGGFLT VFADLCPLTEDGS PGPPTGEGFKDLNRQSPPTHGPWRGP GPGSPGPPRSGQVPDNSTRCFLSDFWSP QGDQRPCSPYTGARPRQGAQAQHLRC PSSRRRARTRGSTR
1738	7918	A	1760	164	404	IRLFFRTRRHSPFLYPSLLLHVPHISC ATALSLPGGWHLTYTSLGISITVGVSP IPPPALTSPLSNTSMWLLIWAYAR
1739	7919	A	1761	3	440	CSTRLD FANRTPRPGGSKLPVLNANL MGSMAAGKGPQPGGGGINVQEILT SIMGSPNSHPSEELLKQPDYSDKIKQ MLVPHGLLGPPIANGFPFGGPGGPK GMQHFPPGPGGPMFPGHGGPGGPVG PRLGLPPPPRGDSFLE
1740	7920	A	1762	129	440	WLPAPATDCYHGAGEQYRGTVSKTR KGVQCQRWSAETHPKPOFTTSEPHA QLEENFCRNPDGDSHGWPCTMDPR TPFDYCALRRFADDQFASILDPEEQ QF
1741	7921	A	1763	2	296	AMVFGGVVPYVPQCRDIRRTHNAHG FSTYVCLVLLVAIIRLFWFARRFESP LLWQSAIMILTMMLMLNCTAVRVA NELNARRSSSTAADSNHEDV
1742	7922	A	1764	2	324	AMVFGGVVPYVPQYRDIRRQTNADG FSTYVCLVLLVANILRILLWFGRRFES PLLWQSAIMILTMMLMLNVHRRSV WPTSSTPGAAPLQLOIASMRKSGSPR EFRT
1743	7923	A	1765	1	412	MKALLALPLLLSTPPCAQVSGIRG DALERFCLQQLDCDDIYAQGYQSD GVYLIYSPGSPVPVFCMDMTTEGGK WTVFQKRFNGSVSFFRGWNDYKLG FGRADGEYWLGLQNMHLTLKQKYE LRVLDLEFEN
1744	7924	A	1766	2	178	VSHTNEIAEKRTHNVLERQRRNELKR SFFALRDQIPELENNKAPKGVILKKT TAYILS
1745	7925	A	1767	270	397	PFNPPLNQVETIGDAYMVVSLGPLGRN GQRHATEISRMALALLD
1746	7926	A	1768	183	477	IPEPPGPPSSLLPLLGKGLNIGGGAG GGGRRDRVPAPLCTFPFPFPFPFPIA TLKESGLCPPICSVTSSQHNFIQSPQFR RHRTRGSLKLLSSY
1747	7927	A	1769	208	395	SLPQVGLSQVDLSQVGLPQVGLSQVG LPQVGLSQVGLPQVGLSQVGLPQVG

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						LSQVGLSQVGL
1748	7928	A	1770	29	115	SGKGNIGKTVIVIMVDVAKALNRPPTCK
1749	7929	A	1771	26	119	SRPTRPIDGLEPGLHGLYVYQYGDLTNNCNR
1750	7930	A	1772	1	76	IDGLEPGLHGLHVHQYGDLTNNCNR
1751	7931	A	1773	1	372	PPLKRRQGGGPPGCGWLNTPPEPAQNLFSFQNKQKPPGGGHTPVPCTPLGGKKPRKPPSPGRGGSQWSKIS
1752	7932	A	1774	2	209	LKILAIQCHWSQRPFVIGDVLQGYSGSEGRAIIFCETKKKNVTMEMAMNPHIKQVRLFFMLSLEIMGMNH
1753	7933	A	1775	3	180	ERGLHGEFGLPGPAGPRGERGPPGESGAAGPTGPIGSRGCRDHKAPSCVCCC
1754	7934	A	1776	1	274	LLHLGAVYSLVLPKAKPLTLWAYFFCLLAALGVTA GAHRIWSHRSYRAKLPLRIFLA VANSMAFQNDIFEWSRDHRAHHKYSETDADPH
1755	7935	A	1777	3	371	KSQCHVSLDMVHLVHARKAQHLATDVGYKTAHHFTALPTDMKVEWAKKAYGLQSDNQYRADVKWMKGMGWVATGSLNVEQA KKGINSRRGEYKIRSTIPGKKKRKQELEREGENERYAQN
1756	7936	A	1778	112	401	QTCPPGRNPRA GTPPPFGTNGAPGGHQTPGAQKSPGGRRAETCPLPCRNPTQFGSLTELQSLISALFALLQKPLFLAMRGPLQGA PLGEKGVGGW
1757	7937	A	1780	127	398	NLGVP GKRNPPGSTPPKRGNGKPPHPGPVNEWFFKKKGVPVGRGGKQPSNIRGPPLPGPPKGGDYRGNSSSRPFWGLSSSRVSP LGP
1758	7938	A	1781	29	176	VVFVLEMRFRHHVGGVQAGLRLTSSDLPALASQSA GITDVSYRA WPPSGI
1759	7939	A	1782	1	335	EVHSV KLCFGLGGPCLLPFIFRPLLLHPRRPRIIPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGHGGVEIPQGVVEACPGLGQDQGPREQQKQGSGRHDTILGDCPRGLF
1760	7940	A	1783	86	306	DVLIQGVSHTVGIEFLIYPKEMKSVQCKDICTPMFIAAPFTIAKIQNGPKCLSVNEWIKRMWDIYTV EYYSLL
1761	7941	A	1784	399	554	QSSDTFYDIRRTVVCPIIDVISDDTFEY MAGSDMTYGGFNWKLNFRWYQWI
1762	7942	A	1785	315	420	VEADLGYPGKAKVIHKESDMIMAFSVNKANCNEI

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1763	7943	A	1786	2	382	LNSSSFPRMYLADVQNTPSAKLNSSS FPRMYLPDVQNTPSAKLNSSSFPRMY LPDVQNTPSAKLNSSSFPRMYLPDVQ NTPSAKLNSSSFPRMYLPDVQNTPSA KLNSSSFPRMYHLDPVQNTPSA
1764	7944	A	1787	3	387	KKKQKKPPPPNICCFQEIQLTPKPSHKL KVG.GWRKIFPPNGNQKPAKVTSSSPD KTGFKATTV
1765	7945	A	1788	3	249	ETFTFHADICTLSEKERQIKQKTALVE LEKHKPKATKEQLKAVMDDFATFVE KCKKADDKETCF AE EGKKLVAA SQA ALCL
1766	7946	A	1789	3	372	GAHAGEYGAEALERMVLYLPTTKTY PFHFDLSHGSAQVKGHRKKVADALT NAVAHVDDMPNTLSALSELHAHKPR VDPVNFKLLRHCLLVTLVSHLPVEITP AEHASLDKFLASVSTALTSKY
1767	7947	A	1790	3	371	GFEKIHLISTQGAVPYALRVELEDWN GRSTIGNYATFMVGP EADKYRLTYA YFGGGDAGDAFDGFDGDDPN DKFF TCHNGMQFSTWDNDHDKVEGICAEH DGSGWWLNKRHAGHLNGVYYQG
1768	7948	A	1791	2	367	LLLFDKRDTSDFDLLTGRDTASEPPQ NDGNSFNSPRLTMEASYNHNFSQQS LRMAKEIFTLPNPNPFVEDDLKNEIC CAAYQYRTWKLGGDIDLVRGEHHC VMTGTNR EEDFINIKTL
1769	7949	A	1792	171	343	LGILTKPEPGQPSQGLHQSHLGSSGFQ IGVNLSMENYALTFGINFFIALMIQPIG TM
1770	7950	A	1793	1	220	DVAFKDLDAVAILVGSMPRREGMERK DLLKVNVKIFKSQGAALDKYAKKSV KVTKCCILWDFSLLAFTYAFSI
1771	7951	A	1794	248	393	LPFLSFLHSHPLPKPOALPSLQQPPT TAVANPPSPQPPPEIQEL
1772	7952	A	1795	50	374	GGFPPPGAVGLKPPLPIPFYSPGGSSSP GEIPLPFGAPFLVPKAKILPPGVLLK GFPFPKNTSSSP
1773	7953	A	1796	3	120	TMYATQWETLDTFTKWLREGKNEI LKLLFLSHFLIP
1774	7954	A	1797	2	151	NYRNLVALGYQLCKPEVIAQLELEE WVIERDSLDDTHPGKCTLLGTAT
1775	7955	A	1798	489	591	GGQALWPRLECSGAIHCHNLELLG SSDFPASD
1776	7956	A	1799	400	8	DSSSSSRKGSPLSPSRNPRGQIWPKG TLALGGQGNPPKPPGEGGTSSSSTK FWFFKKKGGSPRPGGVQNPGRPK TPPGPPKGGKRGGLAPRGREFLSFF LK

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1777	7957	A	1800	32	277	DGQALSLGARLPWGWMDPQLSDGLRLAVTASQHIKIHQLLCFQVDLEFFSYPSHFPPFIILKNFSLSLFKGFSFFCCCCFL
1778	7958	A	1801	242	359	SNLFQREPNWRPHTLPDFKLYYKARVIKTPSYWHKNRHI
1779	7959	A	1802	3	300	PLNKLTELLRHDMAAAGFTERLTFALCSQEDIADKLGVDISATKVAHNSNTAEFQVARTITLLPGLKLTAAARTMPLPLKLFEISDIVIKDSNTDVC
1780	7960	A	1803	1	267	EALDCILPPTSRSDKPLRLPLQDVYKIGGIGTVPVGREETGLVKPGMVVTFAPVNGTTEVKS VEMHHEALSEALPGDNVGFNVQNVSCQ
1781	7961	A	1804	1	346	KDVRRRGNVAGDSKNDPPMEAAAGFTGQVILNHPGQISAGYAPVLDCHTGHIA CKFAELKEKIDRRSGKKLEDGPKFLKSGDAAIVMDMDPGKPMCVESFSDYPPLRGFAVRDMKTN
1782	7962	A	1805	3	360	GMPCAEEYLSVALNQLCELHDKTPTVSDTVTICTTESLANRRPCFLALEVDETYVPKEISAEAFTHADICTLSEKERQIEKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADY
1783	7963	A	1806	3	153	DRGAPGVQPCRLVTMTSVVKTVYSLQPPSALSGGQPAEHLNGNPGTSGD
1784	7964	A	1807	205	288	AMAAQLQPPPPKFKQFSCSLPSNWGYG
1785	7965	A	1808	40	271	GVMGPHAWLIVFSFFVEMGSHYVPQAGLKLPGSSDPASASQSAGITGVSYCTQPTWNL SKYGLTLCNCTTSLSQP
1786	7966	A	1809	2	395	AHCCVEMGMDMIEAISLVREVTGVNVNMRVGIHSGRVHCVGLGRK WQFDVWSDNVTLANHMEAGGKAGRIHITKATLNYLNGDYEVEPGCGGERNAYLKEHSIETFLILRCTQKRKEEKAMIAKMNRQMY
1787	7967	A	1810	1	406	GSAEGHPPPTHTTVQHEGFLLRKREL DANRKSSNRSWVSLYCVLSKGELGFYKDSKGPASGTHGGEPILLSHKATS EVASDYKKKKHVFKLQTQDGEFLLQAKDEEEMNGWLEAVPSSVAEHAIEAKWGQTL P
1788	7968	A	1811	186	404	PENVAVGEERLPGPGCTGLWAGVPPLMSGTSLGPVLWAWRRAGPLPCPGGISAGSSCLPPPRAGSPPLFGHL
1789	7969	A	1812	1	276	GWLKWTNLYLKGYQRRWFVLGNGLLSYYRNQGEAMAHTCRGINLSTAHDITEDSCGILLTSGARSYHLKASSEVDRQQWITALELAKAKAVR

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1790	7970	A	1813	143	355	VFFNLAILIKFKGAIRFTTEGGFLFSPLK KKALENLWKGKGGSALRDGYLFFE NFKKWPQNFFLAKTLKFF
1791	7971	A	1814	2	353	EKSPQTLLYCRKLGLVLDLSHNNLTFL PADIGLLQNLQNLANTGNRIETLPPEL LQCRKLRLRLGNNELEPLPSMVGEL TNLTQIELOGNRLCECLPVLEDSPLLK RSGSREEEDLL
1792	7972	A	1815	1	218	LKKSLEYAIFSQFGQILDILVSRSLKMR GQAFVIFKEVSSATNALRSMQGGPFY DKPMVSIAGTEAVWVCKML
1793	7973	A	1816	99	385	KQSLTWSPRREGRGPARAHGKPGPR GPPHSPALAPGEPETIGASSSSRKIFGF LGKNGVLPGYPGRAGQSPDLGNRPGP PKGRGIRGGAPHPGLL
1794	7974	A	1817	51	261	WGSKDFFPPPPPTGTVQGGGPPAPLIL CFLEKRGVPPVGPGEFNLFPKLGPPG FPKGGKKRGGPPRP
1795	7975	A	1818	284	397	NLQVSCLNABQNQHRLRAFLSRLHRV AQVTPPAGTSTSG
1796	7976	A	1819	1	677	NGLSVPILOHPDLQDVLIPVIGPRKNI KKQQCEAIVGAQCGNAVLRGAHVY APGIVSASQFMKAGDVISVYSIDIKGK CKKGAKFEFDGTVFLNGISELSRKE IFSGLPELKGGMGIRMTPEVYLSPSFDS VLPRYLFQLNLPALVSHVLNPPQGE KILDLCAPGGKTTHIAALMHDQVC CGLLEVHPRPCLTGYHQWRLQNLSKN CCLLLPLEASSERALARC
1797	7977	A	1820	234	330	KFKKFWPGAVGHACNPSTSGGRGGR ITRSGNR
1798	7978	A	1821	3	117	WQVGLELLASNDPPASASQSAGITGV SHRSWLILATF
1799	7979	A	1822	25	418	VSLLLPRLDYNAGILTA TSTQSARI TDISHREQFSRIILTGAKDLYNEDYK TLLKELTDASKWKDTSYSMDGEDNI VKMPNTTPMQSYRFQCNPIRSQYFL KKQKNPNLNFMWGQTRWLTVPVIAL W
1800	7980	A	1823	194	396	KHSFCAPLGSTYAKIGKIQRRLA WPL CKDDTHIYEAFYIFILMKHSSKRRHLPL FQLRWTRHFQICLF
1801	7981	A	1824	73	355	GQGQIFGPPPPFFMFWGKKNRPRGG KNKGEPGVSVSPFGEKGGNGLKKDS SSPFFSPSSSSRTVSPKCCGGKFFVP PSPGPGITGLQRA PPQ
1802	7982	A	1825	186	398	VSSHIVQLARKKVREIHAAIKVRLAC PLVRGFSYPWLQAFPLFSFLPCCRCL ITRFLPERNLLIFITS

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1803	7983	A	1826	3	287	EDITSIPASGFFPPSLSCASLPASSFFPPSVSCASLPASGSPPSLSCASLPASGRLLPSLSCSSLPSPSGPPPSLWKLLGLDFPHDPTTSKIS
1804	7984	A	1827	3	170	LDLLTSSSSRLGLPKCWDYRLEPPRPALSCSKGFLNKLPLLSWILLYGPPQSNSSF
1805	7985	A	1828	3	106	TMYATQWETLTDFTKWLREGGKNEILKLLFLSHF
1806	7986	A	1829	3	182	EVFMHQGSLNRHMRSHTEQKPNECH EYGEKPHKCKEKGKTFTRSSSIRTHE R IYTGKEL
1807	7987	A	1830	203	365	GRKGQGLKRSPGHSLPVPPLCFLRQAKANL DKNKQTKLENTDLA GELTRVLGQ
1808	7988	A	1831	35	226	AFCKNPVTIIPNGESLNSFYLKSGTGKSQLIFDIVLEVLASGRPHDEIKVMQIKKGIKLTL
1809	7989	A	1832	1	130	RKQAQIRKVVYPGLSCFDGVRQPIESIPGISTYRPSFKSEIF
1810	7990	A	1833	218	366	RQGLPYVAQAGLELLGSSDPPTSASQSARITRHKPPRLPTVTVLNTIFK
1811	7991	A	1834	31	235	YGLLVSSGLTVTAVKDSGEWNLEAGALVLADAGLCCEIDFNSLKEHDRITSIHEAMEQQITISVVRLGKR
1812	7992	A	1835	83	362	LPVNSAGKTRVLFWPVAQCPCGHLPEDLPASGPLLPSHHCCQGAPSSPSCCTAVAASWHQVCPPTTATRAVFLKPSSDGVALHVTWLHAAIR
1813	7993	A	1836	190	340	YWEDFEYILDPEAKKPDNWKEAMDGEWERPLMPNPKYKVRGVLSNGCEK
1814	7994	A	1837	43	362	SIQFSQEIYESPFLTETGEYYKQETSSSSSSICSQYMEKV
1815	7995	A	1838	2	268	ETEPRTMASDLESSLTSIDLWPQLTLRATIEKLGASQAQPPGSSRCKSPGSP TDPNATLSKDEAAVHQDGKPRYSYATLITYAINS
1816	7996	A	1839	5	123	NAYWSCIKENYLKKEKRQPTKWENVFANQVSDKGLISRK
1817	7997	A	1840	1	96	DLELLGSSDLPASASQNAIGIIVSHCALLMAS
1818	7998	A	1841	1	385	IGLAEKVPLGWPRPCGCPRNQGPVPQTAWAGAFGLPPLSLTPGKGERMAAETGDMGLVLGQVTRRSRQSKSSSSSSSSSSSS
1819	7999	A	1842	358	0	SSWGPPLPFRPSGGVGGSPGAGFKA PPGPQGPPPPFFKPPKSPRVGARPPFS PRGIPLKPSSSSPRKL VGS
1820	8000	A	1843	357	81	SNSLKPLYPIPMTPMPVNQAKTYRAGKGENNPACVCL

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1821	8001	A	1844	378	526	LLRTCVDFFRLVPFMVFLVLPFMEFL PVFLKCLFPEMLPSTFESKVV
1822	8002	A	1845	1	401	NWISTGKRIKPNLYLTPYIKIKSKWK DLNATSKAIISS
1823	8003	A	1846	438	192	SPGRPTKPKKSQENIFKGNFQDIQLR TSEPDTSANMRDSEAGKLVLAWSE LGVIYVPSEFNVSIVLVLLRII
1824	8004	A	1847	9	238	KPTRPNGWKHITVSWIGRINTLKMNV LPRISYLFHQLPVDPDKQFKDKYVK DACVTFCVLKCTLVSRVLNCGPFG
1825	8005	A	1848	2	320	GRTDRFAFQLPFAEAGADGARLDFV VRYETPEGTFWANNHGRNYTVLLRI APAPTPTDAERGAPSSRQLPQLGATA RVPRVPWRLRPGQLKSCNEAGEGQA CRGRN
1826	8006	A	1849	221	429	KAPRLHPQIQICFHELLSCCTCLATV KPVSSFKYLLTLPGAMAHACNPSILG VQGRQITKSGVRDLYS
1827	8007	A	1850	2	127	GRRSRVDPRAKRCPRCNAQFRVTEA LRGHMVCSDITCDPA
1828	8008	A	1851	1	346	PASSTDWLLSFVAVYERHCLRTTLKAL PEGACHLSCLQIASFLLSKQSRITGPS GLSSYHLKTALLHLLLRQAADWKA GQLDARLHELLCFLEKSLHHKLLHHF FIGNRQAGAGGH
1829	8009	A	1852	71	253	GIRGTLSSWRDSDYDFGLKPLTISYDP ATCLHVVWYNGSYFLVEFVDSTDKSA CIEKKSE
1830	8010	A	1853	109	447	GFNLPALAYFCVAQCGCTGRNLYFHV SGLESRVENKELIPMQQILEEAEPQGG LQEAFFGKRPLFSKCGSTHEDRVEKG SGDPLPLKLENSPEAAGLNSISDVNKN GSIEGEE
1831	8011	A	1854	3	217	LDQWLHDNDNHVAAPHCKAGQGRRT AVMTCAVLLHPGKLLKAQEAALNFYG EVRTTNKKASYFLMLCLSSWI
1832	8012	A	1855	251	463	RAGAHFGLVETLASGFKGIFWLKPPK SWELRGPPIMPAYFLVFYDRGLTPV GRVWLKFGALGDRPAWFSK
1833	8013	A	1856	3	140	LPTFILHYIDIGILIAAPTDELIDCSQSL RKQDTEAGLHIAQDKYH
1834	8014	A	1857	4	284	SLSPLPAGAGTKIPGVGFLLKQKRFF SPVLGVRSKSTKGPPPGKGLLGPPIP KSGEKGKGTFFPKGPFKGPHPPPKG GGPQGLFPLKKP
1835	8015	A	1858	2	368	DFAVFLTILCMVLIDYAIGPSKQLQVP SVFKPTRDDRGWFVTPLPNPNWWTV IAAIIPALLCTILIFMDQQTAVIINRKE HKLKKGCGYHLLDMVAVMLGVCSI MGLPWFVAATVLSIT

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1836	8016	A	1859	1	375	PTRPPTPRPGLPDPWVSQITNTDTLAA VAHILQSPQGGQQLQQLIQLTQIQQQK PQPSILQALDAGLVVQMQUALTAQLT AAAAAANTLTPLEQGVCFNKMLMDR FDGGESEHSEEPKKETPAWATQ
1837	8017	A	1860	1	770	AVEFVKQNPLPSSFPKKKIRLAAPV CSSKTLQAEVPLSDCVQKASKPTST QIMVKTNMYHNEKVNHFHVECKDYV KKAKVKINPVQQRPLLSQIHDTAAK ENTCYCGAVAKRQEKKGMEPLQGH ATPALPFKETQELLSPLEQPEGPSLA AGESSSLASSTVSVDSSQKKKEHNYSL FVSDNLGEQPTKCSPEEDEDEEDVD DEDDHDEFGSEHSELSENEEEEEEEED YEDDKDDDISDTFSEPGIIMLAG
1838	8018	A	1861	251	448	NNYSFHNPNHPRAAALEQFKSLGAEP LEVLDKESGEGQGGYAKEMSKFEIA EMKLFQACQCKEVDI
1839	8019	A	1862	4	145	VSLQRHLSATDTSFSLDLFQLLSSQH ENSLEVIGTLDILAGTYLH
1840	8020	A	1863	3	330	RHGPPRLQTRPGYAALTGTAAVKSAS PQSPGGRPGRAEVSPWPVPLGRG WPKCLRLSAAHPQQFRPEALPAGG GLMGSA GMPGAAALSSAQGVCFPP KFPRPP
1841	8021	A	1864	249	414	KCWFLKNADSRPGA VAHTCNPRTLG GGGGRIKRSVDPDQPDQRGETLSLLK IEKK
1842	8022	A	1865	2	593	PTPEKPRKVHAKWILDTDTFNEWMN EENYEVDNDKKNPVSRKKISAKTLTD EVNSPDSNRRDKKGGNYKRRKRSFP PSPTPEAKKKNAKKGPSPTYTKSRG HREEEQEDLTCKMDEPSPVPNVEEVT LPKTVNTKKDSAPVKGGTMTDLD EQEDESMTTGKDEDENSTGNKGEQ TKNPDLHEENVNKGTHHVV
1843	8023	A	1866	3	166	FPIDRCCEGNFDAINIRGETFFFKGES FHLASYMLVSCPLPVTHWGCGLTLE A
1844	8024	A	1867	3	211	SSFSIPTLVITEQFATAYQGTRARSDN THYWLIIISCIAYVALVTLLIWPVKV ILHKKRYIYRKIKGW
1845	8025	A	1868	3	211	SSFSIPTLVITEQFATAYQGTRARSDN THYWLIIISCIAYVALVTLLIWPVKV ILHKKRYIYRKIKGW
1846	8026	A	1869	209	531	TRGCCTVTCAPALSSTAASPPVATTA SAALLTTRATSSCCVATTGPLAASSTT TQPMPTCAAPASVTLRRPEPAMAQ MRTSSLSWTWADSRSLVRLGPRTPSP POP

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1847	8027	A	1870	2	689	SPLLPLASSLAPERTHLPFGPSLLSPP SFPARPREPRGCVTAAPDKMDTAE DICRVCSEGTPEKPLYHPCVCTGSIK FIHQECLVQWLKHSRKEYCELCKHRF AFTPIYSPDMSRLPIQDIFAGLVTSIG TAIRYWFHYTLVAFALVGVVPLTAC RIYKCLFTGSVSSLLTLPDMLSTENL LADCLQGCFVVTCTLCAFISLVWLRE QIVHGGAPIWLEHAAY
1848	8028	A	1871	1	171	LDTILEFSQNMNTKYVGLQILENVKLT RWKILPRNQCGRKIKNYKFRLLFLA FLL
1849	8029	A	1873	1	245	VCRNSARAAVHTETKQFFLYNTLD DKKDYLEKEHLLNSVHENFSQAMDS PADRDQFLRHMEQIVGIGKSRMKM DNKNP
1850	8030	A	1874	1	131	FPLWTSEQGVGRNKQTYVTWQADC KENAGGDYYWTFPPQPTFV
1851	8031	A	1875	295	384	VGYYQAGSNGQPLPSQYMNLDLSASC RILAD
1852	8032	A	1876	1	131	FPLWTSEQGVGRNKQTYVTWQADC KENAGGDYYWTFPPQPTFV
1853	8033	A	1877	3	426	KTCFNLPLSGARSQAASILTKFQELKD VQDELRLKENEF
1854	8034	A	1878	1	131	FPLWTSEQGVGRNKQTYVTWQADC KENAGGDYYWTFPPQPTFV
1855	8035	A	1879	1	131	FPLWTSEQGVGRNKQTYVTWQADC KENAGGDYYWTFPPQPTFV
1856	8036	A	1880	465	883	PCKKGPPCMGVWGANITLKKKGLF PLPGNKDPWAHPNSQFWPPVRQCP MDPPWKAPKGAIDPIIFGGKPKGV PRVYKALNWRHGVFVASAMRSESTA AAEHKGEHPHHSLSVCVCTQHVLSPF LSQTFLLSTPGV
1857	8037	A	1881	200	455	GSVRCVSARHLVFLVSHIALPGHQ LPQCSWFSFHPQCVLANKSHLVVEE EVRWMEIYLSGLVALRLTSLLA VTS LASIANS
1858	8038	A	1882	1	748	KSYWDSA YDDVMENRVLNLLYA QTVSDIERGWILVTKEQHRQLKSLQE KVSKEFLRLAQTLRHYGYLRFDAC VADFFPEKDCPVVVSAGNSELQLRL PGQQLREGSFRVTRMRCWRVTSSVP LPSGSTSSPGRGRGEVRLLEAFEYLM SKDRLQWVTTTSPQAIMMSICLQSMV DELMVYKSGGSIRKMLRRRVGGTLR RSDSQQAVKSPPLLESPDATRESMVK LSSKLSA VSLRGIGSPSTDA
1859	8039	A	1883	3	181	QRA GIRGYIGLPGLFGPSDGERGLP GVPGKRGKMGMPVLLPQSSEARGGN SMPSEGA

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1860	8040	A	1884	69	234	AWCWFCNLILLGILQVEYHPYLNQSKLLEYCKSKDIVMTAYSALGSDSDKDW
1861	8041	A	1885	2	398	SCPLEQRLGGETDPAHQDHRRCAGPRHGTAPACHGFHLPGRSPTHFVSLSLTPLVCKMGTLPRAAALRCKTPWWGLCTPSHVPGPCSSSPRPVCSFPILHGNILQGGPAQMVPTTGGPPGAPVRLVKHPWP
1862	8042	A	1886	32	315	HIYKYNLHLSADWGNPFCTYTWHPAPTTTLPLHHEPAFPPLLPQPPTQPVSSSESLGALEATVSTWPTPELEPSRHYKRNIREPKSLTS
1863	8043	A	1887	1	165	DISSNIQAIVKEHPFSETEDKNKITAIFYCISLTQQGLQGVELGTFLIKRVVKE
1864	8044	A	1888	1	165	DISSNIQAIVKEHPFSETEDKNKITAIFYCISLTQQGLQGVELGTFLIKRVVKE
1865	8045	A	1889	62	133	FQGFEDCLVFDELMDFNSDLSK
1866	8046	A	1890	198	400	WKLPGAQKFGPKYLTKEGLTKTYGGRPNPKDSDPFFLEGPIMGGTGGQINGKKGKKAILKPKFKKRQN
1867	8047	A	1891	15	319	ANSARGARYVLSLLLDWRGCSLNYYSKSDVPFQNEGPILRGEAQERRLIAHDAQERRLAERRARIQOEYEEQEKREKEEEQRLKNEEHIRLAERLKEA
1868	8048	A	1892	2	161	PRVRDIMESNAQGRCLILPQMPKALFRKKQKKKEKKGNGEGGRERVKEGRKEN
1869	8049	A	1893	1	383	RIHTGEKPYECNICEKAFSHRGSLLTHQRVHTGEKPYECKEKGAFRQSTHLAHHQRHTGEKPYECKESKTFSQNAHLAQHQKIHTGEKPYECKEKGAFSQIAHLVQHQRVHTGEKPYECIECG
1870	8050	A	1894	186	294	DDCLRLSLTRFAAAHWTVASVSVVQGHFCKLFACEY
1871	8051	A	1895	1	401	RREGEEKRGGRRGGKRGGGGGGSSSSPEKERGGRRGGKGGGTS
1872	8052	A	1896	313	833	AETDKIVVGSSVAPGNTAPSPSSPTSP TSDATTSLEMNPNHAIAPRRHAPLEQLARQGSFRGPALSKQMSFPKQLSLRINELPSTMQRKTDPIKNAVPEVEGEAESISLCSQITNAFSTPEDPFSSAPMTKPTVTVAQPSPTQTGTWQSSGAASPGLFQAQHRRTPSE
1873	8053	A	1897	1	375	QQDISFVSSTFVTEMEKTDLDIAVHMTYNTGQTVAAFHSPYWMVNKTGRMLQYKANGIHRKHPPNYKKPLDFSFQPNHFFNNNKVQLMATDSEMTNQFSIDTVGSHGAVCKCKGLKDDYQVGVITD
1874	8054	A	1898	3	109	SLATAAGSEDAEKKVLATKVLGTGVKWINVRNAYGF

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1875	8055	A	1899	3	148	HASVQKHCRGYLVRSLYQLIRMATIT MQAYSRGFLARRRYRKVRPTSV
1876	8056	A	1900	3	124	SGFCAEKLSPALCCICIVRNTHIHTH THTQTHTRAHTH
1877	8057	A	1901	2	333	MPGGCSHICLLSSSYKTRTCRCRTGF NLGSDGRSCKRPKNELFLFYGKGRPG IVRGMDLNTKIADDEYMIPIENLVNPR ALDFHAETNYIYFADTTSLFGRQKID GTERE
1878	8058	A	1902	3	801	FLKICCRYTYGKPMGLGAVQVSVQC KANTYWYREVEREQLPDKCRNLGGQ TDKTGCFSAFVDMATFDLIGYA YSHQ INIVATFVVEEGTGVEANATQNIYISPO MGSMTFEDTNSFYHPNRPFGSKIRVR GHDDSFLLKNHLVFLVIYGTNGTFNQT LVTDNNGLAPFTLETSGWNGTDVSL GKFGMEDLVYNPEQVPRIYQNA YLH LRPFYSTTTRSLGIHRLNGLKCGQPQ EVLVDYIDPADASPDQEISFSYYVRP GNGDG
1879	8059	A	1903	13	411	RWGFTMPDWAGLKLLTSSDLPASAS PSPGITGMSHCAGP
1880	8060	A	1904	123	239	PPFLLGTGLKVEVTHCGTMRKRYR VCNVTRRPASHQT
1881	8061	A	1905	257	379	YFLLQMEREMRHKLKTA FNKIEKV EALTKEELEFEVPM
1882	8062	A	1906	1	403	PDGALQVASPGTDGVLGLHLLTMT SCRTHQGTTLQYAQTSDGQQLVPS NQVVLTASGDMQTYQIRITPSATSL PQTVVMTYAVTITSQTITDDPQLTR DMRVMNYTEARECRRKNKEVVKC LETEVQP
1883	8063	A	1907	281	383	TKQLLCTAKETINVRHRLTEWETIF ANYASDRS
1884	8064	A	1908	60	212	YWEDFEYILDPEAKKPDNWEAMDG EWERPLMPNPKYKVRGVSLSNGCEK
1885	8065	A	1909	2	316	MSLPLVSLVFVFAFGQRIVNRLRTSLF SSILRQEVAFDDKTRTGELINRLSSDT ALLGRSVTENLSNGLRAGAQAQSVGIS MMVCGPGSPWYLPARACLHQASHV
1886	8066	A	1910	1	341	GAHAPHNPVMPASMGSAVNDALKR DKDAIYGHPLPLALVFEKCELATC TPREPGVAGGDVCSDFSFNEDIAVFA KQVRAEKPLFSSNPEDNLMIQAIQV LRFHILLELEK
1887	8067	A	1911	269	514	STSPSHAVVANVQLVLHLMKQHSKA LCNDRVINSIPLAKQVSSRGKSKKLS VTPSSNGINEELSEVLQTLQDEFGQ MSL
1888	8068	A	1912	2	109	KILNKTLANQLQHIKSVIHNNQVEFI PGVQSWFN

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1889	8069	A	1913	62	420	PEIKDLYSYNNLSVESRRRTKQLFEVLHFLAENFISYMGLALVTFQKHVFSPFIIGAFVAIFLGRAAHYPLSFFLNLGR RHKIGWNFQHMMMFSGRLGRMAFA LAIRDTSYARQM
1890	8070	A	1914	2	408	VCMQLVGRHLHLASPQESPFYVLIETSGSNAGHDAEKLGHFLHALGSLGSL VTDGMTATDQRRKVS
1891	8071	A	1915	129	544	LEGKCPSPICVCKNKHVNNRSSTLLTNKLG FVVYCKSAFLTG YDGDGLGILGRRPGNNISSPFMISVKANCTSDFEEYFAKRKLEERDGHAVSIEEYLQRSDTAITYPEAPEELSLRGTP EANGQEENGEAVNHF
1892	8072	A	1916	85	332	AKLQRRQSLSLAPPLCISLPFGSPQAQPPGTIMLPDCLKPPTSTHPPMSFLEVPSPDKPLPHFPANKIPTPKDSSEV
1893	8073	A	1917	99	366	LFLFVPNADPGYVLTQAGSLRSLGNKEPHSPFGLDSFNSTAKDSPLTPKLFNSLLLGPTASNKKTEGSSLRDLLHSGPGKLPQSLDTG
1894	8074	A	1918	2	583	TYPEFPGRQNKSVLRPAVTNGMSOLP SINPSSAGNETTFSGGGPAPVTTPEPDHVPKADSTDIRSEEPLKTDSSASNS NSELKAIRPPCPDTAPPPSALHWLADLA TQKAKEETKEAGSLRSLVNKESHSPFGLDSFNSTAKVSP LTPKLFNSLLGP TASNNKTEGSSLRDLLHSGPGKLPQT PLDTGSCI
1895	8075	A	1919	14	381	WKSPPGFPPPKGSGQPHGGPGSWPFGPSSSRSPRPGPP
1896	8076	A	1920	43	374	GTKRSKWSPGPKVKADWSRVKVM AIVFWDQAQGILLVEFESQQMISAYYECLDKVKALAEKLGKLGHRVLLHH DNVLAHSSHQTRPILQEPWEIIRHPA YSTDLT
1897	8077	A	1921	113	392	LSAAKGSDSRSLASQRPAPRTMLS STQNAAGSYQVRGALDTQKCSPEK SASFSSKVTYSWFSRRITLGYKRPLER EDLFELKESDPSALR
1898	8078	A	1922	109	412	GGIKARRSQARPSVNIDARCLWPQKQASVAAENS VICSFLHYMEKGGKGWH KAWFVVPENEPLVLYIYGAPQVCILL LRVLSATWQSQIQSLTSPWPWKIR
1899	8079	A	1923	131	373	SSEFTAGEFTCLRVASSAHQTSNFSFCSFTLALSMSSCKCSISFRFRVNI VLYLLSSSSCDRSFSSCWSGIRGTAMFS

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1900	8080	A	1925	2	485	PGSTISSAGKMDAGKAGDEKPEKSQR AGAAGGPPEEEAEKPVKTKTVSSSSG GESSRSRAEKRSAAEEAAADLPKPTKI SKFGFAIGSQTTKKAASIKLGSSKP KETVPTLAPKTLVAAAFNEDESE EEMPPEAKMRMKNIGRIDPTSAAGPN SFNKG
1901	8081	A	1926	187	388	VSSHQVLARKKVREIQAAIKVRLAC PLVGGFSSPWLAFFLFSLLPCRCL VTRFLPEGNLVIF
1902	8082	A	1927	2	182	HCDMVITYGLDQLENCQTCGTDYIIS VLNLLTLVCELFFSLMCWFQALKW ICKKLRL
1903	8083	A	1928	187	388	VSSHQVLARKKVREIQAAIKVRLAC PLVGGFSSPWLAFFLFSLLPCRCL VTRFLPEGNLVIF
1904	8084	A	1929	3	457	QHGLLMQLLKLTHNCLNDFIGTSTD ESSDDLCTVQIPTSWRSALDSSITLQ FFDLYHSIPSPFSLVLSCLVQIASVR SLFNNAERAKFLSHLVGVKRIENP QSLSDPNNYHEFCRLRLKSNYQLG ELVKVENYPEVIRLIANF
1905	8085	A	1930	1	90	TKAVPALGKSPPHHSQFQVSYSCVY YPAB
1906	8086	A	1931	2	385	RLIINKHTDESIGDCSFLNTWFMHDT CKYVHYEIDACMDSEAPGMKDHTPS QELALTSVGGDSSADRLFPQWICW DIRYLDVSLGKFADVMADPPWDIHM ELPYGTLDDEMRRLLNIPVLQDDGF
1907	8087	A	1932	235	363	HFKTLFATTLTAHMASLGPFPFRVP LMSTPMGGPVPPIRYG
1908	8088	A	1933	2	887	GFTVPEIKTILGMPAFEVSLQALQKA TFQTPDFIVPLDLRIPSVQNFKDLKN IKIPSRFSTPEFTILNTFHIPSTIDFVE MKVKIIRTIDQMLNSELQWPVPDIYL RDLKVEDIPLARITLPDFRLPEIAIPEFI IPTLNLNDFQVPDLHIPEFQLPHISHTI EVPTFGKLYSILKIQSPLFTLDANADI NGGTTANEAGIAASITAKGESKLEV LNDFDQANAQLSNPKINFLALKESVK FSSKYLRTHEGSEMLFFGNAIEGKSN TVASLHTEKNLTLELSNGVIVKIN
1909	8089	A	1934	155	367	TWSPKFLSALGPKNPRERDKINGP AKKTGERKQATPRGQKTANSQGRRK GRITRSMTNKAALAIATVQG

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1910	8090	A	1935	2	925	SRLVDPTQSGGIRGQALCRGWVDTTY NAHNQLHLQRAQEPGGSQPLQSL EEEDDQEEEEEEEEDEGEDSGTSA ASSPTIMRKSSGSPDSQHCASDGTET LAMVVVEPGDTLSSPEFDSGPFSSQS DETSLSTTASSATPTELLPLGPVDGR SCMSDSAYGTLSPTELDQFVAPGPM ELVPRAPSPRVPSPPSPRLRRRTPV QLLSCPHLLKSKSEALLQLLAGAG THGTPSGPSRSLSELCLAVPAPGIKT GSPQEA GPIWDCRGAPIPGSGPLIGC LAGEPAGSHRKRCDGLPS
1911	8091	A	1936	4	289	LENVWVWAEDMAFVPMAPVWSPEHQ MQRLQVTRKLLTEEQATFPMMGGAT PRYLILASNSHNK WGHPGRYQVR SFSGEPLQPNSSVERGFSWGR
1912	8092	A	1937	26	310	VGFVGKKNLCSYQVCFSDNFPFVA PMLQGRFQGLAPDIRKSSYFSPYVD KNLDLFREKRVLMYCTGGIRCEGSA YLKAKVSHHPGALWAWQ
1913	8093	A	1938	2	379	DISQVTAQSLRSHGVVVPDQTVLFND TIADNIRYGRVTAGNDEVEAAAQAA GIHDAIMAFPEGYRTQVGERGLKLSG GEKQRVAIARTILKAPGILLDEVPRG SPPLLPALCMLKPFLGTVPCT
1914	8094	A	1939	29	359	NGYGVTDLPDQDNMKVLANCAQH RPQCPCPAPSLTPPLPGCHLHLSPTD QSPGKKREGCTPALSLPAFYCIPSP PNSPQGFNVSLCVRIFPPKNTPNFWN POTEF
1915	8095	A	1940	1	197	RITHNLLNLYGLYRKMEIVYSYQRCY RSLTSSALVPHMPFIISFPPLIHSFKC MLTAVTRQVL
1916	8096	A	1941	1	169	EKQRRIERIKQKRAQLQELLQVKIPR CFHYLPCFSTCLLESVCFLVPLSG VW
1917	8097	A	1942	64	355	YFSTGHFLLTHLLLEKLKESAPSRIVN VSSLAAHLGRIHFNLQGEKFYNAGL AYCHSKLANILFTQLARRLKGSGVT TYSVHPGTQSELVRHSS
1918	8098	A	1943	1	81	QMWVDIFPKLGPFGPQVNINPRPK R
1919	8099	A	1944	2	399	FHSLIHPAYERWTFHSHVHPASERWTF HSHVHPASEIQTFHSHVHLASERWTFH SVIHPASERRTFHSHVHPASERRTFHSL IHLASERWTFHSHVHPASERQTFHSL IHLASERWTFHSHVHLASERQTFH
1920	8100	A	1945	267	457	LWSYFYSGCPYIILAHFQKSSEEQIA KLQKLEHEKELARKEQELTKLQTR REFQEQMKVA
1921	8101	A	1946	3	181	LKECEKPLLEKSHCIAEVENDEMPA DLPSLAAECWTRIFPFLTSTCMLWE SAFPITL

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1922	8102	A	1947	3	967	HEVSHIVQLVRKLLIHSRPARLLECLE FDPEEFYHLEAAEGHAREGGQIKTD LPQYIIGQLGLAKDPLEEMVPLSHLEE EQPPAPESPESRALVQGSRKPCESDF ETIKLISNGAYGAVYLVRHRDTRQRF AIKKINKQNLIRNQIQQVFVERDILT FAENPFVVMFCSFETRRHLICMVME YVEGGDCATLLKNMGPPLVPDMARL YFAETVLAEYLHNYGIVHRDLKPDN LLITSLGHIKLTDFGLSKIGLMSMATN LYEGHIEKDAREFIDKQVCGTPEYIAP EVIFRQGYGKPDVWAMGVVLYEF LVGCVPF
1923	8103	A	1948	1	176	LSYIMEKADLVIVFAEGVVENGGINIK VRASVLPSSLLKTWRCLADLGHSSV DYGSF
1924	8104	A	1949	9	101	HHELCCVCGDRASGYHYNALTCGCG KGGHL
1925	8105	A	1950	3	973	GGIRGKCSVALLNETESVLSLDKED TFFYSLVYDPSLKTLLADKGEIRVGPR YQADIPEMPLLEGESDEREQSKLEVYV WDPNSPLTDRIQDLVVARAVGTFA RALDCSSSVRQPSLHMSAAAAASRDIT LFHAMDTLYRHSYDLSSAISVLPVPLG GPVLCRDEMEEWSASEALFEEALEK YKGFNDIRQDFLPWKSLSLSIEYYY MWKTTDRYVQQRLLKAAEAESKLK QVYIPTYSKPNPNQISTSNKGPGAVN GAVGTTFOPQNPLLGRACESCYATQS HQWYSWGPNNMQCRLCAICWLYWK KYGGLKMPTQSEDV
1926	8106	A	1951	2	350	VHRPIAPPWGGQVGPPIPRFKGLSP WPCCVNFAPLKKSPKNPGQGGGPPR CSLFLGGLGWKVS LGPGPGASNPRF PQSPPTGGPKPTPSSSSP
1927	8107	A	1952	105	453	TAFFYCPRASLCLPLGSFVCAQHPL PNPAVNPALPHTKWVPLHTPGMP VDVAPEPTQPGHQVLTSTRDFLCE LTPITPLYRISPSLHLSCSVQHPPTFF LPPLSPSPWPGT
1928	8108	A	1953	3	102	ELKILKHFKHDNIIAKDILRPTVPYGE FKSV
1929	8109	A	1954	1	204	EKVPEAKRLYGKRGDPFYEAQENHN LIGVANVFLECLFCDVLQYAVPIISQ QGEVSTGQPWRTMVVQ
1930	8110	A	1955	1	326	NPPGYLEDSEFVKSGVFNSELVRVSR TPTTQGTGVNFPGEIPSPQYHYDMNS GVNLQRSLSSPSSKRPKTSIDENME PSPTGDFYSPSSPAA GSRTWHERDQ GE
1931	8111	A	1956	3	285	GFVGYKKNLCSYQVCFSDNPFVAP MLQGRFQGLAPDIRKSSYFSPYVDK NLELFREKRVLMYCTGGIRCERSAY

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						LKAKVSHHPGALWAWQ
1932	8112	A	1957	2	111	AKDITSDTSGDFRNALLSLAKVQLRYFRKCLLFYKD
1933	8113	A	1958	312	383	QITFEDLPEVESLPRDRVLGFLIE
1934	8114	A	1959	2	177	SRTSLNFRNTRLRLMSQYGHFPFFRA YLGPHASPHTPIVQVRDALAKTQLDLACLQL
1935	8115	A	1960	219	802	YRAFCLIVQIILSPYFNFISSCKPNPNQISTNSNGKPGA VNGAVGTTFQPNPLLRACESCYAQTSHQWYTSWGPPNMQCR LCAICWLYWKKYGGIKMPTQSEEEKLSPSPITTEDPRVRSHVSRQAMQGMPIVRNTGSPKSAVKTRQAFFLHTTYFTKFARQVCKNTRLRLRQAARRPFVAINYA AIRAECKMLLNS
1936	8116	A	1961	1	363	LTEGPWRRRSGSQACVGGAPPLPTAPS HCTSTRWGMSRVRLEALSPALTAWASVLRAGILYDTYPLSEETWHTHQFNFIKNHAFRLLLKPGGVLA SSSSSSSREL MKSKYLDITIMEFVRPP
1937	8117	A	1962	1	262	CFLILQDPLVKSHVSRQAMQGMPLRNTGSPKGAANTRQAFFLHTTYITKVARQVCKNTRLRLRQAACKRNVDAINYAIRAECKMLLNS
1938	8118	A	1963	2	370	FTRLDFKGIQTGDPNA VVMGLAPEHFHYQILNQAFRVLREGAPLITHIKARYYKRKDGLALGPGPFVLTALQYATDTKATTVVGKPEKTFLEALRCTGCEPEEAVMIGDDCRDDVGGAQDVGML
1939	8119	A	1964	3	541	EVVEGVAGEEDYHDEQEEHGEKNAAEAGQHDHDEHDEGSDMELDLLAAETESDSSENHNSNQDNASGRRSVTAATA GSEAGASSVPAFFSEDDSDNDSSSDSDSSSSQSDIEQETFMLDEPLERTTNS SHANGAAQAPRSQWAVRNTQHQRAASTAPSSSTSPAGKSENVLRLRL
1940	8120	A	1965	3	373	CLPTFGADKAKGERVRSSTIRKTSYLDITITGPYLTGQWPRDPHGHYPSCMKDKATQVKSGNQNLITLHFFCFDHSQ EYVLYSNFPRFETHTSKERTNPLFQENFAVIVFCILAFSTSLKFF
1941	8121	A	1966	2	284	EFEGSDNDDEGEHEEEENEDYLTDS NKENETDEENTEVMIKGGGLKHVPCVEDEDFIQALDKMMLLENLQVLNVIC KDSSQYKTLQPIITFWFM
1942	8122	A	1967	33	232	TLPCFVLASGDLQVTGSGHCYPSTAQKAVGKDNFTLPIEGVNGIEERMTVVWDKAVVRLDLFSGAF
1943	8123	A	1968	3	136	ARDHCDLTKEELEPRVFRDVTVKGI DASDYQTQVLPKGTESSRN

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1944	8124	A	1969	1	399	VIEVNNRNGKTKRPRVIVDYNENM GAVDSADQMLTS YPSEKRRHKV WY KKFFHHLLHITVLNSYILFKKDNPEHT MSHINFRLLALIERMLEKHHKPGQOHL RGRPCSDDVTPRLRSGRHFPKSIPTTS GKQN
1945	8125	A	1970	346	468	SRSINIFNLQDQIEALLMRACEPIQN FCHVSDVVRSGK
1946	8126	A	1971	3	1137	ENIKDSDKMLSFRAHGPEVQAHNKR NLIQHNNSTQTDIFYTDRLEDKPEGP PGSSSFLHKFPFGPLQVCPQACPSA SERLSSSFRSDAS GDRGFGLDVDRGR RPLLPFETEVGPGCVGEASLDKADSE GSNSGGTWPKAMILSSATAVPEKLSVY KKPKQRKSIFDPNTFKRPQTPPKIDYL LPGGPAHSPQPSKRAGPLTPPKPRR SDSIKFOHRLTSSSEATLVGSSPSTS PPSALPDVDPGPEMHASPPRKARVR IASSYVPEGDDSSHLPAKSSCDEDL TSQYVDELGQKRRRPKSAPSRPKLA PVVIPAQFLEEQKCVPASGELSPELQE WAPYSPGHSSRHSNPLYPSPRPSVGT VPRSLTPST
1947	8127	A	1972	2	129	KCKKHPEAKRMPCAEDYLSVVLNQL CVVHEKTPVSDRARPVL
1948	8128	A	1973	143	415	NISLFQFSANPLISLSKLISTTPSKQHN TYFYLFTYLRWSFILVVOAGMQWHN LSSQQPPPEFKLFSCLSLPSSWDYRC PQPHLANYYYY
1949	8129	A	1974	120	406	GEAATQENLAELRPEPELLSPSTVLSR EPELPSPTVLSREPELPSPTVLSRKP DLLSPSTVLSRKPDLASTVLSSKPD LLSPSTVLSRKPDLASTVLSSKPD LSPSTVLSRKP
1950	8130	A	1975	2	111	GTSHSKQACYPLAFGVPAALMAVAL SKWKSVELIEA
1951	8131	A	1976	3	121	RICSPPFMELTSLCGDDTMRLEKNG LTFPFSAYHPSST
1952	8132	A	1977	510	628	GDLCTFSILAEQLREPSFPDVQHGVL IHKVILGSPAHR
1953	8133	A	1978	1	136	AKTSPSPSSSEDEKPTKHHKKGKA LRLKRRFVVVLMALPCIH
1954	8134	A	1979	142	366	EGVRNYLILQPRSLRLNCSFFPNREE ELCHHSSSTPLAADKESQGEKGRLL SQDEGLLLVVEVFVEDVEINTY
1955	8135	A	1980	279	546	WGMIPGQTLVSPETDSAFHPDPDYKAF EDAAEEHPYIPFFATFDSKVLLPAAY LVLPVHLKLSSSFLSQNRWLTWSLPM CCPLNTHQ

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1956	8136	A	1981	2	392	FKALTDSENAIYPSLASKASNNHNTHV GDMRLKCNESPHSTNNGVLNSCLDV RTVIPETSVSSTVSQTMTVHTQTIKT ESSNTINGADVKDSTSLITFTSKSEVD ETYALPATKIIRVETHATATLFSKET
1957	8137	A	1982	3	136	ARDHCDLTKEELEPRVFRDVTVKGID ASDYQTVQLPKGTESSRN
1958	8138	A	1983	3	96	NHFHTGKCLFMSGLEVFQNLHMDH TLPGY
1959	8139	A	1984	1	200	KESNTCASRGLARKPPWRNEGEGRR ARRPRWDPEASPVRRGRITGSPRPPR RGGGARAHVLPGERW
1960	8140	A	1985	134	383	TLFRGRDPWEPPKFSLALGPRKNPRE RAKIKGPAKKPGERKQAPPGQKTA TSQGRRRGRITRPMNTKPEIASAAPA GVTEDP
1961	8141	A	1986	41	444	LAPLGHEIGPEDCRYSEKVTQYINT ADKTRGVKEARLISPEFVHDLKMG GDERLVTCLSLRVSLSNPSVWVES FGHEGLGLLLDILEKLISGKQEVVK KNQHKVIQCLKALMNTQYGLERIMS EERS
1962	8142	A	1987	187	408	SCWSSLPSTETVSRTDSPSKIILDPVR VIAEKVSQVLLRVPHGWGKPRPGHP TECPDLFSAHTPQVQSSIER
1963	8143	A	1988	24	202	KLKPGLIYVFLVQTAFCHVGQAGLKP LTSSDPPASASQSVGIAGMSHRVQCC LRNSCLC
1964	8144	A	1989	2	357	FYGIROGICGKKHSEQVPDILQNAIF NMLNTTNCPSLKDCKPKVIIIQACRGDS PGVVWFKDSVGVSNLSLPTTEEFVD DAINKAHLEKDFMAFCSSTPDNGSW RHPTMGSGFIGRL
1965	8145	A	1990	209	380	SGRKYLQINAYFSSTYTKIGTIQRLAW PLHKDDKQIHEAFHIFKYQKMYIHKF LNL
1966	8146	A	1991	2	86	NKPSGFWMIKSVTTSASGSFESILCPS A
1967	8147	A	1992	261	363	PCFTFFSLALRSFGNALGNCLDKDYL RSLNKL P
1968	8148	A	1993	293	392	YLLKEIKEDLNKQKSPCSWSKILNIV KMATLP
1969	8149	A	1994	1	396	GPAGGQDNYPGSMQWPSPRVPGGH GSQVRGLPIFGFGGKGVSPGGPGGF LLPGSNGLAPLAPPKGGVSLSPCPW APASSPTTMASSSSSSSSSSSSPKLR FSSSSSSSSSSSSSSSSSS
1970	8150	A	1995	160	444	NVTVLSCRMIVDKIDVDKDFVTEGE LKSNIKHAQKKYIYDNVENQWQEFDM MNQDGLISWDEYRNVTYGYLVGKG QDVSLAGITVVLSSQRNKWVWTQ

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1971	8151	A	1996	111	253	NKFFLIFQLEIQNHPPFESLSWADLVQ KKIPPPFNPNVVGIVPNLSF
1972	8152	A	1997	220	350	MLISKSLTVFQPLIFCLLLDMGDEV YDDVDITDFPVSSAEMR
1973	8153	A	1998	3	115	GFCHVGQAGLKLNNSSNLPAASQSP GITVSSHRAWP
1974	8154	A	1999	1	253	DDVWEEDVDVDTPLVFLLSQHLE EFLPIFKREQDLEALLCSDDELQSIQ MQLGPRKKVLNAINRRKQVLQPGQG LVDTSL
1975	8155	A	2000	3	370	GKAFCHRSHLRHQRIHTGKKPKYCD ECGKAFSQSSNLIEHRKTHTGEPYK CQCKGKAQSSSSLEHQRIHTGEPY ECCQCKGKAFCSSALIQHQRIHTGKK PYTCECGKAFRHSALI
1976	8156	A	2001	106	391	GPCPLLRTTPEHRSLSAAAPGAVRPTA GVPIFAELSCCVLMVCVKLKIFHLAL AGLKAGDEILENNRAADALNSSMLK DFLSQPSLGLLVSTY
1977	8157	A	2002	2	252	SHPTSHSPQHLPLTPTNWNSSSTPVDFI FRKAPPVFPWHQHHRAAGPHFSDSH RCSPGGPPHPLTPPVHPHPPPPRETF LRQ
1978	8158	A	2003	252	341	TSFRRHDLMNSTHEDLQDKPASGD QNFL
1979	8159	A	2004	27	330	MRAQLWQTNLSLTDWIPGSMVPFMS RILHAELQQLYGNPQESLDRHLHKVKT VCSKVGGAVILPCHGENMPSTPSPQD MPVLFARPAPCTIRCFCLQKAR
1980	8160	A	2005	171	373	NPRAIFKSVRTCVPVPTQPCRNVKAR SCGVGAGTTSFTLSVWPHRYITQEGH KLETGAPRPATVIN
1981	8161	A	2006	362	493	STYLLLYKYFITKMVMFFSLCRQGD FEKKKKKKGKLPKNYDP
1982	8162	A	2007	248	395	QLHLGYFILKSVIFFDFLMQGLSIVAG SSHKKTTGSKASASPTSTST
1983	8163	A	2008	228	391	GRKGQGLKRPFGHSLPVIPPLCFLRQ AKANLDKNKQTLKENANLAGELRV LGQ
1984	8164	A	2009	577	807	QRVVLVLGRAAAQCSMTMTPGPW LGLPAVPAVTLVKHDDPALVSFHSLG REWWVLHIIGFGGKIQKNTGKSEKY P
1985	8165	A	2010	1	348	DKLRGDISARGAVHISNPITAEFQVAR TTLLPGLLKTITNRKKPLPLKLDEIS DIVVKDSNTEVGAKNYRHLCAVYYN KNPGFEIHLGLDRIMQMLDVPPGED KGGYVIKASQR
1986	8166	A	2011	405	502	LGVLYEYARRHADYSVMLLRLLAKT YETILEK

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1987	8167	A	2012	19	279	KKHQNMVVAWQRGLQGPVVCVTQV GSLPHWPFLFFAGLGNVQIFVKGSN LFKLKVRFLDAKNKVVANGTGTQGG LKVPGVTLLWPPS
1988	8168	A	2013	173	378	VSATSTKICCLFVRSSVWDKQMISL TKSIFFIILFYLLFPRQYKSQFEAQKI WYEHRLIDDMVAQA
1989	8169	A	2014	68	427	AACPGCVHVRATAQVWVWGRCHG APYDSQSSSSSACGCCGGKGMES DTRTKAPPGPSAPGPFPEMQCAGP WAAALPPTLAPHDQLVEIRHQVPTL ARGSHILLPLLSRSSRI
1990	8170	A	2015	182	367	AKDIGLLWNLCRIGNVFSSSDVFFSYL VENKTELCSFGCHGVSKESSSRITLG EQAAALAN
1991	8171	A	2016	1	355	LTALFVELNHKTLILYPSLQAYRLYN SSLPGDSCPDLKLHPATRKDVSRLE ASEDGVSVCSDVPTGLCSLTGLWQ HGISAGLLGTNDNEAGNELMLPDGS MARSLEELSLAWQVG
1992	8172	A	2017	13	197	NCIGLGGAAMLLSCWGLAAVCSITG YTHGRHTLAFMAAKVKYWTQDLLK LNFLCFSRKLDV
1993	8173	A	2018	241	370	QKNTGQRMDDGLPLVISSGLSSEQK MLSELAVILIAKCYTEFD
1994	8174	A	2019	1	363	PVKKAEPHTKDKPYDCPFLLDVRD RDSYQQCHIVGAYSYPATLSRTMNP YSNDILEYKNAHGKJILYDDDERLAS QAATTMCERGFEENLFMLSGGEQGLK VLAQKFPEGLITGSLPA
1995	8175	A	2020	18	364	PKKNLGRGPRGLGDKGVLSVGTNL FFTPKKGAPGKTPPWKKMGPPKKK GSFFPNWGGPKA SSSPK GKSSSPWS SSSQPPPKTKGKTS SPPKGEPLPGPRG NSKGPGRWPWP
1996	8176	A	2022	141	278	SLPDKDGKKCLFLVKCFDKTFEISAS DKKKKQEWIQGKVIFYLP
1997	8177	A	2023	3	360	FFYLRLKQKEMKQDFEEQMALKELL QAAKEEEENFRKTMKFAEDDRIEL MNAQKQRMKQLEHRRAVEKLEIERR QQFLADKQRELEEWQLQQRQGFIN AIEEKRLKLLKEHATNL
1998	8178	A	2024	1	362	DDRALPDFKGIQTSDPNAAVMGLAPE HFHYQILNQAFRLLLDGAFLAIHKAR YYKRKDGSLGPGPFVTALEYATDT KATVVGKPEKTNFLEALRGTCPEPE AVMIGDDCRDDAGGAQ
1999	8179	A	2025	153	287	FSKQKRKGGGRNFQTAHRRNMLKGHL EKEAADRRKKQEEQMETEQ
2000	8180	A	2026	199	377	TALVQPSLSMTPEVKDVGFGSLVIPS GSVASNLATSALPTGNVFNAPTKQAE PEEKVP

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2019	8199	A	2048	1	129	VSPKVVPPQMGDHEVLTKGIQKFPGIN YPVLTPNLKGFEAAVRG
2020	8200	A	2049	2	349	GNFEALRQIQYSRYTAFSLQDPFAPT QHLVLNLLNNAWRVPLKVSALLMSI RLPPLKQNEVANVPSSKRARIEDV PPPTKKLTPELTPFVFTGFEPVQVQQ YIKKLYILGEG
2021	8201	A	2050	174	324	KNSWPGAVAHACNPSLGGKGRQIT RSVDRDHPGQHGELPLPKTSQPS
2022	8202	A	2051	94	289	VARGRPVDECCRPQAQCPVSPSC THE LRCAPTQEVDAEIQVQVCLYAFDLI YLNGEVSSSFLPL
2023	8203	A	2052	85	340	LGRRPSCPAVDMTSDIDTANNRLI SE DLWSVHCGFLRTAQSMRPFKQVICV LGSPRFTSGHHYWEWTLHSSKKQA AVPSAQTI
2024	8204	A	2053	90	363	GHHRIFYSQVYLSHFFCVSFFSLTPQ AKFLPNSGDSLTAMCARDQVVRVAK LSAATQCKKNTKRVAQHKGASHKVSK TLLQNLCPNPPLWF
2025	8205	A	2054	2	350	KDCFITYQGHHDGVDGAPIADVILPGA AYTEKSATYVNTGGAQQTKVAVTP PGLAREDWKIIRLSEIAGMTLPYD TLDQVRNRLIEVSPNLVRYDDIEGANYF QQANELSKLVNQ
2026	8206	A	2055	1	348	KDPESFFKVLMLKDLGLNFHVSVL GETFTDVPDIFSEAKKALGSSVLHWG YLPKDDYFQVLRMADVISTAKHEF FGAAQLEAVYCGCYPLCTKDSICYPEI FPAEYGVSTPEQI
2027	8207	A	2056	1	125	ENYRNLYSVGLCISKPDVISLLEQEKD PWVWIKGGMNRGLCP
2028	8208	A	2057	333	27	PNTASSPASSSSPKKGGFGFFPKGALN PNPKGNNPPGPPKSSQKGGTPRGPI FKGGDRGGTFPGQKSPSGTEGGWKL ALIFG
2029	8209	A	2058	13	109	NAVESWRASGETALRAYVKKHYPNG VCTVSHQ
2030	8210	A	2059	1	342	VAAVAATALKGGGARNARVLRGILA GATANKASHNRTRALQSHSSPEGREE PEPLSPELEYIPKRKGPMPKAVGLG WAIGFPCGILLFILTKREVDRVKQ MKARQNMRLSN
2031	8211	A	2060	1	345	HDHLLHLIHFFFIHHHCHHHNHYS SSSSSSLSPPRS
2032	8212	A	2061	2	481	VYGVKYYKSFRTGLYTRFQGVYL PLLWQSFCKWSPALGYTRGHFSAL VAMENDGYGNRGAGANLNTDDVT ITFLPLVDSEKLLHVHFLSAQELGNE EQQEKLLREWLDCCVTEGGVLVAM QKSSRRRNHPLVTQMVEKWLDRYRQ IRPCTSLF

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2033	8213	A	2062	51	662	FIQFYQEIFESPFLTGETYYKQETSSSSSSNCSQYMEKV
2034	8214	A	2063	242	377	LMILSLGGPELIDPAGLPLPQAQSWVWLVDLERTIALIGRCLG
2035	8215	A	2064	160	341	GPGANLGSLEFLPPGLKGIPRPTPKNWYDVRTSSSLIFVLKKTGFSL
2036	8216	A	2065	3	149	PPCCLGIFPKGEKRIRVQTLGLPVVLA LKDVFFGGDVPAISGVLAHMG
2037	8217	A	2066	291	575	GFQLPGPGLSLDRISGPTHSPGKLSALK GWTQANQINDLRQSVIWLGDWVVSLEHRMQMCCNWNLTDFCIIPYSYNETDYSWEMVKGRLGREDNL
2038	8218	A	2067	180	378	SVTMTLTKGSFTYSSGEYRGGEWKEGRHRHFGQLMFADGGTYLGHFENGLFNGFGVLTFS DGSRV
2039	8219	A	2068	3	82	RKYSDASDCHGEDSQAFCEKFSGGV G
2040	8220	A	2069	3	230	ISRAFATMGETVMSVKIIRNRLTRIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAQETEAQGIEITCPRQHR
2041	8221	A	2070	235	363	RPLFQLFWIEFVMRHKGAHLRLVAAHNLTWFGYHSLDVS GFL
2042	8222	A	2071	3	128	TPNVRRTKRTRKLPLEYWRGERIDYQGRPSGKTYLCYNICQ
2043	8223	A	2072	1	353	LLCVGHRTSRISFLLSSAGAKKPMRDCGCMVSSGSLSSLKAAERTPGALFFSSSTPGRYYNYDSSSRPQRSVMSDQCAGQWFLKACGLGEGDTEVREEEQPERKMGFPWRWEVSI
2044	8224	A	2073	140	356	IWGVKEKLFVFFAVPPNGLVVCYGTIVTEEGKEKKVNIDFEPFKPNTSLYLC DNKFHTEVRSQTQNFIAF
2045	8225	A	2075	85	340	LGRRPSCPAVDMTSDIDTANNRLIISEDLWSVHCGLRTAQSMRPFQVICVLSRPTSGHHYWEWTLWSSKKQA AVPSAQTI
2046	8226	A	2076	107	350	GKERNAGPNFHLFIPELTRTSQCLSV CVSDLGMFAPTQRTGISTSHITRIVDYDVYARRNLQRGYTAKELNVSEIN V
2047	8227	A	2077	260	407	PEALRGLAFOENVNSLVAGFEFLKN APNDASDYDAVRQGVLTGLAK
2048	8228	A	2078	3	243	SGESVELLAHDSVVMIRKGGDQTSLLVVDKETDNMYRMVSNARPIYHALRLGPFTHDLNFCSELGLCSSNWKRHIT HH
2049	8229	A	2079	204	308	QPGLLGVPFKLIASKANDHQGFYLLN SIEHMP

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2050	8230	A	2080	2	273	QALWLSQLQKQDNGCRSSGSLNNA IKVNHSGASFDLSIMISARMRIGSDNV KNSKGKPKQKIKPGWHQKRGDRTKV DCDTLSYRDGGY
2051	8231	A	2081	224	428	SIDGMPSLQHTTPPGMTPPQFAAPTQ PSTPVSSSGQTPTIPGSPSATQIQS TPTVQAAAQAQVTPQ
2052	8232	A	2083	98	408	PSTQIAPIHGQTTSI.PNSLLIIPFFSI LLLFQCQLIYEDSMDLIAKPCVAAKIY RNLYREGSGIGAIDFNL.DWSHNFTNM LG.YTDHQFTLTRL.YLTIHS
2053	8233	A	2084	61	417	FIPVSPN.VLSSIGYPSLQVELETPTGLH YTPPTPFQDDY.FSDISSIESPLRTPSR LSDGLVPSQGNIEHSADGPPVVTAE ASLEDSKLEDSVPLTKMPETVDVDES QLGECMSLEAE
2054	8234	A	2085	93	242	NCDSASPVYDCILALRAGANLKNLM YHAQGAFGRTL.GFQILQDPDFGSGTKI
2055	8235	A	2086	1	355	PKSQSIKEVANLNLIKIRDFCAKSDTK KMKRHVTDWEKIFANSISEKRLVFR YKELSSSSSSSSSSSSSSSLGSRH FLKHKQTKTRVTNNHMKKCSAPLAI
2056	8236	A	2087	79	202	GITLHTVIYIYFFFFYFRERNLAILPRL VSNWSAQTLPPW
2057	8237	A	2088	31	235	YGLLVSSGLTVTAVKDSGEWNLEAG ALVLADAGLCCIDEFNSLKEHRTSI HEAMEQQTISVVRIGKR
2058	8238	A	2089	310	736	AKSEGLAKQICKVVLDFHEKQYSK ELGDAWNTVREILTSFSCWQYAVLL NRFNYPFELEKDLHLGYHTLSQGS PNYPKSKCYLSRTPGRIPSERHQIGN LKYYLLNAASLLPVLALELRDGEK VLDLCAAPGGKSLA
2059	8239	A	2090	403	5	FLSLFETESPCVAQAGVQRDLGSV QAPPPG
2060	8240	A	2091	194	352	KHSFCAPLGSTYAKIGKIQRRALWPL CKDDTHIYEAIFYFILMKHSKKRIILPL
2061	8241	A	2092	194	358	KHSFCAPLGSTYAKIGKIQRRALWPL CKDDTHIYEAIFYFILMKHSKKRIILPL FQ
2062	8242	A	2093	174	324	KNSWPGAVAHACNPSTLGGKGRQIT RSVDRDHPGQHGIEPLLPKTSQPS
2063	8243	A	2094	83	365	LPVNSAGKTRVLFPVPAQQCPGHLP EDLPASGPLPSHHCCGGAPSSPSCT AVAAASWHQVCPPTTATRAVFLKPSS DGGALHVTWLHAATRI
2064	8244	A	2095	1	117	WKGMKFSFFPFTQVKIEQELDKLS PHKIKHTKKVCCN
2065	8245	A	2096	2	154	ESQSVTSADPGFQVPISKAVQLTTN DAIKTLLVELDISVSKCIYFSAQ

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2066	8246	A	2097	1	394	EEFVCKVWEGRWKRVPHDVLDPWLK DNDLLHGHRRPMPSLRACFKSIFRIH TETGNIWTHLLGCVFLCLGIFYMFRP NISFVAPLQEKVGFGLYFLGAILCLSF SWLFHTVYCHSEGVSRFLSKLEYSG
2067	8247	A	2098	2	193	RNGVSPCCPGWSLIPGLKQSTSLSP E CWDYRHETATGHAFFLNETNDNVK VCALVLLKER
2068	8248	A	2099	3	121	FCLGLFLFPQALSGRQIHVIDMDTID VSNLNRQFLR
2069	8249	A	2100	3	358	ARDELTFHLSQIAAIVEMQELKNSTN SSSFLSDEIRSLGQLSSSRAAHLSDV PDQLPGSVLSPPPPLPQFSSLPQPC FPPVQPGSNNICSDSNPATEMSKQNP AANKNTYSHHS
2070	8250	A	2101	2	338	TTRPLQSILLTHTGLCPPTALLGSP YKSLVSQPCPFRSRLSPCPRRSPRGDV GRVTPGAPHSITGPSPLAAPSWSLGS LGSHIQGPGPPSPRPRQLSLGDYGL VTP
2071	8251	A	2102	219	308	TSFRRHDLMNSTHEDLQDKPASGD QNFL
2072	8252	A	2103	2	92	TDMRCRTTFYTALGRLLMVDLGTGR NRSGS
2073	8253	A	2104	102	382	GGRDPSIIHWDTETIKLSILKGHHQY GVSADVDFSADGKRLASVGIDDSHTV VLVWDWKKGEKLSIARGSKDKIFVVK MNPYPVDPKLITAGIKH
2074	8254	A	2105	1	295	NAYILKKSRIKRPPOVPKPKPREWKNP ESQRGLSGTQDPFPGAPVPVVEVGQK FCRIDKSRKLPHSKAKTRSLVEAEA VEEETSIIKAARSELLAEP
2075	8255	A	2107	252	386	LFIIVSCSCLFIADLLCVSVTEGADLSL RLVDGVTECSGRLEVLVP
2076	8256	A	2108	1	396	KINKMKTLKRKKLLNQLSSSVSSN KKGKVSQKLHNTVSSLAATFGSKLGQ QINVSCKGITYIGKRRGRPKPTVLNGI LSGSPTSLAVLEQTAQQAAGSALGQI LPPLLPSASSSEILPSPICSSSGTSG
2077	8257	A	2109	3	153	KNSAREPYSSSKYA TDLSSVALNRNF NQQVRPVS VIRK WQRRVLLTCC
2078	8258	A	2110	249	356	LFFSEMFFSFKVKKTPSDLFLEVPSAT SLQICKDVM
2079	8259	A	2111	151	321	LKIFQRPRESKPESQIPPQRPQRDQV REQINIPQRPGRPSKSSSEGRFLVWG IIR
2080	8260	A	2112	638	790	DNLAAGSRGCREQRLCHCTPAWATT ARLLHKKKKKKKGKGRGAQLWIPV I

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2081	8261	A	2113	1	358	PKSQSIKEVANLNKIRDFCASKDTIK KMKRHVTDWEKIFANSISEKRLVFR YKELSSSSSSSSSSSSSSSSSLGSRH FLKHKQTKTRVTNNHMKKCSAPLAI
2082	8262	A	2114	146	315	NEGSPRVKVKNLIESMQINGSVLKNG SLTNHFSFTSSPARVAVLISGTG
2083	8263	A	2115	33	187	FWFQYHINKLSIMTSENHLNNSDKEV DEVDAALSDLEITLEGKTSILVG
2084	8264	A	2116	2	465	SLNEIYSWIEFITERHPDMLTKIHGSS FEKYPLYVLKVSQKEQAANKAIWDC GIHAREWISPAFLWFIGHTQFYGIIG QYTNLLRLVDFYVMPVVNVVDGYDYS WKKNRMWRKNRSFYANNHCIGTDL NRNFAKSHWCGRLLALFLAMSLH
2085	8265	A	2117	3	591	PGRFRGGPGQVMSAQQSSPVLG LINSVMKSPMTQAGLTSNMGMGTS GPNQQTQSTGMMNSPVNQPAMGM NTGMNAGMNPGLAAGNGQGIMPN QVMNGSIGAGRGRQNMQYPNPGMG SAGNLLTEPLQQSGPOMGGQTGLRG POPLKVS TVLVCVHNHRACEYCHDG WRVCLTLYSSFHYYTPGIYCAVIS
2086	8266	A	2118	1	358	IKDLYTYNNLAVESTSRTKQFLFGLH FLAKNFIFSVMGLALFTFQKHVFSPIFI IGAFAVAIFLGRAAHYPLSFFLNLGR HKIGWNFQHMMMFSSSLKGAMAFAL AIRD TASYARQMMF
2087	8267	A	2119	3	96	CISKPDVISLLEQEKDPWVKGGMNR GLCP
2088	8268	A	2120	3	149	LPFLSFLHSHPLPKPQALPSLQQPPT TAVANPPSPQPPPEIPQEL
2089	8269	A	2121	197	386	WGRPWFCCLGMAETVDITSEMVNG ATEQRTSSKESSPSPYSRDKAKTGL PAQSAATLPART
2090	8270	A	2122	188	388	TFIKFACFSIGAHIQFLNFSTEANHDFL EIQNGPYHTSPMIGQFSGTDLPAALLS TTHTLIHFYS
2091	8271	A	2123	2	393	TGPADFSRHLADAALLVPTPIPLLPR LATPHSSPTSSCVPSGSPSCPLSGLS HLPSCHRPAILCLGLPCSLQTPNACL HTGPPHPSYRITSLPEAVGIRSESHQP PAQALRALGPQWVSGENRRW
2092	8272	A	2124	1	371	IKDLYTYNNLSVESRSRTKQFLFVLH FLAENFIFSVMGLALFTFQKHVFSPIFI IGAFAVAIFLGRAAHYPLSFFLNLGR HKIGWNFQHMMMFSLGAMAFAL AIRD TASYARQMMFTTTL
2093	8273	A	2125	299	368	FLFRYLLGVQEQQCVDEGWSTA
2094	8274	A	2126	190	404	SLLTVLTRSCDKNSPKDLLFMNFFVA YVDQNLGELLHPLGLEEDKAFQIEIG LKTWGSCKLYNRNPMGWAES

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2095	8275	A	2127	2	398	ARAKKPQAPSNNASSLSASLNPVGKN TSSPALPRTAPCISESPRKCISPTPK AKVIPAQNSADLPSTLLPNKCSGKT QPKYLKHNHISRDNAVSHLAHSNS SSKCPKLPKANIPVRPKPSFQSSAKM
2096	8276	A	2128	310	397	TCVLPPQVLYPVCHVRNMLWSAV YLPC
2097	8277	A	2129	44	428	RLKDKFWNFIFYKFIFIGVLNVQTV EVVMWCLWFAGLVFLHLMVQLCKD RFEYLSFSPITPMSSHGRVLSLLVAM LLSCWGSLAAVCSITGYTHGMHTLAF MAAKVKVYWTQDLLKLNFLSRKLD V
2098	8278	A	2130	2	460	RIRHEVLLYVCAHTAIYNVFRNNQY HLQGHANISCLCVSEDRRWIATADK GPDCLVIIWDSFTGIPVHTFIEDSCPEGN GIMAMAMTHDAKYLATISDAEVQKV CIWKWTLAVETPACTLELPEYGVQ NYVTFNPTNNKELVSNKTRACI
2099	8279	A	2131	1	423	DLVLPGSCQDPACSDKAPGMEGTAA LHGDSAPRPQQAKEQGPGERPIPVGD GKVSVSFPPEPDETHDKLQHLAPEE LHTDRESRPFGPSMLPSGPKKEAPRV MDKGTSDETRGAEGTKRSQPDIGLW KAMPSLIQTDGW
2100	8280	A	2132	60	212	YWEDFEYILDPEAKKPDNWKEAMDG EWEPLMPNPKYKVRGVSLNGCEK
2101	8281	A	2133	1	327	DVRTLHQWVNGIRIAKYGKQLYMNY QEALKRTESA YDWTLSSSSSIKSGSS SSIPESQSNHNSQSDSGVSDTQAGH VRSQISVSSVFSEA WKRGQTLEBSSK VTASF
2102	8282	A	2134	2	145	GMPIFLVSSATLSQVLFHPNLSGAAG EFGALQTVRLERYKAFYITGE
2103	8283	A	2135	30	400	LFLPPISTVTHITLPSPEKPGPLCSLHL PLPSDAVSSVPGYGFVDFDPSAAQK AVTALKASGVQAQMAKVRVLPHVC SSKGFVVSTKVPVLRFPPEGLRTMKLS GGQLSVVLSRQSMSTPGC
2104	8284	A	2136	1	69	DAHEWMNEIPTVPTYYPAPKQPQE
2105	8285	A	2137	1	340	RHEAVSTCCSDGKLYDAYVSYSDCP EDRKFNVLKPKQLERRRGYKFLDD RDLLPRAEPSADLLVNLSCRRILVVL SDAFLSRAWCSHSFREGLCRLLELTR RPIFITFEG
2106	8286	A	2138	216	367	LCDIFCAHLISKVYFIFILRFLYEYARR HPDYSVLLRLRAKTYETITLEK

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2107	8287	A	2139	2	627	PAPRHITVDVQLFREDNPPEPSKEITSH EEGGGDVSPRKEPQEPVCPTKIKPNL SSSPRSEETTASSLVWPLPAHLPEEDL PEGGSTVSAPTASGMSSPEIVSREESP QCSNQSSPMGLEPLNLGKAEDNQ ISAEVESGDTQELNVDPDLKESSTFTD ENPSETESEAAAGGIGKLEGGDVK CLSEKDTYDTSIDSLLENLDK
2108	8288	A	2140	3	630	VDPVRVPRVRAPLSSDGLIVSRPSDL LSMMSDEKNLGVSKLVSPSRSTSC SSKQSGRQDSWEVVEGLRGEMNYTQ EPPVQKGFLFKKRWPLKGWHRFF YLDKGILKYAKSQTDIEREKLHGCID VGLSVMSVKKSSKCIDLDTTEHHYHL KVKSEEVFDEWVSXLRHHRMYRQNE IAMFPHEVNHFFSGSTTIDSSSGVVDS IS
2109	8289	A	2141	3	364	LNTLILPKDKDITRKENYRPTILMNID KHLARLRKKERQHKIRDEKGDITDDT AKIQKIISGYEQLYASSSSSSSSSS SSSSSSSSSSSIQNLNTPNTNKIEAIK SLLAKKSPG
2110	8290	A	2142	2	182	HCDMVITYGLDQLENCQTCGTDYIIS VLNLLTLVCELFFSFLMCWFQALKW ICKKLAL
2111	8291	A	2143	2	169	LFQYPTDEGKVEDFTLVERAHQSGV GIPFLWGVRRGVSQLVSVYLSLSF HVP
2112	8292	A	2144	3	152	PKGQTEHDEGMLEYLEDIIGCGRINE PIKVLCCRREILNEHREKGVNHL
2113	8293	A	2145	2	356	LISSTEGHGLCVSPLSRSPGSHANFL MTPLSPTGTQGSFPCVGSLEEDSPFP SFAHKLVRGKAKADAWPKTAPKKD DNSLNSPAPVDRDGEDSDNSYRDPVPR FOKSFQAIDTPLM
2114	8294	A	2146	1	392	RTRGRGRKMATPLGWSKAGSGSVCL ALDQLRDVIESQEELIHQLRNVMLQ DENFVSKEEFQAVEKKLVEEKAHAH KTKVLLAKEEEKLQFALGEVEVLSKQ LEKEKLAFKALSSVSKSVLQESSKK DQ
2115	8295	A	2147	3	472	FSEYLTKKTLTPNLQHFLHSIAMTS ESSCTTIDGLNATKNFLQCLGRFGNT FLFPLYGQGEIPQGFRCMAVFGGIY CLRHVQCFVVDKESGRCKAIIHDFG QRINAKYFIVEDSYLSEETCSNVQYK QISRAVLITDQSILKTLDDQQTSIL
2116	8296	A	2148	80	407	VLVSLCGTDSPPNPFGSHSVSGEAG GYLSWGDASDCFIVGASGAEDRVPE VTRKPRLSATRVGRTEVPRRRLK PAAQDKWTSQQDPDHPNRLLRQDP DASES

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2117	8297	A	2149	1	393	SKANLSGGVWKDNINMALVVDITY DDQLISCGSVNRGTQRIHVFFPHNHTA DIQSEVHCIFSPQIEEPSQCPDCVVSAL GAKVLSSVKDRVINFFVGTNTINSSYFP DHPLHSISVRRLLKETKDGFMLTDQF
2118	8298	A	2150	140	270	VFFFLRWKPFEPKASHKKVDFVSV SQSHPHPSYCPLFCGE
2119	8299	A	2151	87	373	MRNGCAHPKGETRYSICLSVLQAG NLVSIQCEPEGNSCSWQVTVRNFKAE NITLLTFYLLTFAFFSLFSLPQDCFTS FSTGSFFELDGRPFCE
2120	8300	A	2152	27	219	AFCKNPTATITPAGESLNSFYLKSGTR QSQKLIIDIVLEVLASGPRHDEEIKVMQ IKKGKILTL
2121	8301	A	2153	2	344	SNLMEKFKENLRILSSPWTQVCHNFP ALIEYFPGSHNKIAENFAYLKRYVLE RINEHQESLDMNSARDFIDCFLNKTE QEKHNQQAETFVESLIATVTDMDGA GTKTSPTSRY
2122	8302	A	2154	1	602	QVLNYLSLRATEQEKAAMDSARLSA AKSSPMMETINMCLQYLDVSVLGL VPRLCILIRSGVGLGTGGCASVIVSL TTQCPQDLTPYSGKLSALLSGLTDR NSVIQKSCAFAMGHLVRTSRDSSTEK LLQKLNQWYMEKEEPIKYSCTALTIH AIGRYSPPDLKNHAKVPLAFLGM HEIADEEKSEKECNLWTEV
2123	8303	A	2155	2	180	LVQGGQLNPYLRKVRDDHIDDALV RVSWAARLKPNGDMDIQSEFILKV TEKNDTI
2124	8304	A	2156	8	151	SRSAAWHEVEKKERARLKTQKFHART GMIESNRVSGDPQGNQPVGKEG
2125	8305	A	2157	93	436	GIVGELLEENITEFLMEGCRFITPAH YSDVGDERSIVLCGYPLCQKKLQIV PKQKYKISTKTNKYVDITEGKSFCSNF CYQASKFFEAQIPKTPVWVREERHP DFOLAKGR
2126	8306	A	2158	2	423	SSPSRSTWVCEMQASGSISGGEFVAV VGLAQFLRGPMDIIFYAGLARARA SANRVASLLATGEAVIPASDPAPLNH AEFLLTRDVLVLAGASPDLDVKRGEI IGIVTENAAWADALVDALARREPPS GTIHLGPRAK
2127	8307	A	2159	3	291	EPPGKPPFKPFARRJGCPQPTIHPHS DSPSTRPPARPHARPVHTPARPSTCL TVRPHARRPSIWPSTDVSRPQYSLSP STSLALPGQSCGLR
2128	8308	A	2160	3	332	HIHAEATLLFLFGEKGDVIYAIPSC WPLGTIIPSCVLPRITELMGKFDEG KLPDTPHMLGLAIEPVAHDYDVIVI DSAPNLGIGTINVVCAADVMIAPPPG ELF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2129	8309	A	2161	3	423	MPWFRATLAQWRYALRNPIAMCLALTVAYVYLNLDPEYWAMTSAAVVSFPTVAGVSKSLGRIADSLGALAALLAGHTLNEPWFFLLSMSAWLGFCTWACAQFTNNVAYAFQLAGYATAIIAFPMVNKTEASHLWDIAQ
2130	8310	A	2162	163	335	VNKSANYGVLDKLARGYADLSKAEGSSSSSSSSSSSSSPTIHASELRSLKSSRP
2131	8311	A	2163	211	357	RNNPGIPLLGIFLKGKWMCGRGICSLVFVKMLFTTANTHNQQAHQQR
2132	8312	A	2164	1	341	GRGWDTVFSNIVQAVSQTFGGIWLWQIVLALVTLIVAMHIFRNPRLLLFMLTTAQFILLAGVGHATLNEGVPAKIHQSNHAIHLICAAWFGGLLPVLWRMLQIKDRWRLQ
2133	8313	A	2165	3	140	TDSMAVRRQRDTWQNPAGTQLTRLAQGESFPSLHILTPISIALLY
2134	8314	A	2166	2	268	RQITNMFIRCIAGHMLGSRDGDSPVSTPGAERALLSGEGSFCTSQQRWPTTPAPAKQLGAPPPADWKPRLPQGVWEYRPKPSRAPWS
2135	8315	A	2167	56	336	TLKWAVLYFLPLTNLDQAAAHWDTSGLQRLILKKDELRAADCCRLQFQPGKQDKLPVAKLRNLLGQCWERKWLFVMTCMFFGLLSLSHRQNE
2136	8316	A	2168	3	128	TPCGHCRQFMNELNSGLDLRIHLPGREAHALRDYLPDAFGP
2137	8317	A	2169	82	324	KSKLVVAFKGOVPAVYGSRHMVVFPPNSLIQIGSCTHQMGOIAIVSFQNSTPKVIECFNVESRILCMLYVPLQHKPTYF
2138	8318	A	2170	3	131	FARRNNLSVSAPODIGVLRKLKYAAFEALTEKVTLVNPHISP
2139	8319	A	2171	2	181	KRDIWTLGLFSEFPVVFQYKSMVLDAYSEYVNNFSTAVAVLKKTCAKPAFLEFLKVS
2140	8320	A	2172	12	168	FLSEFPVVFQFFKSMVLDASSEYVNNFSTAVAVLKKTCAKPAFLEFLKVS
2141	8321	A	2173	180	354	KGFEPDVRILLTKYSNSNGSQPPWMEQIRDAWGSVMVKNVRETDEVGKGQIRMRTV
2142	8322	A	2174	3	406	SDRQMPAVARLWRLFTNMTYIDEFSELHGKDVVPREALAGQVPSACVGTCFIRLAETALLADGDGIAFHARLITDYINIGFRLKEKGVTEIFGRFSEVDEAIEHCAFLQHARTFNMICVREYFPDITFSTAGP
2143	8323	A	2175	1	80	IERYQLPQSYQRMPPDFRRRLQGCNVN
2144	8324	A	2176	1	181	SWTTLVLEQIDDMHDYYARYLPQMALAVSVPLVNNVAIFPSNWAAALILLGTAPVIPVVK

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2145	8325	A	2177	2	380	CYTTKEGIVTGDGIGMAISHGVPLRN MKLVQYHPAGLPGSGILMTKGYRAE GGILVKNKGATAYLQDYGMGPPEPLG EPKTKYMDLGPDKVSQLWHEWR KGNITSTPRGDDVYLDRLPLGEKDLQ
2146	8326	A	2178	2	93	RGCGEGLLEAANNVVEELETAKLIFIL GDR
2147	8327	A	2179	2	93	VVCGERGQEAANNMEELEETAKLIFI LGDR
2148	8328	A	2180	2	290	GVTCPPYPIFGTKTLAVTCLVFLQR TTLRLFHTETLKHLDINATPVHNM LPKGKTLGRGPGMGQPGTVDVGAER CQPTLSLPSAGHCQSQAAR
2149	8329	A	2181	3	151	KGFEPDVRILLTKYSNSNGSQSPWME EQIRDAWGSVMVNNVRETDELK
2150	8330	A	2182	2	355	LDDWKFRDWMQOLDEEIRYSMRAT VNAQTRDRRGVQPPPTTWIFNATKG QLERRIVRMETGMAWTEDPSPRTRH LISNCQISETVIPNVFSVRVNYLLCRA QKERDETFYPPTRFHK
2151	8331	A	2183	1	106	AKVTDIGRRQTFTNTAIAIMELMNK LAKAPTIDGE
2152	8332	A	2184	66	421	DSRKKTTLGGTMPSPSASAVTTKPV DQAATQTTASAEQATTVDTIASVAAP VDVSAQVTAAVAENSRLMILNCD EAKGRESQARALAEPTGMTVESQAQRI LHAAPQRAQMRSDTA
2153	8333	A	2185	3	107	PILNNLSWQVNPGEHWQIVGPNAG KSPILLSLVTG
2154	8334	A	2186	1	80	IERYQLPQSYQRMPPDFRRRLQVCVN
2155	8335	A	2187	1	80	IERYQLPQSYQRMPPDFRRRLQVCVN
2156	8336	A	2188	3	351	FRLYENLAGMTGTADTEAFESYIYK LDTVVVPTTRPMIGKDLPLVYMT AEKIQAIHEDLKERTAKGQPVLVGTISI EKWELVSNDLTKAGIKHNVLNAKPH ANETAIVAQAGN
2157	8337	A	2189	3	91	VRYWPDQSQIDDAFAHLVRNLADSPI PLP
2158	8338	A	2190	3	211	TLRLFDITETLKHLDINATPVHNMPL GKGTGRGPGMGQPGTVDVGAERC HPTLALPSAGHCQSQAAR
2159	8339	A	2191	119	354	KASPGMQNTIFLGAVECTORMRSFPG HPCQETTQTPPPVASRPTAAAPPLPS PPDSPQLRALPAPSRAMWPAPGFV
2160	8340	A	2192	1	149	LACLHGARGAEGGAWLAWEFDPDH CFSGQMEDKLAWERHTEERISRAP
2161	8341	A	2193	3	287	LMRYVQEQRNGSGIHCITSRAKVEDP GARLQSKVISAPAYHAGLENNVRAD VQEFQRDDQLQIVVATVAFGMGINK PIVRVVFHDIPRNIISP
2162	8342	A	2194	1	95	SIGDAHSGYPVMNSSFPSNSTLTPTP LNDW

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2163	8343	A	2195	6	274	LWAVSLAALGYVVIYQGLSQQSVLF AMCETNTSEASECLSPKFSLNIVLIAL AYTVEAGLWSTLLRPVYITKPRWRHD VTFVLLYGLLD
2164	8344	A	2196	1	199	RVPKTKTKKAPGLPRELKGSHLTISN GVSRGAAFRVASSACFRCPDVEGSK VWPLPLPRALILP
2165	8345	A	2197	1	80	IERYQLPQRYQRMDFRRRFLQVCVN
2166	8346	A	2198	1	144	AEVGEPYFGDGTGFHNKVELENVLL HKLPLVKRLHLIDGSPALVPTVY
2167	8347	A	2199	3	161	TASWGANKLQFYEPRTHTDSSLSKAIH GIVAAARCGLLTQSYQFWREGTEIDLGA
2168	8348	A	2200	3	344	TKQVDYVPGTPCKPQDQNGIWTIVQ AHEWKGYYVARADFEFRNGEMKMN YQLIPVILKKKYVTWEDGKSERVLYTP ELAENQQMISLLSPFHNDKQGLGLKI GETNGRLAADCD
2169	8349	A	2201	3	101	FMDWLAVQYISALNIIYMRDKYRY QHCLIALH
2170	8350	A	2202	9	345	GNRQAWGIHCPRRERTEPDQAOLHT HRSRPLICPGKRSEPNPVHLSWRS RPSAVLVGRGQSRTPPTCTPTGAEPH LPWEGEDRAGPHLPALLQKQSLSCQ VEGTVPRTTR
2171	8351	A	2203	3	110	QNDPDAEPYWRDVGTLLEYWKANL DLASVVPEDLMY
2172	8352	A	2204	3	349	RKRSGERFDSLGNKNALFGHQAQSVY EDLRDISVKGVLVDIGFDGHTVGGGLAV GEPKAYMPRIELHVCQIPADNPRYM MGVGGPEDLVEGVRRGIDMFDVCVMP TRNARNRHLLVS
2173	8353	A	2205	1	118	YLPTADLKPGLPLLEVGNVWVLPV EMSIHISVSSGEV
2174	8354	A	2206	12	107	LRLRRGEIMALLGENGAGKSTLIKAL TGVYHP
2175	8355	A	2207	1	106	KREQLLEVGDFLKKLSPKPYVMLFDL HGMDERLRS
2176	8356	A	2208	1	281	DNGKKPGKILMSGGRCNFTNLVY DPGAYVSNQPHFCKSALARFTQWDFI DLVNKHGIAWHEKTLGQLLCDDSAQ QIVDMLVDECEKANVTF
2177	8357	A	2209	2	116	KYMARTTHEHAKAGNIINALKYAKG EFVSIFFCDHVP
2178	8358	A	2210	3	115	NEALKIREGDAKEIISIKNSIAEMKDA EIERSNKLLS
2179	8359	A	2211	1	347	SKPLLLPSRHKMNLAALVVSFLQIV FVRTDSVGLQVLLALLIMTALVYG WHLVASIGGADMPVVSMLNSYSG WAAAAAGFMLSNGLLIVTGALVGS GAILSSIMCKPTHRS

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2180	8360	A	2212	81	344	PPQKKKDALCPSALKASIVSCSLPFGP ESLHRFCAVPLSSMIPYTHFDVQFLEK FGVTFMREGETGTLKCTMLVTPDLKP VHPRAQVD
2181	8361	A	2213	3	170	GFIKDIRWLFRRMPASPQRNLMLFSA TLSCRVRELAPEQMNNAEYIEVEPEQ NPA
2182	8362	A	2214	2	129	HLMLRLAIETVAHVYDVVIDSAPTL GIGAINVVRPADPPATP
2183	8363	A	2215	2	290	GVTCPPYPYIFQTGKTLAVTCLVFLQR TTLRLFHTETLKHLDQINATPVHNM LPKGKGTGRGPMGQQPGTDVGGAEAR CQPTLSLPAGHCSQHAAR
2184	8364	A	2216	1	99	VGMGLDGRTLVTKNFRLHLPLHTM GPATDPPP
2185	8365	A	2217	1	371	LRELEDHNRELLNPATTRELTSLVRN LNRLKSERERYDKYRTITLDVTHSL KTPLAVLQSTLRSLSRKMSVSDAEP VMLEQISRSQQIGY YLHRASMRGGT LLSRELHPVAPLLDNLSTA
2186	8366	A	2218	2	78	AFRNTTFDGLVAAYRESTKALVEGG
2187	8367	A	2219	1	147	DEANRLMDMGFAHDIEHAGETRW KQTLFSATLEGDAIQDFAEERLE
2188	8368	A	2220	13	164	GGGLEVGAGAANEKRVDALVAAGV DVLLIDSSHGHSEGLVLRQIRETRAKY
2189	8369	A	2221	2	365	STYYSPDFKKNFYTLTSFNELADNFG VTAGLSRRQSDIIAADYVLNDGIVSG RAQYKNVIDAALSKEFTWFASAVFTH DLTLKYTGSSRDYNTSTFPQDFREM GKSYGLAWDMDTQFAWA
2190	8370	A	2222	1	348	GREPSLHRSLLPTLSAIAELHLLSEN DAEQLRVAYLFLRLLEILLQINSIDEQT QTLPCDELNRARLA WAMDFDDWPQ LSGALTAHMTNVRVFNELIGYDESE TQEESESEQWPH
2191	8371	A	2223	1	97	VEYFAHVWQPIQACIDRGMNTEGVF PAP
2192	8372	A	2224	3	256	VIGTGAPKIVVSLMAKDIAVSKSGALA YREAAFDILEWRVAHYAALSNVESV MAAAKFFRETMPKPLFTLPQTKNV DDPVYA
2193	8373	A	2225	1	346	ESRGYTVFIFNRSREKTEEVIPENPGK KLVPYYTVKFEVIESLETPRRIILMVK AGAGSDAAIDSLKPYLDKGDIIDGGN TFFQASLGRNRELSAEGFNFIGTGVSG GEEGALKV
2194	8374	A	2226	3	93	GLVEQTNASLLNEIANKDSKVITQR VLLA
2195	8375	A	2227	2	337	SANDVNKISSINDLRRVLSAITALNF YHGDVPSVMIRIQPENMSPFIIDISTGE HDDYLVQSLDVGTAFPGDQCACSA VNKKELECVKETISKYCAKFTWKEAI SNPPA

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2196	8376	A	2228	1	149	LACLHGARGAEGGAWLAWEPDHP CFSGQMEDKLAWERHTEERISRAP
2197	8377	A	2229	3	162	NAAFDIGFMDYEFSLKRDIPKNTSFC KVTDLSLAVARKMPFGKRNLSLDALCA R
2198	8378	A	2230	1	137	SGEEEARLIYQGVAAHTTGGADQRLV VDIGGASTELVTGTAAPTTLP
2199	8379	A	2231	1	120	FKAAEPLIPKSGARVMSMLEPTKKMS KSDNRRNNVIGLLE
2200	8380	A	2232	1	272	IQSPYPEILPKAGPVGTTALLGMLPDKR GGAASLACKPARLWRVSKQPKGSEA EPLLHAFPLQLQSSNTHQQAQKQON SPSTDPTAASGYF
2201	8381	A	2233	1	359	SIALNGATLLTIASAPALAGEAGEKLG SEYNATYKMINRMERCYPKAMLKEL IYHPTLTEADLSDEQTVTRVYNALVS ELNDQEQHGSQWKFDVHTNAEQNLF EPIVRVTRTHGVDTDYP
2202	8382	A	2234	3	82	ANKQRYDEPTLIQHAERLKMILQFA
2203	8383	A	2235	1	105	AMGHGQMRERELERVMDFFHQRF NVLVCTTIET
2204	8384	A	2236	2	332	EQIVLDCQAGKRSSNNADKLTAIAAP AEIFLLEHGIDGWKKAGLPVAVNKSQ PLPLMRQAHAAGGLILIGVVLGYTV NSGFLLRGFVAGLFLFAGISGFCGM ARLLDK
2205	8385	A	2237	3	128	TOLEMFNAVAEAGSITQAAAKVHRV PSNLTTRVRQLETELGV
2206	8386	A	2238	3	333	EVWIRQGIKARRTRNEARVRALKTM RRERGERREVMGPANMQVEEASRSG KFVFEMEDVCSQVNGKHLVKDFSAQ VLRGDKIAVIGPNGCGKSTLVKMMML GQLHAHSGRI
2207	8387	A	2239	3	287	ITSIHGRPRRSARPELPCRHSYGPDLFP RPSGDDPLPRPSGHPDLPRPSGHW DLPRPSGHPDLPRPSGHPDLPRPS GHELOETQAECSY
2208	8388	A	2240	1	149	LACVHGARGAEGGAWLAWEPDHP CFSGQMEDKLAWERHTEERISRAP
2209	8389	A	2241	1	127	NRJAGNLLDQIEKQLPLHRDGFHTLQ YQRTSAAAEQRSESFG
2210	8390	A	2242	1	343	PGISKALAFPTNTRMVPWFPEHERAS AVGFYTSQFVGLAFLTPVLWQEM LSWHWVFIVPVGGIHWLIWFKVYQP PRLPKGISPKLDYIRHAAGLVDVNA PVNKKVCH
2211	8391	A	2243	3	85	RAKAEQAGDNLSCIMVTPSTHGVY EE
2212	8392	A	2244	1	127	NRIPANLLDQFEKQLPLHRDGFHTLQ YQRTSAAADQRIESFG
2213	8393	A	2245	5	91	APDFLKDIGGLETRNINQLVVEPTLQT TR

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2214	8394	A	2246	3	343	RSGLKMSIPDTWAADKNGVPTTDPFAGHALLPAAGPKGYGLMMMDALSSVLLGLPFGGRQVSSMYDDLHAGRNLGQLHIGINPNFSSSELFRQHLSTMTRELNAITPAPGFNQ
2215	8395	A	2247	3	110	FNGLLLPCQHKGNVAPVVPDDIKPVIQEQTQVVTPT
2216	8396	A	2248	3	176	HHAEADTLLPFYLGKDDVTYAIKPTCWPGLDIIPSCALLRIEAEMLMGKFDEGTLP
2217	8397	A	2249	1	87	KRLHEYKRQHLNLHLIALYKEIRENPQA
2218	8398	A	2250	2	375	VAVLKKTCATKPAFLEFLKQEQEASPDRTTLYSLMMKPIQRFPPQILLIQMLKNTSKGHDPRLPLQMALTELETLAEKLNERKRDADQRCCEVKQIAKAINERYLNKVERGFLQLYSKIIFALC
2219	8399	A	2251	1	205	ELNSLSKELAGVSEVSPFEAEKGSLEESI.WADRSTL.RQFTKPAAGSGGGFNNISWDGFRVPSSRSL
2220	8400	A	2252	3	110	RYRELGTGVPHERIAGFORIVLGGEALDGTSTSRGFD
2221	8401	A	2253	2	139	LLGENIAAGLIAFMVHLRSVEGGA AFQTLTITAKIIPFTIVGL
2222	8402	A	2254	1	90	NGRPICLFKLHEPVQVAHWQFSTVHPWP
2223	8403	A	2255	3	121	KNWEWMFTSADSVSSTHTLTDLPL ESLADQPGAGNVHL
2224	8404	A	2256	2	317	LQTVGACPSPPSLAMLSPIRGLPCS CISQPHMGPCPAAISLAPAPMSPASRPMPTALPACAFPSCTACLHPALSQOPQIWAVNPWFSAVQGPRTYEYQRTAN
2225	8405	A	2257	3	338	NAYVDPMPFGYINVRNLAPIKVINSNGTAGPVVHTIEDRFKALGAPVELIKVHNSPDDNFYGIPIPLPECRNDIRNAVIKHGADMGIAFDGNFARCFLFDEKGPQTE
2226	8406	A	2258	3	213	TLRLFHTETLKLHLQDINIATPVHNMPLSKGTGRGRPMGQQPGTIDVGGAERCQPTLALPSAGHCSQHAAR
2227	8407	A	2259	3	344	RQPLMPNEYNNPVAPPEKKLLQKSI EIDGFTQPIVVTHTDKNAMEIVDGFH RHEIGKSSSLKLLRGLYLPVTCLEGT KNQRIAAATISHNRARGRHITAMSEV TPELRLLGW
2228	8408	A	2260	3	83	ALKGLRVLVVEGNDPQGAASMYHG WVP
2229	8409	A	2261	2	112	AIANKTQNFVEVVAQYQFDFGLRPSIAYLHSGKGDHL
2230	8410	A	2262	3	150	VNEAESQARAIVDQARNAGDFGKLAI AHSADQQALNEGQMGWARIQQLP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2231	8411	A	2263	1	110	GFGNAIGDLPIMGQQTALQMYPSLQT IYDFWLIGE
2232	8412	A	2264	1	80	IERYQLPQSYQRMPDFRRRLQVCVN
2233	8413	A	2265	14	337	LGIGLELMGHQKGEYQYLNPNNDHV NICQSTNDAYPTGFRIAVYSSLIKLV AINQLREGFERKA VQFQDILKMGRQT LQDAVPMTLGQEFRAFSLKKEEVKN LPRP
2234	8414	A	2266	2	123	ISVIGGFLASKGSIDYPLFISTLVGV LVVPSACV
2235	8415	A	2267	3	134	TNSLAANDVAVVHAGYARWRKKLL RYGVELYELKRTREQSSTLH
2236	8416	A	2268	3	82	GIALWFPGPSISFTGENVELQGHAGP
2237	8417	A	2269	3	135	FGLAQLHQLRGRVGRSHHQAYAWLL TPHPKAMPADAKRRRAIA
2238	8418	A	2270	35	201	PVHRKGWEHPGRILLTRFAANNGSQS PWMEEQIRDAWGSMLKNVRETD EVGKG
2239	8419	A	2271	135	344	VNKSANYGVLDKLARGYADLSKAEG SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSPIQV
2240	8420	A	2272	2	354	GSTISLVGEREFLVDFQEREPELSEQA YSEFENTLRIVDAESVTQGGRWVFTT ARHNHLPAGADAWPILIREAARYTG EQKTLPLSPQGILRQCKEVALSCDGD TFSGEQLNML
2241	8421	A	2273	12	168	FLSEFPVPVQFSKSMVLDAYSEYVNN FSTAVALKKTCAKPAFLEFLKVS
2242	8422	A	2274	62	314	DGSWDSEFPQVKLASLPVRSLLMME DTLWAASGGQVFIISVETHAVEVSHL GGYTVMKKCISETAQLTSGAEVKAS CLWLNFL
2243	8423	A	2275	1	237	PASLLPRPSQGGPRNSRKAGPHGPSIR PQACPPALASFPSQAMMRWHQLLQ ADPLPAQRPPRQGGSPSPFGVTAVYS F
2244	8424	A	2276	3	404	YKAFYNSLRQAEALTFLNCALGPDE LRQYVQELSRIAECYVTAHPNAGLPN AFGEYDLADATMAKQIPEWAQAGFL NIVGGCCGTTTPQHIAAMSRAVEGLAP RKLSEIPVACRLSGLEPLNIGEDSLFV NVGD
2245	8425	A	2277	1	258	YIHLGLNLNVVGLSGLLVLYGGGFF AIGAYTALNLNHYGLGFWTCLPIAG LMAAAAGFKLGYPVLRMHGTYIAFS GYRDRMGGP
2246	8426	A	2278	351	419	INGLSGGLFNMFGNISIGITPIA
2247	8427	A	2279	3	81	FPQIGQRVMIDSSSVVIGDVLADDV
2248	8428	A	2280	1	111	VMPESLMVRSSSLTRKHWEWMTLS ADSVSVHTLTD
2249	8429	A	2281	1	104	YLKGLGVKPDTRKAILWYKEAAEQG YAHAYITLG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2250	8430	A	2282	3	95	CRPVGVLKMTDEAGEDAKTVA VPHS KLSKEY
2251	8431	A	2283	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2252	8432	A	2284	3	103	KMADAIDA YQPDYVVLAKYMRVLT PEFVARFPN
2253	8433	A	2285	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2254	8434	A	2286	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2255	8435	A	2287	2	102	LGLILGLINGLSRWGERLLDTSIQMLR NVPHLA
2256	8436	A	2288	3	77	SDPPKLELQKKHTIEVVDPRFKVRD
2257	8437	A	2289	2	82	MRNELFTATRGQGAQLNGYRLRGST AR
2258	8438	A	2290	1	146	GNGADSREATERLYLDVHKQLPKVTA QKGIVSEAGASVYSASELAAQEF
2259	8439	A	2291	2	111	EISKKDITRLGFRSSLLQASFNRYERMQ AGGFTWAML
2260	8440	A	2292	3	83	ALKGLRVLLVEGNDPQGAASMYHG WVP
2261	8441	A	2293	1	96	SAEAIDPQQAIRIEAPVNPALIGAVKV PDGTV
2262	8442	A	2294	3	73	EQGIAFSNALLPWSEVPPPLYQA
2263	8443	A	2295	3	166	RLSASTEYARFEQDDFDLDIVYGEPR PSPYEKIPLA VEELTPLCSQPLAERLN N
2264	8444	A	2296	3	222	FFYKGPADAKERYSRIVWFDQALSDA QRDNANRSAAVATASARIGTIVVAPR QANYHFQYANGSVNTVNTATL
2265	8445	A	2297	3	91	NVATYGGNICNGATSADSATPTLIYD AKL
2266	8446	A	2298	2	456	PPPWGPKGGGSGPRIDAPGKKGNP SSSQKASSSPGGMGTFFIPSSG
2267	8447	A	2299	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2268	8448	A	2300	3	73	VPRVFLFGAKAAPGYVLAKNIIF
2269	8449	A	2301	2	76	QAWSFDFGPRQITVRFDENLNPVIF
2270	8450	A	2302	3	80	REPMRHLLSLKKSEQLARASEMLKA V
2271	8451	A	2303	1	74	TFAKCCRPIDGPDIIAHVSPGKGL
2272	8452	A	2304	2	114	PLTDETHHLFGAEQFAKMKSSAIFINA GRGPVV DENA
2273	8453	A	2305	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2274	8454	A	2306	3	68	TAIEQGNRHLLEPVLEAMNAC
2275	8455	A	2307	3	169	LTSGESEYHVEKSLPVQTEINGNRFTS KAHINGSTTLTYTYSHLLTAQEVSK E QM
2276	8456	A	2308	2	108	HDAHCLALLPGSRGAEVEMLSADFL KTAQLRLQTY

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2277	8457	A	2309	3	97	PVTFGELKTYEKQLQSSGLEPAAINVS LNL
2278	8458	A	2310	1	62	NTADADVYRFLKFFTFMSIE
2279	8459	A	2311	1	65	FSGLTSLWFLQFDGSPFTEL
2280	8460	A	2312	3	83	ALKGLRVLLEEGNDPQGTASMYHG WVP
2281	8461	A	2313	3	94	YIQHVVAACLTGMTSLLAHRSAAVFH DGIR
2282	8462	A	2314	1	71	TIGVFVLGYLYCLTQFFGFASTR
2283	8463	A	2315	1	204	SAWAEETNSYQLPESLEKFSQRFL E DRTKAGGETPRPFLFEAIDQLLADPLS IRDLVCIRALDEIIG
2284	8464	A	2316	2	123	EVTYAIKPTCWPGLDIIPSWLALHRIE TELMGKFDEGKLP
2285	8465	A	2317	2	99	LSGGRLGDVGRSLLRGNSALVDECV AFYEEHF
2286	8466	A	2318	3	61	QMMPTLAPPSVLSAPORRC
2287	8467	A	2319	3	118	PIVIMLDPGHGGEDSGAVGKYKTREK DVLVLIARIRLS
2288	8468	A	2320	2	345	IQSSDDISVRVNSLAATTLFAMTLKN PKLGYVNYRALGRDYHKLRLNRLLK LGEMIQQHCVSLNFKPFVDSAPILERP LAEKAAGLWGTGKHSLLNREAGSFFF LGELLVDIP
2289	8469	A	2321	1	86	SSDGRSRGFINGTA VPLSQLRELQGLL I
2290	8470	A	2322	2	63	AKLQESSPLPVLGAVPWSFD
2291	8471	A	2323	3	115	AADQQAADLSQLASHIGGLRASLASPA EVDELTCGVFG
2292	8472	A	2324	2	93	NLTVFNNVVTSRPYTIELQQUALTFAN EKN
2293	8473	A	2325	1	161	SKTLRLSFGFIQSLSMILTFGTGILWESA GTLSFTVGGTEWNIQGYMYVTVVLI
2294	8474	A	2326	2	236	MKSLAEQMRNHDREQMSKMAHNL P EOYQECAPVEQVAQVFNKLFNELRA AFPASMANFRQTQEDLNEFHQWLLA FOEN
2295	8475	A	2327	3	103	EFAQIKHVLHGISLLGQCPSINAALI CRGEKM
2296	8476	A	2328	3	99	VQFORPAWDGYLRVNALLADKLLPL LQDDDI
2297	8477	A	2329	3	264	GSHPTSEKLLSVLRPASGHVADALGI TEGENVIHRLTLRRVNGVALCLIDHY FADLTWPTLQRFDSGSLHDFMREKT GNAMLRHT
2298	8478	A	2330	1	95	ARQSARAVSELDSSRGITTRDILSDKAI ENAM
2299	8479	A	2331	3	140	FSASLTFEQSYSEVDGDSASMAELCA LISALADVPANQSIATGSV
2300	8480	A	2332	2	72	VCNVDDEQIQKPQRNPADLGRF
2301	8481	A	2333	2	72	ANAERYRRLQTIHERGYGLQMRI

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2302	8482	A	2334	1	263	ELVFEMVIFHIRDNKLQMEAPERLR GETASFDEANGKVYVQKGRRTARH IRQLEKDDVKLIEVPAEYIAGKVVAK DYIDESTGE
2303	8483	A	2335	3	94	GKEEFYETLRYRRMIEVTGVTCLKN HTVT
2304	8484	A	2336	3	103	TSISMLMWTDAIERGPMTALRDGV RGDKKLDV
2305	8485	A	2337	3	77	NLSGRNRRRMVVKMNCAMPAGLLE S
2306	8486	A	2338	3	143	LLGNMGMAGGCVNALRGHSNIQGL TDLGLLSQSLPGYMTLPSEKQT
2307	8487	A	2339	1	116	CFRRLQGVEMLRADKTFDSHLFTG TGKFASSQLMVE
2308	8488	A	2340	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2309	8489	A	2341	3	85	PPGSVPCHIVNSSEAFVQLARQGTTC C
2310	8490	A	2342	2	73	EENALGDHSRVERIATEKLQMCHV
2311	8491	A	2343	3	101	DRGKLVAYPGNYDQYLLEKEALRV EELQNAEF
2312	8492	A	2344	1	117	TVPPMVRMDVSPDVFEATPNLFTL DGRVDVPWARIVVH
2313	8493	A	2345	1	98	EQQWQAIAEGLGAQYGDVPLSLLR DELAQR
2314	8494	A	2346	2	96	NTPLVNRATQGVYPASTVKPYVAV SALSAG
2315	8495	A	2347	3	110	VKTMRASIAWGLPLVARFGQGQVSL PGGCTIGARPV
2316	8496	A	2348	3	122	DVLLPLWEMREEPVKGITCIDLRSVS RVDTGGLALLHLI
2317	8497	A	2349	3	130	MYRAFEVLPMTVMTPYAAFHKELHG MTEEYVLDDEMVRINAN
2318	8498	A	2350	3	91	AAPDIIVRNEKRMLQEAVDALLDNG RRGR
2319	8499	A	2351	3	113	KLPGVVEYIKLGAVPGGTERNFASYG HLMGEMPREVR
2320	8500	A	2352	2	105	KDGSVVVLGYTARIGSDAYNQGLSE RRAQSVVDY
2321	8501	A	2353	1	111	FNPNLFPYENMEGKIDRPEEYADIAT KCVTNFREKNR
2322	8502	A	2354	2	96	ELLGPDSSIMIGRWLQEFFNNRDWP VASAV
2323	8503	A	2355	3	109	APGVLKIVKVYLAVKRRIQPGDKMA GRHGNKGVIS
2324	8504	A	2356	3	91	AAPDIIVRNEKRMLQEAVDALLDNG RRGR
2325	8505	A	2357	1	110	DAIKLDQVFRDIHKQPVSQSLVRAI VAVAQALNLQ
2326	8506	A	2358	3	83	ALKGLRVLLVEGNDPQGTASMYHG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
						WVP
2327	8507	A	2359	1	144	AEEVGFYFGGDTGTEHFNKVELENVLLHNLVVKRLQLADGSPALVTTVY
2328	8508	A	2360	3	91	EIRGPGELLGTRQTGNAEFKVALLLR DQA
2329	8509	A	2361	3	92	IDPSVQGTISVRSNDTFSQQEYYQFFL SIL
2330	8510	A	2362	186	363	AARQWPHFGSLQSLPSGVPPFFCLNL LSKWGYRGSSSRP
2331	8511	A	2363	3	73	DYLRQDFDRECIENLSPGGSADL
2332	8512	A	2364	1	89	ANEPGTYDGISASYSQPGFSGMKFKA IAT
2333	8513	A	2365	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2334	8514	A	2366	2	284	LASVSALLAEALVLKLRQSVAAATLKDNSLTLLTGLLAVSIPLAPWWMGVLCVTFAKSIPNHWKGCVRYNTLSTPQG PPDARGLHAPPTIEVT
2335	8515	A	2367	1	112	IFLMLRLGTGDPALDVLRLSNLPPTPE MLASTRTMLD
2336	8516	A	2368	2	81	LSCYMNINPAASSIHKYGRKLPHFDA
2337	8517	A	2369	1	158	CLAHLLRFRAAMRRQGRSEQKALLY PFGNYLCIAFLGMILLMCTMDMMRL S
2338	8518	A	2370	3	110	VKTMRAISIALGPLVARFGQGGQVSL PGGCTIGARPV
2339	8519	A	2371	2	108	FTSPLCEFDNVLLTPHIGGSTQEAQEN IGLEVAGK
2340	8520	A	2372	3	80	VQPFVEGLADIVDMAAIQKAGLTG V
2341	8521	A	2373	2	160	LTRLCMHMQSKLLENRNKMLKAQGI NETLFMALITLESQENHSIQSELSCA L
2342	8522	A	2374	3	93	NNLTFDRQYDFILSTVVLMLFEAKTIP GLI
2343	8523	A	2375	2	157	KLPYLAQSWIEDEKGNKITSPLTVLPV VHRIDSMNNGQVKVQGMPIINKLPA
2344	8524	A	2376	1	182	DFDVRKARPYSGYENDFEIPVGGGV SDCYTRVMLKVQELRQSLRILEQCLN NMPEGPFK
2345	8525	A	2377	3	175	KGLELDVRILLANYSNSNGCQSPWM EDQPPHAWGSMVLKNIREDEAGK GRIPGWP
2346	8526	A	2378	1	90	NNDPQIGDKLKVVFIPNYSVSLAQLII PAA
2347	8527	A	2379	3	133	IVHSNHLTEVAYRLYRDQKLKLYLW VDQTLKSDGTQLQEHGIC
2348	8528	A	2380	3	111	RENPGKSLALEIHRQGSPLSLTIPER NPGYGASSG
2349	8529	A	2381	382	574	ARELLGPSSEHLPTVTCAAFQBERKV PPPIPKPPKPKGFPTIREKSLDLPDRQR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QEARRRPMMA
2350	8530	A	2382	1	111	FCSRYNWRRMRVKRWLLAGIALCL LTGMRDPFKPPE
2351	8531	A	2383	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2352	8532	A	2384	2	98	LFPFGWAKLLWRLKVSGVVRTARVPL MGVRAEY
2353	8533	A	2385	2	103	QAYPLTTPSGKIEIYSQALADIAATWE LPEGDVI
2354	8534	A	2386	3	83	ALKGLRVLLVEGNDPQGTASMYRG WVH
2355	8535	A	2387	3	97	HVTHFDKTDITELEAFRKQQNEEAAK RKLDV
2356	8536	A	2388	3	67	QNPYGS LNPRKKVGQILEEPL
2357	8537	A	2389	3	128	VPGVVTLLTHKVLQNLDEKVPIRD MRTILETLAEHAIQS
2358	8538	A	2390	2	214	NVANDKIRIMSESKENINHYSLMDFM NVEHSLWKWSNDHHIHS
2359	8539	A	2391	3	69	AGYAANLKASGMKCGYASGWQG
2360	8540	A	2392	2	178	ALCARGIRPLKIKTHHMDMDVKPG KDSYELRKVGAAQTVASQQRWSLM TETPDDRA
2361	8541	A	2393	1	147	GVAAHKGGVYKPSVSVHLAQDLALK GLRVLLVEGNDPQGTASMYHGWVP
2362	8542	A	2394	3	103	ALA YSPGV AAPCLEIEKDPLKAYKYT ARGNLVA
2363	8543	A	2395	1	96	GNVIKVFQFLNIRDWPFGAATSITLTV MGLML
2364	8544	A	2396	3	91	QKHGKPLNVFENIEMFLPVLSRIERT GV
2365	8545	A	2397	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2366	8546	A	2398	3	101	VGRCHVSLHETQPLRQMEENRPLQ GTTEVTPK
2367	8547	A	2399	1	108	WRPLNNPKHLAVSSFSMENPQGFGL LQRGRDFSFE
2368	8548	A	2400	410	657	ARELLGPSSEHLPTVTTCAAFQEERKV PPPIPKPKPKGKFPITREKSLDLPDRQR QEARRRLMAAKRAASFQNSASERA DSI
2369	8549	A	2401	3	131	YQAKCPQASAEPEHYEALFVYAQKR LDKCVFGEEKPTCKQCP
2370	8550	A	2402	3	179	DLTLLHFRNTTEAGATSGSRDKGLHG KLKAGVCYSMLHPINSRHQRVVVGV RLQQVAGR
2371	8551	A	2403	3	367	LFQVVFYAQMAQEEGRFDNDICAAI SDELEERRHPHFVGDSSAENSSEVLAR WEQIKTEERAQKAQHSALDIYRSLP ALMRAQKIQKRCANVGFDMWTLGT VVDIVYEEISYGYPRMVMR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2372	8552	A	2404	3	104	HHNNNSPLPTTPDDESDTTPVPPTPG GDEIIPD
2373	8553	A	2405	2	70	LSREELIRLIDVCRNQQAKNLWC
2374	8554	A	2406	2	64	PEK WYLVAHPGVSIPTVIFK
2375	8555	A	2407	3	118	MDKAGTVDGNVYVNSYGFVYYNNTN GDFDQSFNGDVTNG
2376	8556	A	2408	2	82	DLIDREGMRVLVEKQDTAGSELLPQA K
2377	8557	A	2409	3	646	MFSYTIPFILPRNKGHLFSRFLGPG GQKGVRGAKQGTQGGSPGGFHVGR GGFTGGPRKFFRPGGGSSSLWVSL RGSGSGSGG
2378	8558	A	2410	3	79	KRMLYLFVDQIKSDGTLQEHGDC
2379	8559	A	2411	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2380	8560	A	2412	3	102	GPDDAVNRRISLLVLNKQAEQAILHE NAESQNE
2381	8561	A	2413	1	164	QELLETPAIRKLWRYRGSNVLGTIYE WPPTTTTRALDTLLREIQNAREQHSRL DT
2382	8562	A	2414	1	66	DGFEECCDNGERLVRTFALDCC
2383	8563	A	2415	1	125	SGAGTTTTSLAFRKIFAQLNGHAAEV EGDSFHRYTRPEMDM
2384	8564	A	2416	3	79	KRMLYLFVDQIKSDGTLQEDDGIC
2385	8565	A	2417	3	337	PKPKHNPFLSLVPEQGVKLTPRHYAY LKISEGCNHRCTFCIPSMRGDLVSRPI GEVLSEAKRLVDAGVKEILVISQDTS AYGVDVKHRTGFHNGEPVKTSMVSL CEQLSK
2386	8566	A	2418	3	98	ALPGSQEPAEVLTRKVISLPAFLRGS AVYRHG
2387	8567	A	2419	2	72	SSMQLGSNVFPFRQLTVTRDGI
2388	8568	A	2420	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2389	8569	A	2421	3	87	AWDGTGEPKLENNADTPTSLYEAA FFQ
2390	8570	A	2422	1	101	SRSRLRQQGELVGRQLRQLQQQQLS QQIVAAAD
2391	8571	A	2423	1	74	KRLPDNSAPYTSITIVFLVRKGPNK
2392	8572	A	2424	3	88	AFAFDFQQNQHDNLTWQIKDGYLL YRK
2393	8573	A	2425	3	83	ALKGLRVLLVEGNDPQGTASMYHG WVP
2394	8574	A	2426	3	91	FQYLFPLMCGALTVGALWVNLEESS MVLG
2395	8575	A	2427	354	603	ARELLGPSSEHLPSVARGVQIEETRVS HSIPSKPPESKFPVSRSQVLESHRYG QEGRRRLMSAEVSAISLQNPSSRAH SIM
2396	8576	A	2428	1	81	GDAEPVLNAIAANNWQPEAIFLTHHH H

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2397	8577	A	2429	2	107	VSSLGIRPRGQIEPVLENVQPNASAKAGLQAGD
2398	8578	A	2430	3	83	ALKGLRVLVEGNDPQGTASMYHG WVP
2399	8579	A	2431	3	83	ALKGLRVLVEGNDPQGTASMYHG WVP
2400	8580	A	2432	337	440	PLALCLAPAASLHELCAAKVSEVLHN RVHRTTEEV
2401	8581	A	2433	3	384	KFDYGIKVKFSFWTAAADGHEVFYGM FDAGSTDRVHVVFQTRPPRETPTLT HETFKALKPGLSAYADDVEKSAQGI RYLLDSVFGDM
2402	8582	A	2434	40	458	RPGWGRPERIRPLDRLPAPRKGGVL SERVADRAEHETPTLTHTFKALKPG LSAYADDVEKSAQGI RQLLDVAKQDI PFDFWKGTPPLVMDTAGRLLPGEK GHKLLQKQVKEVFKASPLVGGDCVSI MNGTDEGVSA
2403	8583	A	2435	3	417	SCGTRWNRGERGAPGAANMDDYSL DEFRRRWQEELAAQAPKKRRRPEA AERRARRPENEMNDVPFDIQLPYEL AINIFQYLDRLKELRRCQVSKTWKVI AEDEVLYWYRLCQEGHLPDSSISDYS CWKLIFQECRA
2404	8584	A	2436	1	528	GTSQGPVGFGPGKPGPPGPKDGLPG HPGQRGETGFQGGTKGPPGPGVVG PQQPTGETGPIGERGHPPGPPGQGL PGAAGKEGAKGDPGPGISGKDGP AGLRGFPGERGLSGAQAGPLKGGE G PQGPSPVGSPPGERGSA GTDEPIGLPG RFGPQGPDPAGEKGAPEK V
2405	8585	A	2437	2	251	FVVPESIRIYSMMFCFAERTRLVLK AKGIRWAPRRGTLPPEFGLLQAAG WGGVYNEFYRTFASRYSYTTSTTNDI VNGHP
2406	8586	A	2438	2	416	FVPRKVQIRSLLEDIPDVLDSMHS LGCFRDRNKLLQDLSEENQEKMIY FLLDLRRERYPSQDEDLPPRNEIDPP RKRVDSPMLNRHGRPERKSM EVL SVTDGGSPVPARRAIEAQAHQSKA MFKSLDI
2407	8587	A	2439	25	449	TSSVLQAGKALGDDFENEELGDE AMMALDQSLASLFAEQKLRIQARRD EKNKLQKEKALRRDFQIRVLDLVEVL VTKQPENALVLELLEPLLSIIRSLRSS SSKQEQDLLHKTARIFTHLCRARRY CHDLGERAGAL
2408	8588	A	2440	24	415	RCLCGECWGS CGRPQALTPLSFQLSM KGP GPGVGLTGRPGVPGRGLQPGHG PPGRV GKMGRPGADGARGLPDGTGP KGDRGFDGLPGLPGEKGQRGDGFHV GQPGPGEGDERRAEGPPWPTGQAG EAD

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2409	8589	A	2441	1	399	FRGTCEALGDERRALSFFHQKGLQDFDTLLSGDGNLTYYVGAREAILALDIQDPGVPRLNKNNMILWPASDRKKSECAFKKKSNETQSFNFIRVLDSYNVTHLYTCGTFAFSFACPIELQDSYLLPISEDKAME
2410	8590	A	2442	71	330	FFNQKQPTTRDLTKTWKKNQPSFMVRPPFPKGPFPQASSSSPLRNPAQSGRGWPKPGRGPQRNPQLFSGSGKLSAPAPKLFQCN
2411	8591	A	2443	220	431	KVCSGEEKARTKASPLPPQHILEAMLYDALQQEAGAKVAELSEEEREKLKVAVEQWKQVMSELRRER
2412	8592	A	2444	2	400	FVRRITYAARRFYSSREMKEGGLAPGRRLRTGTRLSLARMPPPLPTRKEYSLAGALKAGYKETRPSERTQMMLNDRFANYIQKGRFLKQQTALTAELNQLRAKEPTKLADVYQTDRLRELPLEHLQTANR
2413	8593	A	2445	266	399	VLALPLSQEEEEVEREIKQEESVDPDYWEKLLRHHYEQQED
2414	8594	A	2446	2	424	VLDLAQRFFKQNLQFIQGAEEYEGKDLQETLAFPGHVAFAKGDGLMGLKKLVEDGVININECADNGSTPMHKAAGQGHECLQWLKMGADSNITNKAGERPSDVAKRFAHLAAVKLLEELQYDIDDETKWWIREFRGN
2415	8595	A	2447	1	434	PSRTLNNSPQTKTKRPNYAGPNPSRKFSDCPRSQKQTPTSHGPSYRSAQGLRGSPGPAAESPLIKWTGEREGGEERGPGRKRGWQSPESGRAPSPRVPTQPLSKPCRRRSRRAVSKRGQGRKTRPKDEPPFFSGPIWRWK
2416	8596	A	2448	72	383	RPLGSVWTPGRCPFLSLTPPPVCVDTFPEFSSLVPGNEQMKVENFEAAVHFYGKAIELNPANAVFYCNRYQLKACPGQRRPGAGASSGMLSRDLRWERPLRCR
2417	8597	A	2449	2	393	PGQVELADFGSAPMASPANSFVGTPYWMAPVELAMDEGQYDGKVDIWSLGITCIELAERKPPFLNMNAMSALYHIAQNDSPTLQSNWTDSEFRFVDSCLQKIPQERPTSAELLRHEFDRDRDLRVIR
2418	8598	A	2450	1	413	FRSRSLSPGRATGTFDNEIVMMNHVYRERFPKATAQMEGRLQELTAYAPGARLALADGVLFHHQIVELARDCLA KSGENLVTSRYFLEMQEKLERLLQDAHERSDQEGVNFIVQLVRKLLIISRPARLLEGLE

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2419	8599	A	2451	1	457	AFPVDDFVFTEPEKPPSPGDRARVGT LQNKRVFLATFAAVLGNFSFGYALV YTSVPVIALERSLDPDLHLTKSQASWF GSVFTLGAAAGGLSAMILNDLLGRKL SIMFSAVPSAAGYALMAGAHGLWML LLGRITLTGFASGLTAACIPVYVS
2420	8600	A	2452	400	448	NCFLBCAYQYDDDGQ
2421	8601	A	2453	2	401	FVQTIQEDSATTSSESLHVMAPQKRPS HRHGS KYLATASTMDHARHGLPRD IDTGILDSIGRPFPGDRGAPKRCSGKD SHHPARTAHYGFGLPQKSHGRTOQENP AVHFFKNIVTPRTPPTQKGKRGSLSL IY
2422	8602	A	2454	2	215	FVANVGSFMFYWKRFDLQQLRELD ATATALANRQDEGEQSRKRLIEQSRE FMKNTPQRRRATIVFALKGS
2423	8603	A	2455	3	427	SSFKDRDHFOLGSLSHLLNAKATGYQ ELPDWREQAPDPSVRNVEVPWTKC SNREKRKEKENPFYSDSEGESGPTES ADSDPESSESSEDSKSSSGSGGESSSES DNEQDEDEEKGRGSEGEQSEEDGK RKTCKRVYCAR
2424	8604	A	2456	118	397	EVAREVGRPRALAPPGQHTGPKVPPA ARDNANAPSPSEDLRQDLSPGWTTTH AQTPQPKLKTPRNMWPRHGLMPAF PTFLPVEGPRKRGGPPPG
2425	8605	A	2457	2	360	FVVDLTQMQTFFWKDLKPCSDGSVRP HGWVLAGQAAGQGWEIWSQTLVNL RKARRAVGEGADGWTRWSSALASR QNIGAWHLGGLTRSVRRNLGLCSGN REAMVTVGGAHVTPARWGETE
2426	8606	A	2458	9	395	TTPHGETGRKVTQRRGVSRCSCGGG QNHRNSGRVPEGGRFCTSAAVVRA AEGSRGGVGPWADEARVAHARGSG CAGRSRGGRPSSVFNPAPQPSSEGTR EGRGEPDPGESVG
2427	8607	A	2459	66	326	VRGGGRHSYRKDRAGEVGGEWE SAGGGGREGKGGREEAPGRQERAG GKLHSPPSRSVATGPRKKDPVPLSEV SSQLQKRGHST
2428	8608	A	2460	256	867	DERQVRYRLRAFLPESGFTILPCTRYS METNGAKIVSTRAWKKNEKLELLVG CIAELREADEGLLRAGENDFSIMYST RKRSACLWLGPAAFINHDCKPNCKF VPADGNAACVKVLRIEPPGEDEVTCF YGEFFGEKNEHCCHTCERKGE FRTRPREPALPPRLDKYQLRETKRR LQOGLGQWQPTGAPSGSLRAPIA
2429	8609	A	2461	3	436	APRLNSRVDDFVPLNHVMKAMQSL MSRGYVKEQFAWRHFYWYLTNEGIG YLRDYLHLPEISSSSSSSSST

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2430	8610	A	2462	2	454	STAPDCPGRFRAMETYIRQRLIMS PLITSHVIGENEPLTSVLNKVIAAKDV NHKGQGLWVSLKLLPGDLTQVQKNF SHLVDRSTAIARKMGFEIILPGDVRN DIYVTLIHGEFDKGGKNTPKNVEVTM SVHDEEGKLEKAHPGAGY
2431	8611	A	2464	2	433	GQNSRVDDFVVDGHCEGINISCDPYR FMMKHLAFLRKRMNNNPSRGPYHLR TPNRIFWRTVRGMLPHKTKRGQAAL DRLKGFDPPIPPYEKKKRTVDTAGLK VRRMKPTRNAAAYVGRLAHEGGWKY HAVTATLWEKJENAKRI
2432	8612	A	2465	2	403	FVLIKKKGKLQIVVLWRPTFRGNLKL NLWEGERGKTGEKFWGKLLLDKPPK GPPKKTGGQKTPPRGGKEKRGGRGTPS SSPGFLRGKKKSGKSSSSQGGKTEKY KKPGGAGHPFKGGPSSSSQLFFQKPG
2433	8613	A	2466	1	413	FRMTDSEGPQRPLCLFSLTLLSQKVP EKSDAVLRCIISGQPKPEVTWYKNGQ AIDSGSIISNYEFFENQYIHVLHLSCTT KNDAAVYQISAKNSKPGMICCSASVEV ECSENPNQLSPNLEDDRDGRGWKHETG THEE
2434	8614	A	2467	4	451	GEACKDFISSSSIFEHAPHNEWNPHS NAKCEEAASRCGRKRYKCECGKTFSS RKDSLVOHQVRVHTGERPYECGECGK TFSRKPILAQHQRIHVEMPEYECGICG KVVTSSNLIVHQVRVHTGARPYKSSE CGKAYSHTKSSRREFRNGS
2435	8615	A	2468	2	415	AFPGRRFREAGGVPVEERKQASVYG LTWEAGGSAIAEAGSGREGMVQA GA EKDAQSISLRKEQWETKHQRTERKIP KYVPPHLSDPDKKWLGTPIEEMRRMP QCGRILPLLRPSANHTVTIWNGERTA GSRWELIQTAL
2436	8616	A	2469	22	465	SWIDDFATSIDMDSGDGVTHGTPIYE GYALPHAILRLDLAQRDLTDYLMKIL TERGYSFTTTAEREIGRDIKEKLCYVA LDFEQEMGTAASSSCEKSYELPDGQ DITIGNERVRCPEALIQPSFLSMESCGI HETTFNSIMKCDGDI
2437	8617	A	2470	153	416	RSPGYKGRSWLPLQLSWLGPAPSPGS EGRSWLPLQPSWLGHAPSLGSGNRSS LPLQLSWLGRAPSPGYEGRSSLPLQL SWLGHAPSTK
2438	8618	A	2471	197	396	CWAVRYCVLRHAALRGHGGGAAG AGRIALLYKPIDRVTLSTVLHDDLK HTPVDHPDYPLLVDAL
2439	8619	A	2472	3	291	QPDGQMPSPDKTIGGGEDSFNTFTTET VAGKHVPRPVCVDLEPTVIDEIRGT YRQLFHPEQLITGKEDAANNYARGH YTIGKEIIDLVLDRITLA

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2440	8620	A	2473	3	530	KVSLVQVVSSLQSSVVEAFIKVLCVSNPVVPSIPSFSPANAGITLPTRGYKC LECGDSFALEKSLTQRYDRRSVRIEV TCNHCTKNLVFYNKCSLLSHARGHK EKGVMQCSHLILKPPVADQMIVSPS SNTSTSTSLQSPVGAGTHTVTIKIQSG ITGTVISAHTNTPTPAMI
2441	8621	A	2474	32	354	SFFDIVLDFILMDAFEDLENPPASVLA VLRNRWLSDFSFKETVGHCPALRPTLA HISPCGCLAPSLSLALAPGLGPHPLD PRLPGLGDQSLPWRSLQGPALLPGAP V
2442	8622	A	2475	2	402	PTASLIQSHTPDAHYKERHSGMRGKP VRTNGSPVLSRLIYCKSPPTQPTTPE EITSPFSSAALTTARSHSCLLGEVGAY ALGRQSGPSRRRRHQQRRTKQVLL PSQAASTAQWCPSPPLCPAFLAETS QH
2443	8623	A	2476	1	416	LLGTAPSLQNNQPVFNHAIYSYVNI KNRFOGQPCYKAFLEILHTYQKEOR NAKEAGGNYTPALTEQEVYQAVRL FKNQEDLLSEFGQFLPDANSSVLLSK TIAEKVDSVRNDHGGTVKKPQLNKN PORPSQNGCQ
2444	8624	A	2477	3	434	ELPNFRDDDFVSPPTVGPVGRFCVA GSRARLCVDESKRGFDEVYGGYISF YMKQIFFLDDSGPPFGHMVVALGGY LGGFDGNFLWNRIGAEYSSNPVWVS LRLPALAGALSVPMAYQIVLELHFS HCAAMGAALLMLIENA
2445	8625	A	2478	1	148	FRASGRGRSRKDAAGSSSHGDDQPASR GKLOARALGHHHPSPSNWHEAS
2446	8626	A	2479	3	456	LOETMTFKDVEVTFSSQDEWGWLDSA QRNLRYRDVMLENYRNMASMVGPFT KPALISWL EARGPWGLNMQAAQHK GNPVAARTGDVLQSKTNKILFTQEPL KEAEPLAVSSGCPATSVSEIGLRDSF HQSRPKVQCDTIQVVRVKKESVY
2447	8627	A	2480	2	393	FKMPMDLKGPIQIDVKGPKLDLKGPKAEVTPADVEMSLSSMEVDVQAPRA KLDGARLEGLDSLADKGVTAKDSKF KMPKFKMPSFRVSAPEGIEALVDVS ELKVEADMSLPSMQGDCLKTTDISIQP PNV
2448	8628	A	2481	2	420	YKSGTVFHLNLTLSYIKQIFPMEERIFN FHTIDKSLKTHSVVKKHKQVRGEKK LLKCNDEKIFISKISTLALHQRIHTGE KPYECIECGKAFSQSAHLAQHQRIHT GEKPFECTECGKAFSQNAHLVQHPCI AAALDSR

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2449	8629	A	2482	1	371	STPCTLTVSETQLLCEAPNLTGQHKVTVRAGGFEFSPGTLQVYSDSLTLPAIVGIGGGGGLLLVIVAVLIAYKRKSRDADRTLKRLQLQMDNLESRALECKEAFaelQTDihelTNDLDC
2450	8630	A	2483	18	373	RSPPPIADQGGQGHCGSTARPRAPSMPGHPLLRSKSPRMELYLPLAPLPRRLINPGSCFPAAATPDSGLRGLSCNQGTICPVIPRGERAQPPSPHMPAPPSSRGRRQLDPRCARPV
2451	8631	A	2484	2	378	PWQFAQFILTQTQLSLFPMYVVVGYIEPSKFQKIYMNMSVTLFSILMFNGNSMYLSSYYSSLLMTWAILKRNEIQKLGVSKLNFWLIQGSAAWCGTILKFLPSKILGVSDHIRPSDLIAAIV
2452	8632	A	2485	1	370	VPNAKLTVNVDVNDNTQPKFPGITYYMERILEGATPGTTLIAVAVDPDKGLNGLVTYTLDDLVPVGVVQLEDSSAGKVIANRTVDYEEVHWLNFTRASDNGSPPRAAEITYVLEIVDLV
2453	8633	A	2486	3	256	FFAFFAFATCGSGYSKGLQLSVDCAKTESDLSIEVEFEYFPFCAPT LGYQQTWERKKGQGGTGQYLPQVAPAAQLPPRGYIHWDH
2454	8634	A	2487	3	416	PRDLRQHERTHSAERPFKCDLCPMGFKQQYALMRHRRTHKTEEPFKCGLCEKGFQPSHLLYHQHVHTLETLFKCPVCQKGFQDQSAELLRHKCLPGAAERPFKCPVCNKAYKRASALQKHQLAHCAATAEKPLRCTNGE
2455	8635	A	2488	1	364	PVTVLA VESEFTPVPAWSPVTVLAVESGFTPVPAWSPVTVLAVESGFTPVPAWSPVTVLAVGSEFTLVPAWFPVTVLAACIFLGS
2456	8636	A	2489	3	334	PPATQGPDPYRTPNTVMRNYFPFSPGPLATPRGKSQLGANESSTVPSIVNGFYRERAGPSLGQSIEAGKAPGLMPAVQNWLVVEVPTVSPISRFTYHMSAGVPNSSSETA
2457	8637	A	2490	3	438	VSLSSFFLSLPYGVAVGVAFLVVLVVFQTFQRNGYALAQVMDITDIYVNPKTYNRAODIQIGIKITCYSPLYFANSEIFRQKVIATGMDPOKVLAKQKYLKKQEKRMRPTQQRSLFMKIKTVSLQELQODFENAPPTDPMY
2458	8638	A	2491	3	218	KKNYSDSLSPSAVPRSSSTPPKVNVKNLVRSFPGYFFFLRQSFALAAQAGVQWRNIGSPQCLPPGCGQNS

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2459	8639	A	2492	2	441	LGEGALPGPARGVPTGPSHSDSGRSS SSKSTGSLGGRVAGLLGSGTRASPD SSSCGERSPPPPPPPSDEALLHCVLE GKLDRDREAELOQLRDSLDENEATMC QAYEERQKHWQREAREALRECAQA RMAKRPLWRMQDNVNVNS
2460	8640	A	2493	1	384	QKQKQTRWINTPTAYLRVNVADDEVQ RSMGSLRPKSTWMKADEVKSSSGM PIRIENANQFVPLYTDPQEVLEMRNKI RDQNRHDVKSAGPQSQLLASVIAEKS RSPSTESQLMSKKEEDTKDDSEECI
2461	8641	A	2494	1	2250	MENSLRCVWVPKLAFLVFGASLLSA HLQVNTGFOIKAFALRFLSESDAVT MRGGNVLLDSCAESDRGVPIKWKK DGIHLLALGMDERKQQLSNGSLLIQNI LHSHHHKPDDEGLYQCEASLGDSGSIS RTAKVAVAGPLRFLSQTESVTAFMG DITVLLKCEVIGEMPMTIHWQKNQDQL TPIPGDSRVVVLPSGALQISRLQPGDI GIYRCSARNPASSRTGNEAEVRLSDP GLHRQLYFLQRPNSNVVIAIEGKDAVLE CCVSGYPPPSFTWLRGEEVQLRSKK YSLGGSNLLISNVTDSDSGMYTCVV TYKNENISASAEITVLVPPWFLNHPS NLYAYESMDIEFECTVSGKVPVTNVW MKNGDVPVPSDYFQIVGGSNLRILGV VKSDEGFYQCAENEAGNAQTSACL IVPKPAIPSSSVLPSPRDVVPVLVSSR FVRLSWRPAAEAKGNIQTFTVFFSRE GDNREARLNTTQPGSLQLTVGNLKPE AMYTFRVVAAYNEWGPGESSQPIKVA TQPELQVPGPVENLQAVSTSPSILIT WEPPAYANGPVQGYRLFCTEVSTGK EQNIEVDGLSYKLEGLKKFTEYSRLF LAYNRYGPGVSTDDITVTVLSDVPESA PPQNVSLVSVNSRSIKVSWLPPPSGTQ NGFITGYKIRHRKTTRRGEMETLEPN NLWYLFGLGEGSQYSFQVSAMTVN GTGPPSNWYTAETPENDLDESQVPDQ PSSLHVRPQTNCIMSWTTPPLN
2462	8642	A	2495	1	398	TEFMGNPEHRVCNLLKDLQPEDSGS YNFRFEISEVNRWSDVKGLVTVTTEE PRVPTIASPVLELEGTEVDFNCSTPYV CLQEQVRLQWQGGQDPAVSFTNSQK FEPTGVGHLETLHMAMSWQDHGRIL RCQF
2463	8643	A	2496	4	244	GVPSHFRIEKDITVVVQDLGNIFTRL LKRWWHQALLRSBGDKVRMDPPCTN TTAASTYLNPNPYVRKALNIPQQLPQW DMCK
2464	8644	A	2497	1	158	EMGFHHFGQAGLELLISSNPASAFQ SVGITGVSHCARASITSELCSLPWAL

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2465	8645	A	2498	1	410	TAAAAGDPIACYTDIPKIYASRTHSQ LTQVISELRNTSYRLKVCVLGSRQEL CIHPEVKKQESNHLQIHLCRKKVASR SCHFYNNVEEKSLEQELASPILDIEDL VKSGSKHRVCPYYLSRNLKQQADIIF MPSV
2466	8646	A	2499	2	405	HIEELSGVRTAVTMAVMCVAGLFFIP VAGLTGFHVVLVARGRTTNEQVTGK FRGGVNPPTNGCYNNVSRVLCSSPAP RYLGRPKKEKTIVIRPPFLRPEVSDGQ ITVKIMDNGIQGELRRRTKSKNLLEITE SHV
2467	8647	A	2502	3	439	LCNPTKVRDWNIOQLPSDAFSTENGII VTRGNRWALMIDPQAQALKWIKNM EGGQQLKIIDLQMSDYLRLIEHAHFG YPVLLQNVQEYLDPTLNPMNLKSA RIGGRLLMRIGDKVEEYNTNFRLYITT KLSNPCIAAAQRITL
2468	8648	A	2503	3	470	HPNTGGSLPDMTNIHFPSPLTPLDAGE EPTFPALSSSSSTGNLAANLTHLGIG AGQGMSTPGSSPQHRPAGVSPSLST EARRQQASPTI.SPLSPITQAVAMDAL SLEQQLPYAFTTQAGSQQPPQPPQPK QHPPPASQQPCIAARSIGSMHTAQ
2469	8649	A	2504	3	431	LQEILRKFLYLEREFROITISKEFTFSE KNNECHEPEKSFSLSDTIDADQRLRI QNTDDNDKYDMSFNQNSASGKHEHL NLTEDFQSSECKESLMDLSHLNKWES IPNTEKSYKCDVCGKIFHQSSALTRH QRIHTREKPCI
2470	8650	A	2505	86	306	RKKMGDSSWFLIPWCLVVDIWSVGC MAEMVLHKVLFPGRDCLIRGTGTW PWRLGWACGPEKLCVHRHFLFL
2471	8651	A	2506	1	377	HGGEQPARAPGFQHSLYLLFLGLARM AWESPGPKGDCPQQTWAEQTVSPLP LLPSIRSVSGTGGWSARGLLSRNR THVVRQCSHTASFEVLMDVSRCEMG IFLWPLCPPLSPPNPLLLKLNQPI
2472	8652	A	2508	22	194	GRNIVFYGSQTGTAAEEFANRLSMFA HRYGMRGMSADPEEYDLSVCHRVL PDGGSG
2473	8653	A	2509	1	446	ECHQKQKQALREQLQVHIQTIGILVSE KAELQTLAHTQHAARQKEGESEDL ASRLQYSRRRVGELERALSAVSTQOK KADRYNKELTKERDALRLEYKNTQ SNEDLKQEKSELEKLRVIVTEKAG MQLNLEEMYAAAVEDQDSSRH
2474	8654	A	2510	3	408	SVTINQLNENIESLKQKKQVVEHQLE EAKKAINEIHKAQTEQLETNILTLEK ADLKTTLTYHTKRAARHFEESKDLA GHLQYALQRIQELERALCAVSTQQQE EDRSLSCSEAVLQWRLQRTIKEQALL NAHVY

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2475	8655	A	2511	2	127	LPDLASCLDVGNESGCGERTLPDWQ GQDPAEGGQGTSSSS
2476	8656	A	2512	3	202	EGCGVNIFAEELGRYYVTSFTVAVSII AKKEVLLDQPGREGRCQVGSGLFSP EASDSGWLRIWF
2477	8657	A	2513	484	3	KGFSKIFANPTKDKASHAGEKHFKCN ECOKSFQKFSDLTQHKQIHAGEKPYT CEERGKDFGWYTDLNQHKKIHTGEK PYKCEECGKAFNRSTNLTAHKRIHNR EKA YTGEDRDRAFGWSTNLNEYKKI HTGDKPYKCKEKGKAFMHSSHLNKH EKIHTGECI
2478	8658	A	2514	2	412	SDLALRNCLLTSDLTVRIGDYGLAHS NYKEDYYLTPTLWPLRWAAPPELLG ELHGTFFMVVDQSRNSIWSLGVTLW ELFEFGAQPYRHLSDEEVLAFVVRQ HVKLARPRKLPLYADYWDYLQSCW RPPAQRPCI
2479	8659	A	2515	3	374	TKYVTEHWCEDHFFGYQYLVNGVNPV MLHCISLSPSKLPTNDMVAPLLGQD TCLQTELERGNIFLADYWLAEAPTH CINGRQQYVAAPLCLLWSPQALVP LAJQLSQTPEQNSPIFLICI
2480	8660	A	2516	3	419	LADLKNQMVEPLSLAPTA VSSVSGDQ LQVKAHLSQSEVEGLEGLQSQVEN NQALSVLKDKQKRLQEQEELKLEQ EEMIREQEAQRVRDLERLCEQIERLR EQQKTVREQGERLQKQEQRLRKHEW EAGALSIPRGFP
2481	8661	A	2517	3	186	VLQLIHERDNICKQIHLPAQSGSSRVL EAMRRGSGLLGEGASLTFFCFNDQT VSLPRT
2482	8662	A	2518	2	176	QLIHERDNICNQHILPAQSGSSRVLEP MRRGSGLLGEGASLTFFCFNDQTVS LLPRT
2483	8663	A	2519	2	398	VARVYEKLITGCYNILANHADPNSSL DESILEECLQYLEKQLESSQARKAME EFFSDSGELVQIMMATANENLSGKFC NRVLKFFAKLFQLTEKSPNPSLLHLC GSLAQLACVEPVRQLQAWITRMTTSP MY
2484	8664	A	2521	2	391	QSSPSAQEHLASLQEQVAVLTRQNQD LMEKVVQILENFEKDETQMEVEALAE VIPLALYDSLRAEFDQLRRQHAELQ ALRQQETREVPREEGAAGSEVAG ATATKNGPHTHMLNGSVAPETKVNG ACI
2485	8665	A	2522	90	454	GTNLLYYSVFTLLMKTYPRLGNLQKF HVAGEFLKIMAEGRHVSALFQSRV ITVLLQLFEVHEEHVRMVLLSHIEAY VEHFSQEQLKKVLPQVRGQVCSGVV TEPEGRVLKERVLEVFR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2486	8666	A	2523	3	389	GTLSPVPVSVSESLSPERSQLLYLLAEAVVILFIILLGVIMAKRRKKHGSLLWLPFGFTLRRDASNHKRRPEVQGDVGLKNLSVQVSEANIIGTGTSEQWVDD EGPQPKVKVAGDKSLSEEDDPCI
2487	8667	A	2524	3	500	FNKAIEIFIDVSTMKFDMLLQQENSWLFRENECLADYHPCSFADPIPWHVCRSYSLPCFLYSPLPLTLHLVLSCLLAIMCSVKPDGVPQLCRTDDIGELCVCAVATGTSYYGLSGMTKNTEFVGGGESYHGHHLLWLRQLARLARCIVIDVEC KIHFSKTCI
2488	8668	A	2525	2	126	IQPSQILLELMNSDLKAQLRELITAVRETEVGGGEKVVIM
2489	8669	A	2526	2	387	LCPLTEEVHDDSAIRENGFNIFVSNIALERSLPDIRHASCKHKMYLERLPNTSIHAFHNEGWTSLRTIHSINRTPGSLIAEIIIVDDFSEREHLKDKLEEYMARFSKVRIVRTKKREGLIRTPV
2490	8670	A	2527	187	397	GSEGPMPSSAIYSAPQNHWSGRQYSHALFKTMSHMLCIGYGGQAPVGMPPDVWLTMLSMIVGACIAAAV
2491	8671	A	2528	26	412	ARWDCPSGPAGCRPKSWGCCGECGGNGNRSSSKERQSGVGLPAAAAAAV DAAAAAASVEGRQPPGLGAVGPAGRPAGSPGGRMPAGRVAGAAATGLGVSWLRGKNSGVPGAALPPAAPSVASLV AHSGP
2492	8672	A	2529	3	394	GVQAGHAQRLQLQKEALDEQLSQVR EADRHGSPRRELPHAAAGADASDHSGSPQEQLDEKDARRFQLKIAELSAIRKLEVRNALLSEERNELLKRVREAESQYKPLLDKNKRLSRKNEDLSHALRMA
2493	8673	A	2530	1	385	PASPIRVSDLRMDMIAHYNHAGPPHTMQPDRASPSRQAFKKPGTLVYIEKPRSAAGLSLVLDGLPLMEKQVFAYSTATIPKDRETRERMAMEKQIASLTGLVQSALFGPITSYKSDASSEKLY
2494	8674	A	2531	1	425	SRNSIHLVEHWRHITGOKPYKCSFCDKYFNRRNSNLARHQRIHTGEKPHKCNB CGKAFRECSGLTTHLVHTGEKPYKCNECGKNFRHKFSLTNHQSHHTAEKPYKCNBCATVFSLLSYLARQIIHSTEKH VCGRSEVHART
2495	8675	A	2532	3	384	WAFSLEIVLSSSLASAPCSSPEYAPSSPAHVGVSSSLASAPTSVLSPSSSPARVMSSSMVSTPYSSLASLTSSSPAGVGVSSSLASAPSSCLARVSSSLASAPSSSLASLTSSSPASVGVSSSLET

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=L-lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2496	8676	A	2533	1	452	GHPVMAAGSPCGHIGLWDLEDKCLI NQMRNAIISTAIA GLTFLHREPLVTN GADNALRIWIFDQPTGEGRLLRFRMG HSAPLTNIRYYGQNGQQLSASQDGT LQSFSTVHEKFNKSLGHGLINKKRVK RKGLQNTMSVRLPPITKFCRS
2497	8677	A	2534	2	410	DSRNKIEELQQRKFADHKAQLARTQ KLQOELEAANQSLAELRDQRQGERL EHAAALRALQDQVSIQSADAEQEQVE GLLAENNALRTSLAALQEQIQTAKTQE LNMLREHTPLGLAELQQQQNEYEDL MGQICIAAALA
2498	8678	A	2535	3	398	DGRIENSLCLYTHGEYITLVNSGSG LSHYVANQSVQEDPRMMAFFDSLVR REIEGWSSDSDSLSESTILQHAGVS ERSGYTDESSASLPRSPPTVDESAN NALHLGLPLRVNTNTVASTPPPMYS
2499	8679	A	2536	392	1	LSAVDKKGDTPLHIAIRGRSRKLAEL LLRNPDKGRLLYRPNKAGETPYNIDC SHQKSILTQIFGARHLSPTETDGDMLG YDLYSSALADILSEPTMQPPICVGLYA QWGSCKSLKLEDEMKTFAHGCI
2500	8680	A	2537	3	392	ASQLSLHQRIHAGENPHECKEKGKAF ISDSLIRHQSVHTGEKPYKCKECKG SFRRGSELTRHQRAHTGEKPYECKEC GKAFTCTDLVRHQKVRTGERPHKC KECGKAFIRSELTHERSHSGEKPCI
2501	8681	A	2538	1	402	LICDSA VPASFWDGMLVPIGDKPSTIA DRLYLGAFTSVRGFSMHISGPQSEGV YLGVEAYWAGGLHLYTLPVVRPGQG GFGELFTRFFLNAGNLCNLIYGE KAHIRKLAECIRWSYGAGIVRLGTIA QCI
2502	8682	A	2539	2	423	RVNKQDADLIRPKRYEKKPKPVFSS SAAGTPQQTSPAALPVFNAKDLQYD FIPSSDEEPLSQVLSGSSAEAEANDPDG PSAFRRKAGCQYYAPHLDQTGNWP WTSKDGGLGDVRYRYCLPTLVHQ RCIGFARMGKRV
2503	8683	A	2540	3	427	TEGQGSIEIQGDLPLSRGHETSGKG LEKTSNLNKRDFLGFMDTDSALSEVP QLKQEI SECLIASSFEDDSRVASPLDQ NGSFNVVIEKEPLDDYDYLEGCEPEG VTVKQEETDEETDVVYNSDDDDHIKK QLKRHYVLR
2504	8684	A	2541	2	428	RCSVGTYNSSGAYRFSSEGAQSSFED SEEDFDSRFDTDDELSYRRDSVYSCV TLPYFHSFLYMKGGLMNSWKRRWC VLKDETFWFRSKQEAALKOGWLHKK GGGSSTLRRNWKRRWVFLRQSKLM YFENDSEELKGTGTCIA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2505	8685	A	2542	1	622	ASQAGPGSSRRKCSPGSPDTPNATLS KDEAAVHQDQKPRYSYATLITYAINS SPAKKMTLSEIYRWICDNFPYKKNAG IGWKNISRHNLSLNKCFRKVPRPRDD PGKGSYWTIDTCPDISRKRRIHPDDDD LSQDSPEQEAASKSPRGGVAGSGEASL PPEGNPQMISLQSPSTIASYSQGTGSVD GGAVAAGASGRESAEGPPPLYNTN
2506	8686	A	2543	17	183	SLRRCVHQKCNATVSSVFSKPESSIP IWAALVQQEYCVQLWVPYFKDKDQK QV
2507	8687	A	2544	1	421	NAELTRVPLKRLDLIFVTFQDSRMAK RVRKDYKYVQCGVQPOQSSVTIVK SYWVRVTPMAHPKDIWIKHLSVRRFF WWARFIANTLFFLFFFLTPAIMINT IDTYNVRPIEKQNPVITQCIAAALN GPFS
2508	8688	A	2545	3	422	NKATLFEVMLSDECMDDVVGCLEVD PALAQPKRHREFLTITAKFKFVPIPD SELRQKIHQTYRVQYIQDILPTPSVFE ENFLSTLTSFIFFNKVEIVSMLQDEK PLSEVFAQLTEATDDDKRHVFGRC YQNTSAA
2509	8689	A	2546	2	424	EEKLYECSECGKFFMDTSTLIHQVRVH TGEKPYECNKCGKFFRYCFTLNRHQR VHSGERPYPECECGKFFVDSCITLKS QRVHAGERPFECISCGKSFRCRSTLDT HQSHTGERPYPECECGKFFRHNVFA RVGFLNTSF
2510	8690	A	2547	1	392	ASNYVSDWWEFFVYLRSRNPLMVNS NYYMMAFLYVTPPLQAARAGNAV HALLYRHRLSRQEIPTLLMGMRPL CSDQYEFIFITRIPGVQKDYIRHLHD RQHGAVFHRGRFRFGDPLPKQPCMR PL
2511	8691	A	2548	2	379	QMPGDYSCEARGQRVSFRLRISEPKM MFAKEQSVHNEVQAEAGASAMLSCE VAQAQTEVTWYKDGKLLSSSKVG MEVGKCTRLVLVQAAGKADAGEYSC EAGGQRVSFHLHITEPKGVFAKEHCI
2512	8692	A	2549	213	374	RPKMTAEPRDMDFPHGWSEDSYYEA LAKAQKIQMVLEKAKKERTKIEFVT GVY
2513	8693	A	2550	205	389	VAPRDHTIGHVWGQVDACPHGQQLR SSSSACVLHLFQPPGGVPGTQPLPNS MDPTPVLRPL
2514	8694	A	2551	3	404	AAVRAARAVNYVAGTVEFIMDSNH NCFMEMNTRLQVEHPVTMITGTD LVEWQLRVRIFFLLKISS
2515	8695	A	2552	3	405	QRFIYRIYASRIEELFSIVRDFPDSRP AIEDLKCYCLERTDQRQQLLVSLKAA ETRLHPGVNTCDIITLYISAIALRVL DPSMVILEVACEPIRRYLRTREDTVR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						QIVAGLTGDSGDTGDLAVELSKTELY
2516	8696	A	2553	3	402	GNNGFVVHVLNNKEFHFTSSTEVFM HQLRKLSDKQVDHENDDADREDEEH SQEDRERGLHMKLDHDLSDRESEA GTGSSEHEDGEREGSPRTYSRLSVPM PLPTVLLDRKIETLLTEWKNKNDMLF TIHPMY
2517	8697	A	2554	110	397	VGPRMTTEPQSLLDVLGSDAIFSCAW TGNPSLTIVWMKRGSGVALSNEKTLT LKSVRQEDAGKYVCRAVVPVVGAGE REVTLTVNGPPHSSTTGE
2518	8698	A	2556	397	2	RSPLAPGEGYSRLFLKAQALLFGGYR DALVCSPGQPVTFSEEVFLAQKPGAP LQAFHRRAVHLQLFKQFIEARLEKLN KGEFSDQFEQITGCGASSGALRSY QLWADNLKKGCGALLHSVKAMY
2519	8699	A	2557	251	396	ELGWMGWVHVFKLSPSTSAVSPAHTS YSEPMSTLRYASSAKNINKPRV
2520	8700	A	2558	3	406	YEFIVSPSSARAGGPDNSVLLLRLEPK VLSAPPQEVTLKPGNGTVFVSWVPPP AENHNGIIRGYQVWSLGNLSPAN WTVVGEQTQLEIAIHMTGSFCVQVA AVTGAAAGEPPPVCLLLEQAIDKAS QEYSV
2521	8701	A	2559	1	410	QDSEFKVSPSSARARVPASNVLRL PEKVTSAPPQEVTLKPGNGTVFVSWV PPPAEIHNGIIRGYQVWSLGNLSPAN NWTVVGEQTQLEIAIHMTGSPSYCVQV AAVTGAGAEPPRPVCLLLEQAIDKA SQEYSV
2522	8702	A	2560	3	560	YAVRVSQYSLCSQIFLDDSTAIQHY LTMHVSVLEPIPHITQKADADRLSIP DEQLPSFAVSTVHIMKRRNGGSLNN YSSSIPSTASTSQEV PQFSVPPTANTTT SVCNRSMRCSLTFTSEKGESEPKERK APENHADTIGSGRAIPKQGMLLKRS GKWLKTWKKYVTLCSNGVLTYYSS SL
2523	8703	A	2561	3	231	MVSGNEVEYLDLNFHSGVISFKRPFIN HTVGQPPSYSLKITASDGKSYASPSTF NITVVKDPHSEVPVTCDKTGYV
2524	8704	A	2562	2	231	IQGALLEDTEETKNVLEHMEELQEYV ALVRVGPDPSPAHHRTGHTGHRAT QAWALGSRQCYNCALEVLPAPWQSL
2525	8705	A	2563	3	232	GMWGFHDDRDLVRKALYTMRTGA ERBALKRRWRWQQTQONKESGLVY TEEEWEREWTELLKLASSEPRTHFSK NV

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2526	8706	A	2564	1	280	LGMWGFPPDRDLVLRKALYTMRTG AEREALKRRWRWQQTQQNKESGLV YTEEWEWERWTELLKLASSEPTPFS KNVLRTLYRIPAYVRGHAT
2527	8707	A	2565	3	419	THADPHNSRRGFFSHVWGILLVRKH PAVKEKSTLDLSDLEAEKLVMPQR RYYKPGLLLMCFILPTLPWYF WGET FQNSVFVATFLRYAVVLNATWLVNS AAHLFGYRPYDKNISPRENLVSLGA VGEGFHNHYLCHI
2528	8708	A	2566	3	426	FPPGDSYGMQGSVEEVLKTVATIRDK GRANHSAFLFGFGDGGGGPTQTMLD RLKLSNTDGLPRVQLSSPRLFSAL ESDSEQLCTWVGELFLEPHNGTYTTH AQIKGNRECEIMHDVELLSLALA RSAQFLYPAALY
2529	8709	A	2567	1	390	LWNKPLVGVNHCIGHIEMGRLTGAT SPPVLVYSGGNTQV
2530	8710	A	2568	2	393	EIGAETGARSQGAIEVETKATAIAIHR ANSQAKAMVGAEPETQSEKVVAGT LVMTAEAVTLTEVKAKAREYAMKEA VTQTDAAEGKIVKKEAVTQTKAKAW ALVAKTEAKREAMTQTKAETHILAE KETV
2531	8711	A	2569	2	423	TKVLDAGIHRCSQRCRHPCTCRQE VEKHCRCKHTQRMPCPKPYLCETK CVKMRDCQKHQCRKCCPGNCPDCD QNCGRITLGCNRNHCPSVCHRGSCYP CPETVDVKCNCNGNTKVTVPCGERT TRPPCKCEQYMSGV
2532	8712	A	2570	98	303	DAVLLKADTWLGAVAHACSPNTVG GQGRQDRLSPGVKDQPGQYGKTLSL QKIQKQPRRVVGGCEMEM
2533	8713	A	2571	4	416	EAADVAILSLNIIASAKYLKSSHNSRT FYRFEAVWSSLSHNSLLVNRVTPYGE KIYMTLSAYLELDHCIQPAVITKDVC MVFYSRDAKISPPRSMRSLFGSGYSK SPDSNRVTGIYELSLCKMSDTGSPGM QRRSV
2534	8714	A	2572	4	391	LPTGPRGQQAQPPRAEKNGLPASV GPGEQNGTGGYQRAFPRTNPEKHSQ RKSNLAQVEHWAARAKQKDSRSLPLD QTLPRQGPQQLSPFENYQTLPKSTR HPSGSSPPPRNLPSDYKYAQDRASL Y
2535	8715	A	2573	3	383	RRSITSPPSASTTKRPSIDDSMESPV DDVFYPGTGCSPTAASSQSSGWPNP VDAGPASKKSGKLDLCSALSSQSS PRMAFTPHPLPVLGGVRPGSPRAAAS ALPLPWTSVIQKKKYFPHPCI
2536	8716	A	2574	20	248	DQDFSKQKNFINMTCRFCWQLPETD YECTNSTSCMTVSCPRQRYPANCTVR DHVHCLGRSEFKDIQQNVFLQVY

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2537	8717	A	2575	3	394	MYARDAVV G A L P M A A M I A P V E C P S A A A S D A F A M A S P M N G E E C M L A V D I E D R L S P N P W Q E K R E I V S S D V V T P S A V T P S A L S A S A G P F I V T D D P G A A S I F A E T M T K T E E V A D M L L E L C V T E L D V A T R L A
2538	8718	A	2576	1	395	L R N L F I G G L S F E T T D D S L R H E F E K W G A L T D C V V M R D P R T K R S R G F G F V T Y S C V E E V D A A M C A R P L K V D G R V V E P K R A V S R E D S V K P G A H L T V K K I F V G G I K E D P Q E Y N L R A Y F E K Y G T I E T I V M Q D R Q S V
2539	8719	A	2577	1	395	R A T S G M R L S D M S P R S N T A C C A S P P A L V S P G S F S G L V Y K N V T P V Y T A L K G R A T Q I S N M P F M D E S S G S D D C S S Q A S F R I S V P S S E S R K T S G L S P R A I K R G V S M S S L S S E G D Y A I P P D A C S L D S D Y S E P V
2540	8720	A	2578	174	367	D T E I G F N I I G H L L L N D T N Y G Y L T W E W T E R L R S Y I Y P L I F A S I Y K I L L L G K D S V Q L L V S L N K S N
2541	8721	A	2579	2	399	R Q Q N A V G R E K E L L S S Q R D R F E G R P V P D G D A K Q R S P K M R Q R P P P R R D M T P R G L N L P K P I P P Q V E E E Y T I A E F Q T T I P D G I S F Q A G L K V E V I E K N L S G W W Y I Q I E D K E G W A P A T F I D K Y K K T S N A S R P N V
2542	8722	A	2580	1	388	L A H T V F A L H I P Y C R S R V I D H F F C D V P A M L L A C T D T W V Y E Y M V F V S T S L F L L P F F I G I T S S C G R V L F A V Y H M S K E G R K K A F T T I S T H L T V V I S Y Y A P F V Y T Y L R P R N L R S P A E D K I L A V F Y I L T P L Y
2543	8723	A	2581	1	384	R A F C V G Q Y L E P D Q E G A V A P D L G S L S S P L I D T E R N L G L L L G L R A S Y L A M S T P L S P V E I C A K W L Q S S I F S G G L Q P S Q I H Y S Y I E E K D E V L C S S P G G T P A S K S R L C S H R R A L G D H S Q A F M Q A I A D N M C I
2544	8724	A	2582	3	274	C E V A V N W Y A P L V A P I S K D R T T C T V P L I D Y I D G N D Y S I E P Q Q G D E D G F A R G A W D W S L L W K R I P L S H K E K A K R K H K T E P Y R S P A M A G G L F A
2545	8725	A	2583	3	395	S A S R A L K E K L S K D I D S L I G K D S O V K S Q I S E L N L L M K E T E C N G E R A K E E A I T H F E K L F E V L E E R K S S V L K A I D S S K K L R L D K F Q T Q M E E Y Q G L L E N N G L V G Y A Q E V L K E T D Q S C F V Q T A Q L H L R I Q K A T C I
2546	8726	A	2584	1	123	N T V W G L M L G D M R L P F F Q V E D E L S S P V V V F R F Q E L P G S G R
2547	8727	A	2585	3	394	E T E L K V H L K I V E E E A N L L S R R I V E L E V E N R G L R A E M D D M K D H G G C G G G P E A R L A F S A L G G G E C G E S L A E L R R H L Q F V E E E A E L L R R S A E L E D Q N K L L L N E L A K F R S E H E L D V A L S E D S C S V L S E P S Q E E

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2548	8728	A	2586	1	297	STMSMSYVTLTGPGPWGFRLOGGKD FNMPLTISRVSAPCHSLAPDAGATLGG GGHVCPSPVWQSFSLSESRACTIPWD WPGPLVSDTACCCLQRAGLLCM
2549	8729	A	2587	2	394	WSLACILYEMCCMNHAFAGSNFLSIV LKIVEGDTPSLPERYPKELNAIMESML NKNPSLRPSAIEILKIPYLDEQLQNL CRYSEMTELDKNDLDCQKEAAHINA MOKRIHLQTLRALSEVQKMTPRERM Y
2550	8730	A	2588	3	393	PSGKASKGNKSKAKKSKSPKVPKVE NEDQSGQLQKSLKFNLMSPDAGDSPI HLPLNYPGSHDLGRHYRSNPLPSIQ LQHQSASAKKHQVQVQDMPANTFV GTGNPPSTGSEQYSEYSGRTKPPSI
2551	8731	A	2589	2	407	VKPENLLVWDGAAEQVVRICDFGN AQELTPGEQYQCYGTPEFVAPPEIVN QSPVSGVTDIWPVGVVAFLLCTGISPF VGENDRITLNMIRNYNLAFEETFLS LSMKARAFLLKVLVQEQLRPHAEEM YCGRCR
2552	8732	A	2590	1	1491	DMSESKAKKIEIKVDGQTLKSLIDYI YTAIEIVTEENVQVLLPAASLLQLMD VRQNCDFLQSLQHLPTNCLGIRAFAD VHTCTDILLQANAYAEQHFPPEVMLG EEFLSLSLDQVCSLISSDKLTVSSEK VFEAIVISWINYEKETRLEHMAKLME HVRLPLLPRDYLQTVVEEALIKNNN TCKDFLEIAMKYHLPLDQRLLIKPN RTKPRTPVSLPKVMIVVGGQAPKAIR SVECYDFEEDRWQIAELPSRRCRAG VVFMAGHVYAVGGFNGSLRVRTVD VYDGVKDQWTSIASMQERRSLTGAA VLNDLLYAVGGFDGSTGLASVEAYS YKTNEWFFVAPMNTRRSSVGVGVVE GKLYAVGGYDGASRQCLSTVEQYNP ATNEWYVADMSTRSGAGVGVLSG QLYATGGHDGPLVRKSVEYVDPGNT TWKQVADMNMCRNAGVCVAVNGL LYVVGDDGSGCNLASVEYYNPVTDK WTLPLTNMSTGRSYA
2553	8733	A	2591	3	320	MSSPTKTWALVRIFGRHMLFSYQ RSLPRQPVSPVQDTRVKYLESVRPILS DEDFDWTAVLAQEFLRLQASLLQWY LRLKSWWASNYVSPATATNAPPEGL RL
2554	8734	A	2592	1	398	NDVILCSKIVPTKETMPSNNSVAQVQ SNPGFVAISDGAHSASNNPPLLNTNR TQKLPTPVNQA TLSTQTSQSEKLLVCS APTHLTPNILLNQTPLC TPNVSSSLP NHMPSSINLLVQNQQTITNSAILTGC

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2555	8735	A	2593	2	385	SELAESAACEKPNFNFSQPPYEEVEDE GFEADDDAFKDSNPSEHGSDQRTS GIRTSDDSSSEDPYMNDDTVVPTSPSA DSTVLLAPSVQDSGSLHNSSSGESTY CMPQNAAGDLPSTESDYDYPQECI
2556	8736	A	2594	2	175	FVKRLARCCAGSRLGPGNSSSSSSPPS PSASPAPQPSAQPPQARDNKQRV GSPV MRPL
2557	8737	A	2595	3	381	GRPGLPQGRHLCLWLLCAFTLKLCA EAPVQEEKLSASTSNLPCWLVEEFVV AECCSPCSNFRAKTTPECGPTGYVEKI TCSSSKRNEFKSCRSALMEQRLFVKF EGAVVVCVALIFASNVIIORLY
2558	8738	A	2596	2	390	CPFPKKKSGRTFQYINVPSEVSTFLCA GHDTWAAASISWVLYCLALNPEHQEK CRFEVRALGDGSSITWDQLGEMSCP TMCIKETCLRLIPAVPSISRDLKPLTFP DGCTLPAGITVVLKKWGLHNNPV
2559	8739	A	2597	1	430	LSSWGNAAAVAGDPDIACYPDIPKIIYA SRTHSQLTQVISELRNTSYRHKVCVL GSREQLCHHPEVKKQESNHLQHILCR KKVASRSCHFYNVVEEKSLEQLASP ILDIEDLVKSGSTHRVCPYLSKKMK QQADMYAAALRV
2560	8740	A	2598	163	426	CLWTRRGVSCPYSLSGCSQQDAQEFL KLLMERLRLLEINRRGRAPPIRANGP VPSPPRRGGALVEEHLSNDERTYAR ALEHTFLRRY
2561	8741	A	2599	46	395	PVLLSLPSPSLAGGVPSAAEDVAKP EPHRWGREVVVGGLVYREAI GTIGT WKGADGRLGWPRAGRRCRCAWEAVR GGGTDSRPHALSVDVQSGPHMTPY SLLKEDVKWPPTLQPPT
2562	8742	A	2600	3	407	AAITTLRYDQLAGRLASGSKDTDIIV WDVINESGLYRLKGHKDAITRALFLR EKNLLVTSGKDA MVKWWDLDTQJHC FKAMVGHRTVEVWGLVLLSEKRLIT GVSDSELRVWDIAYLQKEKETBEPGP CIASALE
2563	8743	A	2601	3	394	LTALYVL DHGLRVTVSLKELQSNLG VPPVRGSCPLTMPLPFDLITDYHGL QQMKRHHMGLSFKKYRCRIRVIDTFGT KPAYNHBEYATLHGYRTNWGYWNL NPKQFMTMPHTPDNSFMGFVSEEL NETE
2564	8744	A	2602	2	390	SSLSTPAASSIWSPASISPGSAPASVSV PEPLAAPNTSCMQRSVAAGAAATAA ASYPMYSYGQGSYGQGYPTPSSSYFG GVDSSYLAPMHSHHHPQLSPMAP SSMAGHHHHHPHAHPLSQSSGHHH

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2565	8745	A	2603	2	392	WHNTTFFGVFQAQWGDMLYLSAICEY QLEEIQRVFEQPYKEYHEEAQKWDR YTDVPSPRPGSCINWHRRHGYTSS LELDPNILNFVKKHPLMEQVGPWRWS RPLL VKKGTFNTHL VADRVTGLDGA TMY
2566	8746	A	2604	3	439	AIKQGNPSATFGDVSKIVASMWDSL GEEQKQAYKRKTEAAKKEYLKALAA YRASLVSKSSPDQGETKSTQANPPAK MLPPKQPMYAMPGLAFLPDAVGPAGL POWGLPWASPGRWAPSLCCQASVR PRRRHPSRSAPHCTSSC
2567	8747	A	2605	3	302	TSIISFNSDCSARALASGRPVSISSIS EDLECYSSATAPVSEVSIQFLPLPKMS LDEKAQDAGSRSSISWSEMSAGS EGEQSCHSFIATCFGH
2568	8748	A	2606	125	448	QDVLAAQDAAGDNLEMTPTSRGSAKS RGPLEEHLHTLQLEKEPDALPRPRT H YRGRYAWASEDDASSLTADNLEKF GKLSAFPEPPEDGTLSEALYCGRSR GTEQG
2569	8749	A	2607	402	2	QAPRPGSAESALSVRTSPPTFAMYK FRPAFTGPKVPFCGPGQGVPGPDSL TLTGDDSIKSLDFVSEPSLDPYPGPG GLHAAYPSPPLSASDAFSGALRSLSK ASSRRGGDHVALQPLRSEGGPTTHQC I
2570	8750	A	2608	1	359	VVIYFQGLRVDLPIKSGRCGGQYNTY PIKLFYTSNPIILQSAVVSNHYVFSQM LSARFSGNLLVSLGTWSDTSSGGPA RAYVPVGGLCYYLSPPEFSGSVLED PVHADVYIVFMLGHV
2571	8751	A	2609	57	366	REERPSSSPACRFPTNRNPQTQQPWL Q PGRGQAPGQSFQEGNRGPTVRRAP K PAVVPKNTTDAPTKGRSWTPKGD PQPSVEPPSNRCESARLTATLQGA GPRL
2572	8752	A	2610	41	384	LGMATGIGSLHPPVPVARGALSTGL WLGWAAKGGGFHRLPHPTGTPLPGL RRAGSNSSRLQPHTLRGRGTGGAR VMFRSPTAAMLLLEPGAAGTASSPP WLGPAPYSCSPT
2573	8753	A	2611	2	395	LSPMTFLAPHPPAFLHAPFAPSLVTS FAHLPPRNCFSHTCSFSSSLPGSHSL A PFCLKSLPFCIFDSFVYPLAHL LLHTCSSQHFCQSPALFL
2574	8754	A	2612	3	380	LAEAVCSHFTQNLWTVQGIEDSFHKL IPKGHEKRGHENLRKTCCKSINECK VYKGGYNRINQCLLTQKKTQSNICVK VFHKPSNSNKDKIRYTGDKTFKCK ECKGKSFHVLRLTQHKRIHTGCSI
2575	8755	A	2614	1	235	AAAAPGKMLGMYVPDRFSLKSRVQ DGMGLYTARRVRKGEKGFPAAGEKR MPEDLDENMDYRLMWEIFCTGCWYI

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						LER
2576	8756	A	2615	2	377	DHSILLCSSSVATAFIASLLQGIIMVGVI VGSKKTGINPDNVATPIADSGDLIT LAILAWISQGLYSCLETYYYISPLVGV FFLALTPIWIIIAAKHPATRTVLHSGV EPVIPAMDISSIGGMY
2577	8757	A	2616	3	376	KRLHIRENSYQCEECVKVKRFSTILT RHKRVHAGEKPKCECGKAFKHSS TLTHKMIHTGENPYICEEGKALYH SSHLTTHKVIHTGEKPKCECGKAF NHPSALPSHKFIKVENPNYV
2578	8758	A	2617	1	380	SSPLSQNDSCSTGRSADLLPPGDTGR RRHDSLHDRAAPSRAERFRIQEEHRE AKLTLRPPSLAAPYAPVQSWQHQP LIFESCGYEANYLGSMLIKDLRGTEST QDACAKMRKSTEHRMKKIFTIV
2579	8759	A	2618	3	413	HVLHMCAGPVTKIMLSEKLLISVCA VNNHVRTWSVIRYRGMISTPGSPTL ASYKILAMESAHGHVGCSDGNIGIPY GERHDQQVFIRKVVPSDSQFLVRLSS TGQRVCSVRSKEGSPTTACNAALSS KLRSQVS
2580	8760	A	2619	1	393	LLRHIRKLEENEKKQYRESYISDNL LDMDQLEKRSRASGSSAGSMKHRL SRHSTASHSSHTSGIEADTKPRDTGP EDSYSSSAIHRKLTCSSTSHGSSHT SGVESGGDKLKEDLQDVYAAALGI
2581	8761	A	2620	411	1	SSSSSLKVLILDNATHICCKELENA HANIGVLFMPNNTKSLIQLNRIHIA FKAHMY
2582	8762	A	2621	2	443	LEKGEPPWILEEKFPSQSHLEINTSR NYSIMKFNEFNKGKCFCEKHEIHS EEEEPEYNKNGNSFWLNDLIWHQKI KNWEQSFEYNECGKAFENSLFLVH KRGYTQKTKYTEHGKTCDSMFFIT HQQICAAQRITORT
2583	8763	A	2622	3	410	VLEGNRVBEQLRLRELTAALKGAL KEEVASRIDQVEHVHRQQYQDTEQL RRSMQDQTQDHAVLEAERQKMSAL VRGLQRELEETSEETGRWQSMFQKN KEDLRATKQELJQLRMEKEEMEBEL GEKIEVLQRCI
2584	8764	A	2623	1	428	NPSAGSILENQRSNLMNLIIRISDLQ QSCHEYDIPMLPHVQKYLNSVQYIEL QKFVEDDNYKLSLKIEPGTSTPSAAS REDLVGPEVGASPSGRKSVAAEGA LLPQTPPSPRNLIPIGHRRKCHSLGYNF IHKMNTAAV
2585	8765	A	2624	138	396	FPCHHHHHCHDHYHHHHHHCHHCH HHHHHHCHHHHHHHHHHHCHRDHYHH HHHCHHHCHHHHHHHHHHHHHHHYH

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						HHCHDHHYHHHHMY
2586	8766	A	2625	1	408	PQLTELEDAARCIHSGTDETHLADLE DQVATAAAQVHHAELQISDIESRISAL TIAGLNIAPCVRFRTRRRDQKQRTQVQ TIDTSRQQRRLPAPPVKAETIETSSV TTIKTFNNHFLQGSS\TNKTKERKDT HGI
2587	8767	A	2626	1	439	RTGEKVKVEHVVSYLEKKYPYVEVN SILGIDSAAYDRNRKEARGYYEQTGVG PLPVVLFNGMPFEREQLDPDELETIT MHKILETTTTFQRAVYLGLPHDQDA VEYIMNQPNV\PRINSRLTAERDYL DLTANVVRSEDPA SDR
2588	8768	A	2627	438	2	TQRLVISEPDGELTPGWD\TQDRMGV ESRTNIQELGNRNQREAGGENLPETQ AHMGETQDQI.RCKIDAETQTPWEVN QDKNGSEDAVETQTFEKKDKKEAGE EDGEIEQAQGLGKQGQ\TGDENGEE TQTRVLR.ALETIPASS
2589	8769	A	2628	3	402	CGRHIP\TDFETGLGPWNRSKGSWRN HRAGGHERPSWPRRDHSRNSAQGSF LVSVAEPTGTPAILSSPEFQASGTSNCS LVFYQYLSGSEAGCLQLFLQTLGPGA PRAPVLLRRRRGELGTAWVRDRVDI QSAMY
2590	8770	A	2629	2	621	KPGEIVDANFGQQPLFDIEDYMWRE RAKVQGTVHCFPISARLGEWQAVLQ NMVSSYL VHHGYCATATAFARM TET PIQEEQASIKNRQIKQLVLEVRVGEA IESTQRFYPLMEHNP\NLLFMLKCRQ FVEMVNGTDEVRSLSSRSPKSQDSY PGSPSLSPRHGPSSSHMHTGADSPSC SNGVASTKSKQNCIAAALEDTSK
2591	8771	A	2630	3	394	LSGERRYSPPLFTH\THYVPDIVRCVP PFREIAFLEPREITLPEAKDKLSQOILE LFETCQQQISDLKKELCR\TQLRREIQ LLFPQSRLLF.VGSSLN\GFGTRSSDGL CL.VVKEEPCFFQV\NQKTEARMA
2592	8772	A	2631	2	390	LQSLRNPPFWGNIFREKKANGLFGTG ATQGLRYLNHPPTQASPQCTVCP\SGL ERAPSPSPAPRPACNGLVVPPTITSP GRAGSSAQRTSSPKISRRTLGPWPA ACFPGPPLTSALEDWLSRHCAPN
2593	8773	A	2632	2	382	FKPTIGYPPLTGPVPVPLADLLYALLF LGQAKGWIPKPVVLGFGMHIEETQV FRESQSVENLVISLLQHSLYVGPAGSV IQLPLSSCSRYSYCDICILARDPYCG WDPGTHACAAAATTIANRTACI

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2594	8774	A	2633	1	379	PLMSLRKPAECGATVFETDVMVSSD GVFFMHDEHLRTTNVASVFPTRT APRSDFSWTELKRLNAGSWFLERRPF WGAKPLAGPDQKEAESQTVPAIEEL LEEAAALNLSIMFDLRRPQNHHVY
2595	8775	A	2634	1	203	PLPKSFSFLSPVTSVSRDPSLGNLGKE LGPNLQVRGLVALPPWSALLFLFGG IGALGLTLLPAGWL
2596	8776	A	2635	100	385	IANGAFPPSAIYTRKDLLQRSTHIATK TFQALRIFVNNELNELYTGLKTAQKF LRPGGRLVALSFHSLEDRIKRFLLGI SMTERYNLSVRQQHV
2597	8777	A	2636	1	389	NKEDVGLGELSSSEEGSVSGDRGSIVD PEEEKEEEEEDEDFAHHSNDEQNRHT TQMSDEEEDDDGCDLFADEKEEEDI EDIEENTRPKRSRPTSFADELAAIRKG DAVGRVDEEPTTLPAGEAKPRKTV
2598	8778	A	2637	3	413	SAAVAKRALAHGLKCKSQFTITPGSE QIRATIERNGYAQIMRDLGGIVLANA CGPCIGQWDRDKIKGKENTIVTSYN RNFTGRNDANPETHAFVTSPEIVTALP PAGTLKFNPKNYLTGKNGEAPALG GP
2599	8779	A	2638	1	121	AAALAKCSSGASLDSHLHRLHRDS TISNESSQCSSGRQ
2600	8780	A	2639	3	409	SPMPFHPSQVSPRARFPVTSITSPNRTG ARTLADIKAKAQLVKAQRAAAAAA AAAAAASVGGTIPGPGGGGQPGGE GGGEGQTARGGSPGSDRVSETGKGPTL ELAGTGSRGGTRELLPCGPETQQQSE TKTTLV
2601	8781	A	2640	3	404	RLAQLLEGYARYSVSVFPFPFQPGRM ALESQSPGCTTLLSTGSEAGDSEIDPI QPPELQLVTPMAEGDTGLPRVWAAAP DRGPVPSTSGISSEMLASGPIEVGSLP AGERVSRPEAAVPGYQHPSETMNAH TCI
2602	8782	A	2642	2	406	SLCQAANRSLGCLWCADGQPACKRYG PLCPGPAVELLCPAPSIDAVEPLTGPP EGGLALTILGSNLGRAFADVQYAVSV ASRPCNPEPSLYRTSARIVCVTSPAPN GTTGPVRVAIKSQPPGISQPCIAAAL ED
2603	8783	A	2643	1	410	LWWNINSTARAPPASIKPPSGGTGRG TGCPLLPSPSLELPSPAPRTGCRAN SCSSRPRLPFLEAPSTGSCPMAREAH PATSHPPATLDPAGADPGDHKWATT GASPLYCSNTRAQALWNVTEPGRGK TPWKHV

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2604	8784	A	2644	1	413	EEGMDLPDSSGLFQHQTTYNRVSPCR RTECMESFPHSSSLRQHQGDYDGGM LFSCGDEGKAFLDTFTLLDSQMTAE VRPFRCLPCGNVFKESALINHRKHS GEISHVCKECGKAFLHLLHLMKHQKF HTGKRHV
2605	8785	A	2645	1	381	GKVVEKEKASQLQNSSSSSGKEGV RPSHSLPTTSLEFSSVSAEKSPVFAVT PGSTERSMTTPRSSTAPFESTPCPLPIS PTAAPRTVKEQTVSAGDNVIALPDN EVELKAFVAQAPPEVATYSYV
2606	8786	A	2646	1	384	VGPEALWAHVMTMNDQNLGFKAGYV IQVLEASNKDWWWGSEDKAEAWFP ASFVRLRVNQELSENSSTPSEQDE EASQSRHRHCENKQMQRTNVIREIM DTERVYIKHLRDICEGYIRQCRKHTG CI
2607	8787	A	2647	3	579	KCEECGKVFKKNALLVQHERIHTQV KPYECTECGKTFSKSTHLLQRHFHTG EKPYKCECGKAFNRRSHLTRHQRI HSGEKPYKCSVCGKAFTRSTFVLHH RSHAGEKPFVCKECGIAFRDRPGFIRL YIHTGKPYECIECIECGKAFNRRSY RTWHQQRHTGCKPFECNECGKAFCE SADLIQHYII
2608	8788	A	2648	3	410	LPKSHFISARHQRRLVDPAAASKKELS LPRRGSFCTRNSNRKSLIGNQSPALPR PHSPLSAHAGNSPQDSPRNFSPASAH FSFARRNDRTDGRRWLSASLPSSGYG TNTPSSTVSSSCSSQELHLQLPQPTP DLY
2609	8789	A	2649	1	411	KPYECHECGKAFSHRSALIRHHIHTG EKPYECNECGKAFNQSSYLTOHQRIH TGEKPYECNECGKAFQSFTLTQHQV IHTGEKPYK.CNECGKAFSDRSGLIQH QRTHTERPYECNECGKAFGYCSALT QHQRLLY
2610	8790	A	2650	3	397	GCVFQSGSSREVTPIRAQPOGSGPOP STPPQVLSAVIISPPSGRRERISRLFSSA SSTAKENSKKIKMKFPHTVPTREPKS KINKGGIPQRNINDSLEITKLDFSIIVSE GEMSSFAPQFRACNIQNPPAV
2611	8791	A	2651	292	387	SSFSVGIGYNIWVPMASCDFSIRTYT YADCI
2612	8792	A	2652	3	694	VINVSPLEWGHVLLVPEPARQLPQRL LPGALRAGIEAVLLSLHPGRVGFNSL GGLASVNHLLHGYLAHLRPVEQA PSEPLDPGGHLHLLQDLPAAGFLFYTR GPGPDLESLSRVCRATDYLTDEIAH NLFVTRGRPPGKTSPPSALTGVVIL WARKSSFGIKDGEAFNVALWELAGH LPVKTSQDFSSLTEAAAVALIQDCRLP PSQAEDVQAALVALMSQEEQ

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2613	8793	A	2653	1	379	RKL TTFPKCFLGSEFVSWLLEIGEIH PEEGVHLGQALLENGIIHPTDKHQF KPEQMLYRFRYDDGTFFPRNEMQDV ISKGVRLYCRHLHSLFTPVIRDKDYHLR TYKSVVMANKLIDWLI AQGVY
2614	8794	A	2654	2	402	RKL TTFPKCFLGSEFVSWLLEIGEIH PEEGVHLGQALLENGIIHPTDKHQF KPEQMLYRFRYDDGTFFPRNEMQDV ISKGVRLYCRHLHSLFTPVIRDKDYQISP YKSVVMANKLIDWLI AQGVYSSAVA IH
2615	8795	A	2655	165	384	EKRGGFWPQGGRRGEGKIGIKGTT.GPG GKRNFPGSPKPGKGGPQNGQFL VSQKKRGFPMVTRGGENPRPQ
2616	8796	A	2656	1	393	RHSTIVLATNDKRDQEKYGLLNVTKIA ENGKKVRKNWLLSSWAVLQGSLLFT KTQGSSTS WFGSNQSKPEFTVLDKGA TIEMASKDKSSKNVFEKTRQGTTEL LIQSDNDTVINDWFKVLSSTINNQA V CI
2617	8797	A	2657	3	175	MAGLINGYCRLNGTSSQSFILRPQKK GERALPSIPKLAHSEKQGMRAAPPV SGKGL
2618	8798	A	2658	1	361	RVPPIIHVQRTDQLPQSIQQAAMRYLR SQCVDDQVGIIRKSGVKSRIQNVQRMN ETSPDNVNYEGQSAVDVDMIKQYF RNLHEPIITSELASTFLQIYQLLPKDQ WLAAAQAAATMLLRNV
2619	8799	A	2659	2	348	KVGPARLARKMGVKLGKRVFVGN RGVEFGVCNSVYSSLSLQKQSWCC PTSPFPKFLSGHTSPLHDANGSLDQV GYSIRFEDCTSERITVLRMTDGMLLR EFLSEPDLASRYRL
2620	8800	A	2660	1	397	KLPHRVDTGTFVVYDGLAFFNKERT RNIVKFDLRTRIKSGEAIANANYHDT SPYRWGGKSDIDLAVDENGLWVIYA TEQNNKGIVISQLNPYTLRIEGTWD AYDKRSASNAFMICGILYVVKSVYED DVY
2621	8801	A	2661	3	397	IIEGHKAGVGVQVIAEAGKSRSCDGTG AMNFEVCGYDAFPVGYEYAGFPHM DDKQKAREIKFSYIIHAEQNAWTCR CQEIPEERSMIFVTKPCDECVPLIK GAGIKQIYAGDVGKKKKANISYMR FGE
2622	8802	A	2662	3	404	AQPVWQWQVTVWAVHQALHGKIDF PVLGAGLEPSQPPDCRAEYTFQAE RLCQATYEGEWCRGRPHGKGTILKWP DGRNHVGNFCQGLEHGFGRILLPQAS EDKFDCKYKCHWREGSMCGYGICEYS TDEVYKGI

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2623	8803	A	2663	3	408	YLKEDVPTCGYLVLSNSRWREWRWC RVKDNKLIHFHKDRDTLLKTHIVSPLRG CEVIPGLDCKHPLTFRLRNGQEVAV LEASSSED MGRWIGILLAETGSDTPE ALHYDYIDVEMSA SVIQTDKQTFCFM NRRV
2624	8804	A	2664	2	177	ROPTINRSLLANCINALSDKGSSKY IN YRDSKLTRLKVPATAGPGHWAPR VRLPD
2625	8805	A	2665	1	465	ITQGPVVDWNDIAGLDLVKAVIKEEV IWPVLRSDAFSGLTALPSILIFGPRGT GKTLGLRCIASQLGATFFKIAGSGLV AKWLGEAEKIIHASFVACRQPSVIF VSDIDMLSSQVNEHSPVSRMRTEF LMQLDVTLSAEDQIVVICATM
2626	8806	A	2666	38	393	LRRFSPSQEKLFGKGGSDRFQKVQ EMVESNEAKLVALVNKFYGLKQNT YCFPHSLRWIVSQMYTILSCVDRLEV GEVRAMCTDLLACFICPAVNPEQY GIISDAPINEVARMA
2627	8807	A	2667	2	443	VHTSRVILFTPLDAYRFELMRFRITVF DEKTLPTFLRTATSVSGAEVEVQSWL RMSGFSAIRDPLTQVPCENVMI RYP VPSEWVKIFRRFSLVGEKSLKAKVNR GARFGSTSVSGSEPVIRTVTGADKYE HSIAGAVEDTISRPA
2628	8808	A	2668	1	424	QPD LALARSLLPAAELPVETPKRAGA EVSVSEVSSPGPPKQADLPDAKDS PG POPTDPPASEAPDRPSKPERAAMNGA DPISPORVRGAVEAPGTPKSLIPGSD PGPAVNRTESPMGALQPEAEIEWPG RPQSHPPAPLY
2629	8809	A	2669	1	420	AYSWLISYSGPVIDGDVIPDPEILMEQ GEFLNYDIMLVGNQGEGLKFVEGVV DPEDGVSGTDFDYSVSNFVDNLYGY PEGKDTLRETIKFMYTWDWADRDNPE TRRTTLVALFTDHWVEPSVVTADL HARYGSPTYFYAF
2630	8810	A	2670	2	392	PRPAEPQQLDALDFLVGSGCDHNVK DKEGNTALHLAAGRGHMAVLQRLV DIGLDLFEQNAEGLTALHSAAGGSH DCVQLLLRAGSTVNALTKNLSCLLH YAALSGSEDVSRVLIHAGGCTNVVD HTPVC
2631	8811	A	2671	2	396	CPSRCRAYERVTRSTIAKIYQQSAEA YSHTERVSLARSYGASLCPSGYSPIDY RDGSMVMNMLHIHNIVWSQACLGACA P LLEKKLSPPEPCSDVVG LPSGDVG HLRDGSYHGSAVASSSSSSSS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2632	8812	A	2672	3	436	KRLESSWHGRPPLEKNREKISAPPHR RAQKVMIRSSSSSSSYMSGSPGGSPGS GSAEKSSDDVDISTHPSLPLAREPVPV LSIASSRLPQESPPLPESRDSHPPLRLK KSFEILVRKPMSSKPKPPPKYFKGQ WYAAAAQRIYQG
2633	8813	A	2673	298	852	PGLPRCAGAMAGKGSWKQFVTGTLWA VAGCGTREGCVSNLLPGHGAWLHTG TLAEKMHSPGFTLLPWPVLSASTQLC RPPAPASRGHPQPNMSSAAHLLCRQV KSRLAFGKPLVEQGTELDADIAQSRVK IEHARFLVLAHMLDLAGNKAAL DIAMIKMVAPSMASRVIDRAIPAFWS NRGWAA
2634	8814	A	2674	435	8	SSSSSSSSSSSSSSSSSSSSSSPEAE MDELTEVGFGRKWMIMNFAELKDYVQ TQCKEAKIRDERLQLLTRITSLERSLM TRRSRKTQHEWRSRCRCGSPIT
2635	8815	A	2675	1	398	GSMVVPKEQSWIPKIFKKTCTTFIV DSTDPGGTLCCQGRPRTAHPAVAME DAFGAAVTVVWDSDAHTTEKPTDAY GELDTFGAGRKHSNFLRLSDRTPAA VYSLGTRTWGLRAPNLVVSVLGGS
2636	8816	A	2676	1	437	PETKGDGRGKQGLERGERGEPGAPGP KKGQGESGTROPKGSGDRGEKGD GAQGPGRPPGQKGDQGATEIIDYNGN LHEALQRITTLTVTGPPGPPGQGLQG PKGEQGSPIGMDGEQGLKSGKGD MGDPVFWPLWSNLGVS
2637	8817	A	2677	1	377	EPAVVDNVLPIDINQIPAEGGGRIVLY GDTNCLDDSRQKDCFWHLDALQY TSYGVTPPSLSLGNRQRPSPGAGSVT PERMEGSHLHRYSKVLEAHLGDPKP RPLPACPOKTWAKPQPVLRPL
2638	8818	A	2678	3	388	GPQFLNHKRNQARENFSKWKKCGK GFTRSSHLTKHRIHLGEKPYICEKCG KAFNQSSTLNHKKRIHSAQKYKCEE CGKAFK WSSSLNEHKRIHAGEKPFSC EECGNVFTTSSDLAKHKRIHTGDV
2639	8819	A	2679	424	2	HLNFKNNFLNLYPNTFLNFSHVS HLGNNKLQNBGGAFGLGLSALKQLHL NNNELKILRADTFLGLENLEYLQADY NLIKYIERGAFNKLHLKVLILNDNLI SFLPDNIFRFASTHLDIRGLYCGRSE DQATSRHDI
2640	8820	A	2680	379	0	FGSLFFSSLLFSSLPFSSLLFSSLPFSS LF
2641	8821	A	2681	2	283	RVDPRVRVLVDIKDTEPLIQAKTTL GSKVVNSCHROMAEIAVNAVLTAD MERRDVFDELKVEGVGGRLDTK LIKVMVLMQRETKTSLF
2642	8822	A	2682	2	182	WPMQWARASGLKIFFLIETFRCAVQ AGLELLDSSNLPASAFQSAIGTVSLC AWPGLFL

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2643	8823	A	2683	108	386	HYEGEKHYECNEFGKFSKKSNTQH QRMYTGKEPKDECKENEKALKLYHT QNERTHAGEKVYDCKCKGKFHEKA CLTQHQRNTNTTGKPSKCI
2644	8824	A	2684	99	397	CWLTAKHRLSLQAPQQCSLHCSERL PGSPLEAAPAQPGQSSFDRTAPGPM PGPREGTA GNTRSPTAGLGLPLPV PAALGEVTLPGITDLPVVER
2645	8825	A	2685	2	151	RGNSQSPGAKYIIRDNGDRDLRFHPK PSDLHLQTGYKARSRPGPLSAT
2646	8826	A	2686	2	373	VDQPCPSLQAWSPEVHLHYMNMIV PCPTGECSELLELQHPVQADITLWV TSFFMESSQVLFDTIELLENKESVHLG PLDTFCDIPLTIKLHVDGKVSQVKVY TFDERIEDAALLTSQPHCI
2647	8827	A	2687	4	412	ARSLPAAELPVETPKRAGAESVWEV SSPGPPKQADLPDAKDSPPGQPTDPP ASEAPDGPSPKPERAAMNGADPSPQR VRGAVEAPGTPKSLIPGSDPGPAVN RTESPMGALQPDAAEWPGRPGSHPP APPVY
2648	8828	A	2688	1	409	SSGTGAASYYVNTGETEVGFVPTFGP CYLNLGSPREYTGFPDYPDELNTGK GEGVAYRGRILVELA TFLEKTPPDKK LEPISNDLLVVEKYQRRRKYSLAV FHSATMLQDVGEAIQFEVSIIGNYGNK FDTTMY
2649	8829	A	2689	3	463	SGLVYSFCPAPASCOAPLPTVGLPHF CTGSNLPALMPASSLASWPPPALLET SLHSGNLPHEL PNSALSASLHLSWPP CTSSPPNSLDLHPGLLLPTFIVLGISQ PSVLFFLPFFIISPFLSTSRPLPASSSP LSILFSNLPSPFTLQN
2650	8830	A	2690	289	478	SQVSARNFALSVPPGQGGCDKTRSRVT LQEWNDPHDHDLEAQLIYRQCIAAA VEDPRMRSDTDT
2651	8831	A	2691	3	459	AIDLDEGVNGEVITYSFRKTIKPLPKM FHLNSLTGEISTLEGLDYETEAFYEME VQAQDGPGLSTAKVLLITVLDVNDN APEVTMTSLSSSPEDTLPGLTIALFYL QDRDSGKNGEVTCITPENLFPKLEKSI DNYYKLVTTKNLDREVYS
2652	8832	A	2693	459	60	SSSSPRANFWPGKKNPGAPGKKVPSR GGGKKRGKAGGPPGKGKGQGGPKR GEVFF
2653	8833	A	2694	351	440	LMTSGEISSYQDAIKIEIENGRPCIAAF G
2654	8834	A	2695	38	461	HQPSLKHTNFTTQEA VAGISVGPGRGP RGGRPFGQCADCGMVFTWVTHFIEHQ KTHREEGPPPCPEGKVFHLNSVLT HGKIHLPEPPRKKA PRSKGPRESVPPR DGAQGPVAPRSPKRPFGQSCVCGKAFP WMVHLIDHQKL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
2655	8835	A	2696	1	440	PCHSVPPHSHLLNSHYEKLDPVGYRV VTDKGFNFSPADEAFVCQKKNHFQIT IHQVWVGSPKPFVETEMGLKPIEMFYL KVFGTKVEATNQIIAIEQSQADRKKI FNPVKIDLLADQVTKVTGLRHLFSEA TANNMRKKGKPNPDHV
2656	8836	A	2697	1	366	QKSHKMVKMKMCDYLSNSGLCSQET LEINNVSASASLSAGCHSTNALSTV NQKKPIGHHTLRTPDITDALDSS LTDSIAPALGEKHCCCLCTPFTGELSPL QLSLQALATTSPFTLS
2657	8837	A	2698	298	0	GFTPRGGGRGGKRGNGSGKNVMV EPHRHEGVFICRGKEDALVTKNLVP ESVYGEKRVISIEGDDKIEYRASNPFR SKLSSS
2658	8838	A	2699	11	208	VLFLVTGRPPRGSQAAQGGPAKQLL PLERVYQEIALLKLDHVNVLKIEVL DDPAEDNLYLGE
2659	8839	A	2700	3	380	KKFWARAPGFFPLTPPLGGPKPGGFF GGKGLGPPLPPGETTAPFSSSSSGER GPSFYPPSSSSSSSRKIP
2660	8840	A	2701	3	389	ALQRRLNKHRLSLFYNERGLFKSEE PPTEEEEESPGDGEPTLDGELVLLQD PLVPPPPSQAPLSAERVAFFKGLPWA PKVRQKDIEHFLEMSRNKFIGFTLQ DITDLVGLPRPIHESVKTLLQHCI
2661	8841	A	2702	3	424	SFPIKHCPVMLVLALLQTASWHTVR HELISTMMPHFHGNHPIAIIHMYA GGQGSQSIRELIMHAMAWEYMRGEQ YDQAEISRULDVAQDLKALSMLLNG TPFAFVIDLAALASREYLLKDKWLT DKIRELCMRSL
2662	8842	A	2703	1	408	QPTVIDLRETDQGYKGLSVRSVCWR GDHILVGTQDSEIFEIVVQERNKPLFI MQGHCEGELWALAVHPTKPLAVTGS DDRSVRIWSLVDHALLARCNMEEPIR CAAVNADGIHLALGMKDGSTVLRV RDMTECI
2663	8843	A	2704	2	403	EGGGPYAGSSTKLAEDAALWQVAES KTPLGVAFSSLQEVIIQLVDSHPDIHL NVRDRQGLTPCACTMTFKSSKSAEAI LKRESGADEQVDNKGRTFLHVAVQT SDIESVFLISVRANVNSRVQASKLT PHSY
2664	8844	A	2705	1	151	LDAWNRELLDKYCVAYGVGIIFFFK VHKKGQPRAVQSPCLSSVPEFSVK
2665	8845	A	2706	1	273	STLPSAVSAPLTPVLVLLQLQRLTPKL FHEVVQAFRAAVATIRGDQESAEN KFQVTDSSAFNALVTFCIRDLIGCLQ KLLFGKVAKDSSR

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2666	8846	A	2707	64	285	GPLVIFQAPGTPILARQVAPTPIIKPVF QAPATVQPRATLQRLPGVQVKQQA DFLRPQGPFSVFLKQRSGLR
2667	8847	A	2708	308	543	DPVTMTSSNPADPIGDQWEEEEEFGN YAVDLVKHIRSEFGDYFDICVAGEWL DHPGGGDGAREAMPREPVGVRFT Q
2668	8848	A	2709	24	386	DFSRVFLTELPIPSPNHSHLTPHTHK THINAHSRDVSPLARLLPSPCISQHN PNPHYPTQTPTIQKFVANSITKPGHMVS FQSSSVVVTKQAVATVSSSACLFGKN HSGYYLQLFSSL
2669	8849	A	2710	1	437	GPYLLQFLTPTVRFTGALTPCLRSVLH AQKRQEAAGADAFLIQYDAHASLPSPY AVTGRLLVVSPPYLGDGRGA AAVR LLSVLHPSIHLPLGQHWETTVPKLLGF LDEHTEETLPQQEWEKKMFLRDT LASIAAAVDDTNYRP
2670	8850	A	2711	3	439	KGKAAQENGAPCEPSRNPLEPFASLE QNRREAHVRVSRKQKLQLEDEFYT FVNLLDVARALRLPEEVDFLYQYW KLKRKVNFNKPLTPKKDEEDNLAKE EQDVLFRLLQLFRILSRSHRVSRKQ KLQHLEDEFYTFVNLL
2671	8851	A	2712	1	400	LESVRDSGKKHNGLTCEELA EKDDIK YRTSIEEKMTAARIKCPKCGTGLIKS EGCNRMSSRCGAQMCYLRCVRSNGY DHFCQHRSPGAPQCECSRCSLWTD PEDDEKLEIEIQKAEAEQKRRNGEN MYC
2672	8852	A	2713	3	433	TEDSEDVSRKSVPVPGALDKGSLEET EESIDALVSSQLSTNTHRLASGLSTS LNSMMSVYSETGDYGNVKSVEILL HISYCYKTGGLYIFVKNCRLPGDEK KQSTDAYVKSYPKPAKSRKNKNETKI STGTVLRLRLCR
2673	8853	A	2714	264	444	ASSSEDPPVTNSSSPFGAQLAVQKY EPLFPFSDCRENKMMLTMLQA
2674	8854	A	2715	1	448	ELKIYWGTTTSGKPHVAYFVPMKIA DFLKAGCEVTILCADLHAYLDNMKA PWELLELRVSSYENVLKAMLQSIGVP LEKLKFIKGTDSQLSKEYTLDVYRLSS VVTQHDSSKAAAQVVKQVEHPKLN GLLYPALYCGRSGGVLATVRG
2675	8855	A	2717	3	490	FFSPNGIPAGENPFCKQCQCAFSSHS SLRIHERHTHTGEKPYKCNECGAFHS STCLHAHKRHTHTGEKPYECKQCGKA FSSSHSFQIHERHTHTGEKPYECKCGK AFKCPSSVRRHERHTSRKKPYECKHC GKVLSYLTSFQNLHGMHTGEISHKCS LCGTVY
2676	8856	A	2718	1	87	PDEGSVYCVARNYLGEAVSRNASLE VACK

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2677	8857	A	2719	102	371	LVGGCKPGEFLLLFNLLFSKQVICVHDVSSIYRVPLLEEQGVVDYFLRRLDLPIERQPKMLMKWKEMADRFACNEELGVLASFLL
2678	8858	A	2720	2	424	MLRSWTRERVIGDAAKNQVAMNPTNTVFDKAKRVIGRRFDDAVVQSDMKHWPFMVGNDAGRPKVQVEYKGETKSFYPPEVSSMVLTKMKETAAYLVKTVTNAVVTVPAYFNDSQRQATKDAGTIGLNLRIINEPTAGA
2679	8859	A	2721	3	216	GPAHRRGPAGCPGHGLSLPAWGGVGAKGGGNEVAPSHSGSCLPLRLYLHAKNIHHRVLKSTSIYLSLWG
2680	8860	A	2722	2	108	VDQKYKRQAQADRVNLRLRGYYNQSEAGSHTSPL
2681	8861	A	2723	2	392	FPSGLTNLCLAKTAFSPRGLQALGQTFGANPAFASSRLRYDLSKNPGLLATDEANALYSFLAQPNALVHLDSLGTDCVIDLLGALLHGCCSHLTLYNLARNSCSHRGLSTGRVERPRRPSSSSAAPTH
2682	8862	A	2724	3	420	GAYNVSCSKHMQHIRMSLRGKAVVLMATNTMMRKAJRGHLENNPALEKLLPHIRNRVGFVLTKEDLTITDMLLANMVPAAARAGAIAPCEVTVPAQNTGLGPEKTCFFQALGITTKISRGTDILVSGPLTVLTKQMG
2683	8863	A	2725	3	395	QILSTVIYDSELOLELPAVSPEDDGEYWCVADNQYQGRATAFNLSVEFAPVLLESHCAAADRTVQCGLVVNYIPDPAVFVVLSPPVSVKVCWEQWLYLLFAVVLVSLYTRIVLYVIYNLLLYVALFLS
2684	8864	A	2726	1	354	ROIISRQKQVPMFSGELLSPRCSFTCGKSQVTSSEGLLCLTCSSSHQSLPSQNPILKNITDYLIEEVSAAEEELGSSGGAPEEPKPEGNPAEINVERDEKLIKVPVAARGTWGLGR
2685	8865	A	2727	226	586	EPPYFMFCLSVNTRTVLSPVSTTQWIDKGANMIQWRRHSLVNKLFRNFFLHNLFFYPQRKKIHLNLTNSKTNISKWIMQLNINYKTRKSIAENIRQNLHDTELGKVFFIINKHKPLK
2686	8866	A	2728	3	398	NTIFSDSPYACTLVQENCLNLHMINFIIHNEVQEAFFKELLQIHQYVMALS EEFDPDIAGWTGKYYLEEKIVSLSKNLLGALTDHFSEYIGRASIFTCQLSRQGEQFLHRNIQEYLMILTEPDGKGKQK
2687	8867	A	2729	2	388	KFQNALLVRYTKKVPQVSTPTLVEVSRNLRKVGSKCKKHPEAKRMPCAEDYLSAVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYGPKEFNAETTFTHADICTLSEKERQILKRTALV

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2688	8868	A	2730	1	392	VKFGINYDYPNSSDYIHRIGRTARST KTGTAYTFFTPNNIRQGSDI.SVLREA NQAINPKLLQLVEDRGSGRSRGTGG MKDDRRRYFYFEGKRGGFTFLDRER YERGVCILDAREFGALITKGVDSAPR
2689	8869	A	2731	15	425	RLFTIRKALSQKGGGLAQAFYSAQE VSLILSDVVGDPEVVIASGPTVASSHN VQDCLHLNRYGLRAALPRSVKTVLS RADSDPHGPHTCGHVLNVIGSNVLA LAEAQRQAEALGYQAVVLNAAMQG GCKKYGPP
2690	8870	A	2732	267	434	IQPDFSISGFPFKGDPNSPVLLDPVL CALTKKKHKPTGSLVLCYQIVRGGCG AR
2691	8871	A	2733	369	481	ICVKTFPPLALQVRMAAAEHRHSSGL PCWPYLTAETL
2692	8872	A	2734	1	409	FNMSRRGLPLVKRGPPRSGGPPPKR SAPSGPVRISGMSGGRAPVSRGRDSY GGPPRREPLPSRRDVYLSPRDDGYST KDSYSSRDYPSRRDTRDYAPPPRDY YRDYGHRSRRDDYPSRGYSRDRDYG RDRDYS
2693	8873	A	2735	3	413	PGAIEYKGANIQLLDLPGIEGAAQKG GRGRQVIAVARTADVIIMTLDATKGE VHRPLLEKELESVGIRLNKHKPNIFYK PKKGGGISFNSTVTLTQCSEKLVQLIL HEYNIFFNAEVLFREDCSPDEFIEAIVG HSA
2694	8874	A	2736	2	400	PLVQCGGIPFDYSHPRDVVSNLSHL GAPGGPPAQGLPYCPERSPLMGVP SVAFIPVPSLAEIVERNPRVEPGGRYR PAGCEPRSRTAIIVPHRAREHHLRLLL YHLHPLLRQQLAYGIYVIHQAGNGT L
2695	8875	A	2737	8	453	YSAVEFPTPLRHLMTGYTPLTTDQS VRAAFSVPGQAGPGPNRPCPSLSLFT APGATLCGPQGAALRDWHRVGDFLA DLLSTLPLPLASAKEPKGDCALSAG RVPVLSYQVASVRKTTVLDVMRRL LQPKNMVMYSTGRDRQTNHC
2696	8876	A	2738	16	451	LVEFNKSLAADTKKQNDAPQAVSMP ATETKKASHVADTKVNTKAQETEA PSQAPADEPEPDSAAAQSQENQDTRP KVKAKKARKVKHLDGEEDGSSDQSH ASGTTGGRRVSKALMASMARAIRG PIAFWARRASKTRLAAWAP
2697	8877	A	2739	707	966	PYPMPCCSISTVLACGRPQATAVYKV SEYARRFGVPVIADGGIQNVGHIAKA LALGASTVMMGSLAATTEAPGEYF FSDGIRLKK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2698	8878	A	2740	9	469	HAYCQLGTREIANGHRITASDAGFLV GSHVQYRCPLPGYSILQGAAMLTCTYSR DTGTPKWSDRVPKCALKYEPCLNPG VPENGYQTLYKHHYQAGETLRFFCY EGFELIGEVTITCGPGHPSQWTSQPPL CKVA YEELLDNRKLEVTQTIDSSRQL
2699	8879	A	2741	1	468	PATPILARGALDRILKLDGQGPALQG FLVFHSGGGTGSGLTSLMERLSVD YGKSKLFEISYPAQVSTAVVEPYN CILTTHITLHSDCAFMDNEAIDYDIC RTNLDIERATYTNLRLRIPVSCITAS LRFDGALNVLDLTELHNLVPYAR
2700	8880	A	2742	14	445	NHAYSELGTRDKITGQSLRYGFVEYI DPKDAEKAINTLNGLRLQTKTKIVSY ARPPSSASIRDANLYVSGLPKTMTOKE LEQLFSQYGRITSRILGDQVTGVSRG GGFIRFDKRIEAEAIKRLKGQKPNGA TEPNTVKGANHS
2701	8881	A	2743	3	386	EVAELIDQHETMMKLVLEDPLVLSLR LEGGTVLARLRREELGTEDSRDLTLEA ATSLYDRVDEEVHRLVLTSSNRLQQ LEHLRELASLLKGNDOVRAAGGRRP GOHPLQARLAKATLSPSHCVFRALI
2702	8882	A	2744	2	449	PPEEPRLWTRAIRAKCMFFKDKTML CPMHKIKGPCBCEQLNSFAVFRVYIE RDEGKHIASIIQRRLRHMFVGGVLV VHAIGQLLPHQMADFHSAATLYPEG YEATRIYWSLRTTQSRCCYRCPIGENP GRTDTESLGPDPCPGTTGYS
2703	8883	A	2745	3	468	CLRQAWHEVVKVATQADNPLDLVLS RKLHLGPNDGRDPRLSLPGKLVFVS STGSHFSMLGIGDIDMPGLLCPVLR YDNYKKQASGSDSCGAPGANISGRM QKVSYPHCTLIGYFVGLLTATVASRI HRAAQPALLYLVFPTLLPLTMAVYLG G
2704	8884	A	2746	3	444	LEGPYAKLGRTRFVIDHQRLSGQGYCF SASLPPLAAAAAIEALNIMEENPGIFA VLKFKCGQIHKALQGISGLKVVGESL SPAHLQLLESTGSRREQDVRLLQEIVD QCMNRSIALTQARYLEKEEKWLPPPS IRVVGTEGEQTEEELE
2705	8885	A	2747	1	426	PCTPSLARGRTGTYRQVHFPEQLITG KEDAAANNYARGHYTIGKEIDI.VLDR IRKLADQCTGLQGFLDFHSGGGTGS GFTSLMERLSVDYGGKSKLEFSIYP APQVSTAVVEPYKSLITHTTLEHSD WAFMVDNRRGHL
2706	8886	A	2748	340	468	PNSPGLTSHRDMQPLLSALPNVGMF DPSFRVPGTQAASNTNT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2707	8887	A	2749	2	456	LYLHTPLCLARGEAAKSPNGLVVVSIFI KVSDDSNPFVNRMLNRDITITRTYKN DAYLLQGLNIEELYPETSSFTYDGS M TIPPCYETASWIIMNKPVIYTRMQMH SLRLLSQNPQSFQLSMSDNFRPVQPL NNRCIRTNINFSLOGKDW
2708	8888	A	2750	294	417	NQVCVHTPRGVRVEGWLCDSPHRVR AHLGCFSNASCITNCF
2709	8889	A	2751	104	432	IGDSLTPDDSLKCPSLIFPRSFVHRGR PEPLDFHLMFLPSLLHQASAEQQR FFMPA WNLIIQTYAQ TDMGHQMEY SVYINIGWAGPCELTMCGVPPRAKIGV MMLR
2710	8890	A	2752	2	410	GDVLQSVLCGADALIPVQTGAAGSAS LTLLGNGLSIYQVQVVGTSSEVVAMT LETKPQRDRDQRTVLCHMAGLQPGGH TAVGICPGLGARGAHMLLQNELFLN VGTKDFPDGELRGHVAALPYCGHSA RQTWWALAA
2711	8891	A	2753	2	178	FFFSFYMNLFLYNVLKTPGLGISFFL FFFIKLLYNNWPDFDFNLSSEICHD LKKK
2712	8892	A	2754	7	424	TRYAGRGAGMQSSLYVCCWRCVPG DSTAGIWNLEKSNNGSGTQLVMRLCI REGGHDVPSNKKVTSLEWNTNGTL ATGSYDGFARIWTDGNLASTLDQH KGPIFALKWHRKGHYLSAAVDKTTII WDAHTGEAQQQF
2713	8893	A	2755	9	421	PSVRFDVYNVDSKTNISPKDKFLGQA FLALGEVIGGQGSRVERTLTGVPGKK CGTILLTAEEELNNCRDIA TMQLCANK LDKKDFFGKSDPL VFYRSNEDGTFTI CHKTEVVKNLTLPVWQPFWIPGRAL WNGDYDR
2714	8894	A	2756	2	428	QYALRIYCYWGARKQEQEVOEPRLIF SFNEMDNRYEGLEVISPTFEGVLYL NQMGGFNFVDDGSLPGCAGLKLSDG RKRSMSLVWEFITASGYLSGRKIRSR FQTLVAQAVDKCTYRHVVKMVA DT NEVKLIIRDYVVOI
2715	8895	A	2757	68	465	TFIQALMAGTLKPRGCKLACLFQKW QRMVPPPAEPTRQQPSYRRKRKMSG GSTMSSGGGNTNISNKKKSPASTFA LSSQVPDMVMVVEPTLMGGEFGDED ERLITRLQNTQFDAANGIVAEPRAKN GVGIA
2716	8896	A	2758	25	450	PKSARKKEEARQAEFVIIGQALKLSI VRGDAPSSLAASGICKKEPWEPCFC SNFPHEAVCADPWGQALLVSTDAGV LLVDDDLPSVPVDFRTPVQMHVL ETLDLLVLRADKGDARLFFVRLSAL QKLEGKQAWBEH

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2717	8897	A	2759	3	450	LGNSDLTVPTGMVKHMTARDLCQLL VYLRLHCVDNDRSLAKHHPLPIKRG LLDHALAGQAESTIPGQRKFLFMKNY AKYELFIYPMNFPPDQDTWCCQSN GSQTOLLQNLNSSSCPEIQGLFHVKE LGKKSWWKKLYVCLRRSGLYC
2718	8898	A	2760	1	412	LKRVNPEEFISYPLREKIDLRNIFAN VDPGAFTNLFNRLSLRLKGNRVKLV LGVFTGLSNLTKLDISENKIVLLDY MFQDLHNLKSLEVGGNDLVYISHRA FSGLLSLEQLTLEKYNLTAVPTALFL PVARPN
2719	8899	A	2761	6	266	PDLRLPGRGSGTRQKGAEGKPPGHSS HVLCMGISSDGEYLAGSDRSKLILW EAQCQCHLYTPTGHRDAVSVRSWVY VSGSLVGTG
2720	8900	A	2762	3	460	YQVLAPTAAYDQTGALVVGPGARTG LGAPVRLMAPTPVLISSAAAAQAAAA AAGGSASSLTGSTNGLFRPIGTQPPQQ QQQQPSNNLQNSFYGSSSLTNSSQSS SLFSGHGPFGSGTSLGFGSGNSLGA ISALSGLAFFVPRPSSQCGA
2721	8901	A	2763	1	480	SDSENNVNFQFMPSCRGVYELTSHIN RILHCTDNGATCFKGHKWYLVVSGG TGILSMFAAKAGAKKVFGEICSSISDY SEKIIKANHLNIIITIFKGKVEEELPV EKVDIISEWMGYCLFYESMLNTVIFA RDKWLKPGGLMFPDRAALYVVAIED RQ
2722	8902	A	2764	291	486	LSLTCVPSSVQEEEMNTWQIAISSAIS DKHEVSASTOSTPASSRAQLTPNVV TITSESSPGKRE
2723	8903	A	2765	2	411	VSEGGDYLSCEVGYFVDEDRWVNL HIHNLHDGHAVAVTESYVVVAGSME PGFAKTVERYNPNLNTWEHVCSLMT RKHSFGLTEVKGKLYSIGGHGNFSPG FKDVTVYNPELDKWHNLISAPKILRD VKALAIEDR
2724	8904	A	2766	39	471	GEMLNQDQSLSEISNTLTNEKMKIEECI KKGKKDYEEESHQRAAAAEVSVLEN WKESEVYKLQIMQSQAEAYLKKLELI SHDPAAYPDMESDICSWELFLSNVTK ETEKAKYQFEEQIKAIKNGSRVSELSK VQISELSPACNTG
2725	8905	A	2767	3	399	LRSQGKEAFAFRKVVQATMVRDRQH GPVVNVKRIQVKRSRSGGLAGPDG TKSVFGQMCAMNSFGPDSLILPHR VWKVKFGESVDDCGGGYSEPIADIC EELHNLGLTPLLIVTPNGRDESGANRE CYLLRP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2726	8906	A	2768	50	436	LPHLCPLPAVGHAGASGAAGDARSS AGA WFAQLDLKLKTTFDPRRLGLGA SCGQAGYPRGTGSGGLCAGCLPHLP RPAAGDPDPGRTDHVGGQTHAAVPP AIQLP VSPVHP VALDKAHTCLGP AGV
2727	8907	A	2769	3	391	CAPATPSLARGIVK GKARLPVKWMA PQSIFDCVYTGGSDV WTYGILLWEIFS LGLNPYPGILANSKLYKLVKDGYQM AQPAFAFKNIYSIMQACWALEPTHRS TFQQICSFLQEQAQEDRRERDYNLP
2728	8908	A	2770	21	425	LQPAWHEGCVYINGHKW WITGILDP RCQLCVFMGKTDPHAPRHRQLGLGA VPMDTPGIKIRPLTVYGLEADPGGHG EVRFEHV RVKENVVLGPGRGFELAQ GRLGPGRIHHCMLIGFSERALALMK ARVKS
2729	8909	A	2771	10	437	PALLFPGTQWETKTI FTGHTAVFED VSWHLLHESLFGSVADDQKLMWDT RSNNTSKPSHSVDAHTAEVNCLSFNP YSEFILATGSADKTVALWDLRLNKLK LHFSFESHKDEIFQYQWSPHNETLASS GTDRLNVWDL
2730	8910	A	2772	26	464	RARTFCLFGTFLLEVTLL WIIQPNVN GGIENTLQKEVMQYDYYSYDFIFLL AAFRFKGVILAYAGSRLRHWWAIAL TAVTIAFLLSKVLSKLFSSQAFQYE LPHISFLAWIETWFLDFKVLPPAEAE NRLLIVQDASERA
2731	8911	A	2773	6	472	RRFMLTPFLSRGECVTPESENLTSS SGAIDQSSCTGTPLSSTISSPEGPASNS LAQSVMSMASSQINTDTVSSMSGYI APGTTEEAGEALSSQPASRAPSEKGE LPAESPDNSNFAGLPAGEQDAQGNDVI EEEDGSPTEQEGHRTCAFLSME
2732	8912	A	2774	30	459	LQTRADRQALNEHFQSIQLTEDQAS GERQRLVETHATRVIALINDQRAAL EGLLAALQADPPQAERVLLALRRYLR AEQKEQRHTLRHYQHGAADVTEKA QQMRFQVHTLQVIERVNSQLGLLE QNPHLAQELRPOQE
2733	8913	A	2775	47	444	RHLEILQLSRNRHRTIEIGAFNGLANL NTLELFDNRLTTIPNGAFVYLSKLKEL WLRNPNIESIPSYAFNRIPSLRLDLGE LKRLSYISQGAFAEGLSNLRDLNLC NLREIPNLTPLIKLDELDSLGNHL
2734	8914	A	2776	1	441	PSYRIPGRREWQNTIRRLRLPTEASGL GSPFPNTRKELHSWKAENEAFTLADL KQLPELNPVLMPTGNEGTPLRFALE LIRACRLPPRIITQLQVQFPKGTGSSRY GNVPFEYEDSQTVEQEELAYTAEGEE IPHGTYLADIPASP

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2735	8915	A	2777	I	397	GRPTNSLRVLQEQLSQRQLRKEEAH NFSQKMVQLKEAQQRALLRRFELO SLSLQRRLEQIFWSQEKNNMLVQESQQ FKHNFLLLFMKLRWFLKRWQKGKVL PSEGDDFLEVNSMKFLCLLMEEEQY NAAAL
2736	8916	A	2778	21	463	RHEDLLAPDNALKIVDFGSAQPYNP QALRPLGHRGTGLEFMAPEMVGGEPI GSAIDIWGAAGVLTYYMLSGRSPFYEP DPQETDARIVGGRFADFQLYPNTSQS ATLFLRKGLSVHPWSRPSLQDCLAHP WLQDAYLMLKRRQTLTF
2737	8917	A	2779	294	464	HSRTSLRLTWSRRQKARAQLCLTRR DVATMNEQGFCKIEGRSKDMIKRG ENIYPGD
2738	8918	A	2780	3	410	RPSYHMQMSEPIVPAAPPPQGFQKE YHDPLEYHGVPGMPGPAHGFQSPM GIKQEPRDYCVDSVPNCQSSYMRG GYFSSSHIEGFSEYKDPRLYFDITCVV PERLEGKVKQEPTMYREGPPYQRRGS LQLWQVLV
2739	8919	A	2781	154	246	ICSQSTRLEKQQAASKEELEVVKVR SEIAL
2740	8920	A	2782	38	454	LGARGSGKESQEWAEASFVKNEL KGVEVGADTGSKSIEKGESEDEEEK LDDDDKSHESFQPSGAASRGKKFDE ESNASMSTARDETREGFYMEDGDP GAQLLHERTLAFSVWPKDRVMNRL YHICEAAVKGTW
2741	8921	A	2783	24	459	PLTTPSLARGLVPRRSPISSSKGGKGV DKIGPILLTKACKKGTSGLDKGEEQY GADGETEGQGLDTPAFLMGTEQLS TELDISKIPTPAPTLLKMTSSVPVPGPT GSAGPSLPGGALPTSVRSIVTTLGPSE LISAVPTTKSNHG
2742	8922	A	2784	2	424	AGGRGVVQAQRGPQPPGEGAGIPGHP TPPATLPSEPVVEGQASPWPRPRVLP HPALTLPVSSDASSPSPAPRPERPESL LVSGPSVLTLEGLGTVRPEQDPAKSP GSPLLRLGLSSGDVAAPEPIMGEPGQ ASEEFQPL
2743	8923	A	2785	1	452	ARGDADGCEALGTVAVPFDDDDKIV GGYTCEENSLPYQVSLNSGSHFCGGS LISEQWVVSAAHCYKTRIQVRLGEHN IKVLEGNQEFINAAKIRHPKYNRDTL DNDIMLIKLSPPAVINARVSTISLPTAP PAAGTECLISGWGNTLSF
2744	8924	A	2786	3	445	LWRSHEDRDRDAFHRCIFLCCREQF CCAGLRVFRNQLPRKNDIFYSEPPSE NPPPETGESVCLQKSGAHLCRDCGC LGPNTRCSRCHIAIYCGKEHQLDWR LRHRQACAQPDHLDHIIISDNHLPFEP EVIIEADEIMEVAEK

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2745	8925	A	2787	3	437	GIRHEKKPTFMDEEVQSILTKMTGLN LQKIFKPAIQELKPPTYKLMTQAOLE EATRQAVAAKVRCLKMPVLEERVPI NDVLAEDKILEGTETTKYVFTDISYSI PHRERFIVVREPSGTLRKASWEERDR MIQVYFPKEGGKI
2746	8926	A	2788	3	450	LAVIILITSQEYAVKIKKQPGHIRSRV FREVEMLYQCQGLRNVLELIEFFEEE DRFYLVFEKMRGGSILSHIKRRHFY ELEASVVVQDVASALDFLHNKGIAH RDLKPFENILCEHPYQVSPVKICDFDLG SGIKLNGDCSPISITPEL
2747	8927	A	2789	137	330	PSSQSDRDCPSVSIKSPMSIKTPQWL GTVAHACNPSTLG/G*GKWIT*GQEFE TSLANMVKPHLY
2748	8928	A	2790	1	373	FETESRSVAQAGVQ*RDLSLQAPPPA GSHLSLPSSWDHRRPPRPPN/CNFNL VETGFHRAQAGLELLTSGNPPASAS QSAGITGVSHRAQHQ*VLILRLVGS R VLEPEVGRVHLVFGAQMVKF
2749	8929	A	2791	1	167	PPRPANP*FLAMGRFHVQQAGLELL TSNPPASASQSARITGMISHRAQPQM PFE
2750	8930	A	2792	1	446	SPKSPFPQAGVQVHGHGVSHPPLPPR VQ*TFPLNPLRNWGHVPIPTLSKFLN FFFFW*RWGFTMLPRLILSS/GSPNPP ASASQASAGTTDVNHCARHAVLFGGT LLSLSHPCTFWLTLRHLEETRPGTNEL EEAKVPVLPOSSYYPS
2751	8931	A	2793	1	181	RISCPSS*SSWDYRHYVPPGLVHSCIFS RNRL/TLIARLV*NYWPQVIHWPWP PKVLGLQV
2752	8932	A	2794	1	272	VDFFFF*DGVSLLCCPGWSVVA*SQLT ASSTSRPTPFRLSLPSSWDHMRPPPH LANFLYF**RRGFTMVS/SPDLVIRPP WPPKVLGLQA
2753	8933	A	2795	1	439	GSLISIAQDGIQWHYHGSGLQPQLPGL R*SSHLSLGS*DYMHAPPHSA/NFCIF SKNGISPCPGWVLKTPGDSNRSHST LALPNVAEGVSPPTPRPQFSNLFTTL PTNLWSGGKKAKHFLHFNILKLVT LLLVFCQDPSTNTW
2754	8934	A	2796	20	484	IRGRVDLLHTLEGHALPIRSLTFSPDS QLLVTASDDGYIKIYDVCRFLLSVTL LPHASASSLLGAGKLTKHGKLQCCS* QAKRLWGRRHFNRSKKEEEGEKME KQEISQHKRGVKKREGAKENKVTK TKQKGQINPQRTLQRQVSWMLHPSL
2755	8935	A	2797	111	422	GAPKCR*G*KKTGTLTGG*GNCKAPG QL*KTFHQFLISITY/P*GPAISLLKIDP RELKTVVPTKTRT*LFAASFITKT*K YPRYPSTGDGISCYGFLELIH

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2756	8936	A	2798	2	352	LSWSHPVAAQARVQWCDLGSLLHPPPP ASK*FSCLSLLSSWDYRCRPPSPANFC VSVEMEFHHV/GPLKLLTSSDLPALPF QSAGITGVSHRAQAPNNLIGILNPVP PGSQWTSHEFAV
2757	8937	A	2799	3	244	KKNQGGAPGKPLFPFPFWGPGPGVPL GAPVWNPPGPKGQNPFFLSSSS*SSSS FSLFYPPFSSGGLGKKTPLTPKGGGPIK
2758	8938	A	2800	2	233	GPAVNPTPEAPARGFPGA/GGNSPSG PPRGNPFFFKNPPHYPLGAGAFFPPP PGG*AQKMPLPKKERGLTPNGPP
2759	8939	A	2801	3	646	YCSSLNFIPLSSFFFF*DRVSLVLPRL YNGTISGHCKLCLLGSSDSPASTSRV A/GTAGARHHAWLIF/VFLVNTGFH HVGKDLGLDLLNLVIYPPRPVKVLGL QA
2760	8940	A	2802	5	302	DSLAVSQAGIQWCDFS*LEPSPRLK QSSQLLSPSSCDYRCMPRPANVIFV ETGFHHVTQAGLKLSSSNPPALVSQ SVRVGTGMSHQSRPGCQYSN
2761	8941	A	2803	2	747	FFFRWSLDSVAQAGVQRCLNGLSLQA PPPGFKPFSYLSLPE*RGLKSAQRPRL ANVF/VFVFLSRDGGFTLLSPG*SGIS* PRDPPPSASQSA/GITGMSHHARPTYN F*TSFLFFL*LRAPMILLIQGRKVLVLD KLPLSITGLAS*ISRKYSFIHLYLFIFFETE SCSVAQAGVQWRDLGSLQVLPPRPF THSPCLSLPSSWNRYRHAPARPAKFCI FGRDGVSPYWPWGSQTPDLVIHLPRP PKVLGLQV
2762	8942	A	2804	2	327	FFFLMRQSLDSVAQAGVQWHDGLGSL QALPGGTFPSCLSLSSWDYRWPPPP CPG*FFVFLVEMGF/VLARMVSIS*P YDPPVASCSAGITGVSHRAWC/FWV L*CFE
2763	8943	A	2805	69	181	IIITLRYFYFFILAKIKVC*HLNQ NSGETGLRAEDKLVAHPYER*FWQL TVK*QI*IPFGLAIPLEVVYTDILTYLE CTQLLITLFTVITENKKKPNYQLVD WLNKL*YYSISVE
2764	8944	A	2806	2	272	FGDRVLLCHPGWSAVVQSWFPTTSA SWVMQSSHLSSSSWDERHASQSPA NFLHFV*RWGLTMLPRLASNS*AQVI CLPWPPKVLGLQA
2765	8945	A	2807	1	277	FFFF*DGVLRLCRPG*SAVA*SRLTVAQ PPGLKRSCCLSPRGSWDYRCTSPLLA NFCIFYR/DRGFTMLPRLVSNS*AQAI RLSWPSKLQGLQA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,765	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
2766	8946	A	2808	2	385	FVQVAGGNRPSPGPGREKVRPKKT NFGNLRQDQV*KRLASSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SSFPHPGGGPPEAPFPREANPEESLNP KGQGSRNRLPHGSQPGG
2767	8947	A	2809	548	288	ISAHCKLCLPGSRHSPASAS*VAGTTA PTATPG*FFVFLVEMGFHCVSQDGLD LL/NLVIHPWPVKLLRLQV
2768	8948	A	2810	3	301	SRHILPWLEGLASLAPPSLLAAVVP PLLVPSPFPD/CLNIG/GTPGCSQTSPL STSTS*ASSFIPWFQSPSLHSACL DVCL QLGSPPRITAVCTPLPPP
2769	8949	A	2811	1	281	FFFFEMESRSVARLECSDLILAHCKL CLPGSHHSPASASRVAGTTGTCHHTQ LIF*RIFLVEIGFHCVSQDGLDLL/NLVI HPPRPVKVLGLQA
2770	8950	A	2812	25	279	TPRLGILWPWKGSIASLGPSPVLKGE LSSPSSLSPGWDRHAPTHA*LIIFCR/ DRGFVTLPRLISNSWAQVHPPWSPK MLGLQA
2771	8951	A	2813	2	1085	AHCNLLHLLGLSDPTASAPQVAGRTG ATTALVANCIFRRDRVSPCCPIWSRA PELK*SAHVLGLPKCWGLQA*ATVPG PENL*THTNSQ/WGHPHQTNQSYR* KRITCVHFCTNKKDINCE*CMIFNYK* TGQMLLHYLKLKGQWKLSSVSTLI LFIFIGSLQPVPTFRKFSCLSHLSSRD HKHALPCPANSFVLIETGFHRVGHAG S*TPGPSTDSACLGLPKSSGITGVNHS AQPYNYCYLNLNF*SLQLERPHPHSV ASIYL/LHLLPGLERSSSVLPSSWDY RLTPLSLDKFCRFWRDLLPRCLGWS QTPGLRMIHLPSPKALGHEPPRAAS TFYTKCKHHSSIIKVIPQLP
2772	8952	A	2814	1	246	TNLGGKPIP/MGRFSPPKNFL*KGPPP GGPPVPSSSSSRKPGRGENPPGRPIPD LKTPPTHNNLPQKGRGGPPGPPLKT PFP
2773	8953	A	2815	3	84	PPHPQGPPPPGRPPGCRDL*RRQVFS MKPGRTPERTA WSH/HPGCLGSRPR RPSAPA*SSSWASEA*PTAARPR*PIPR GRLPRGGLQAAETK GARFSQ
2774	8954	A	2816	3	301	FFLRWSFTLVAQAGVQ*RNGLSLQPP PSQFKFLSCLSLSSWDYRCPAPRPG NF/SVFLVETGFHHVGGAGLKL.TSG DSPASASQASGATGMSHSAWPG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,785	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2775	8955	A	2817	1	405	HYIPASSLGAPNIRAISSSLIMNKLKCH HCSYAAKCKQTLKKHLIHTGVRSFS CDFFTWRKHVRKHFLVRKCD/KKCK CMVCKIMLAASVGVVRHGS*PYGFCV DCSNKSQPGRPASVDERQDTE/FPHD KDYEEENVGEADEKWVDDGDQNDP SQ*DERQDTESLMIKTMRRMK
2776	8956	A	2818	2	668	LPPALSEIPRLPLPGWRHLPTSSA HPPR/PP/RSPCLFACPLPLCK/PGSPGQ DSVYLPGPSAQEGCAIDLFMGPGLS EPGREPGGPGPHCLFPHRNSGTQSDG EGKTGLLGSCTPGPHPAQTWGWG KGPE*AGSVWAGNRDGIPSSGPWAS TS*PQ*GEREPGQEGPGGAP*PGLYLP EKQPGLVMERALLSDERVLKEIQTSL EGDRGSGNWRSHR
2777	8957	A	2819	1	339	ILLNRSASSTILMRQSLASCQH/PGW SKVVR*LTATSASRVQAILCLSLPSS WDHRRPPPHLANFL*F**RWGFTMLA RLVLNS/WT/SVHPRPKHLVGLPAL HRARPPFF
2778	8958	A	2820	3	289	AQAGVQWPDLSLQLPPGFK*FPCL SLPSSWDYRRVPVYANFLYFSRDGV S/HVGQAGLKLTSQDPHASTSQNARI IGMSHRAQLFFQLFILT
2779	8959	A	2821	1	292	FF*DRVLLCCPGWSAVA*SRLTAKW ASWAQAIPPSSAPKVGWGPKGVCPP \HLAKLCFFGIFCRRQGSALLPRLVSN FWAEVILSPQPPKVLRLQA
2780	8960	A	2822	3	199	IYPKDYKISCCYKD/TCTLMFIAATYS TN*PKTWNP/TKLSQPMIDWIKRW HHIPPMVEVRRFSSL
2781	8961	A	2823	2	1189	QFVTITADGSTAYMELSSLSRSDTA VYCATSPITGSGGVQTSYYFMEVW GTGTAVTVSSASTKGPSVFP/LAPSCN STSGGTAALVCMVKESFV*PGTVSW SSRTLNSGVHAFPIAQSSGLYSLSS VTVPVSSMGTQTYTCNVNHKPSNT KVDKRVKPKSPDKTHTCPPCPAPELL GGPSVFLFPKPKDITLMISRTPEVTCV VVDVSHEDPEVQVNVYVDGMEVH NAKTKPREBQFNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPVYTVLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWIKNSIQ ENRYKITTIPVLDSDGSFFLYSKLTVD KSRWQQGNVFSQVMHEALHNHYT QKSLSLSPGK
2782	8962	A	2824	13	395	FPQVQVNRLLRKRKTESRCIPQAGVQW YDLGSLQPLPPRFK*FSCLSLPSWYD RRPPPCP/ANF*FLVEMGFHYVGQAG LKLTSGLDPLASQSAIGTGMSLRP A*TFCFYKKCCCVYFSPSPGADV

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2783	8963	A	2825	1	996	FRRTPALGLSLRALLAYIFSLAGEMD MTKHSFFSVINQQAIIISGESIYWSQKP TPSSNATPWSEPAADVDELTAAYALLA QLTKPSLTQKEIAKATSIVAWLAKQR NAYGGFSSQTQDTVVALQALVAKYATT AYVPSEBINLVKSTENFORTFNIAQV NRLVFQQDITLPNVPVGYTLEASGGQ CVYVQTVLRYNLPPTNMKTFSLSVEI GKARCEQPTSPRSLTLTIGARYVGSR SSCNMAIVEVKMLSGFSPMEGTNQLL LQQPLVKKVEFGT*HHLNIYGF*KLIIK NTQTYTFTISQSVLVTNLKPATIKVYD YYLPDEQATIQYSDPCE
2784	8964	A	2826	1	124	FFFF*DRVSLCRQAGVQQ/QLGSLQP RPSRFK*FSCLSPLSSWDYKCA SPRPA NFCIF**RWGFTM*TRMVSIS*PCDPL TLDSQSAGITSVTHCARPALPVCQLL ASSAKNPLSRGVCSPCLCSV*HPL*GV QQHKSRLTATSAFPVQVILLPQPE
2785	8965	A	2827	2	372	LRQSFALAAQAGVQ/WHDFGSPQ/PS PPGFKRFSCLSPLSSWDYSHAPHPA NF/DIFL.VETGFLHVGGSPPELLTSSDL PASAS/QSAGITGV/T/HCTQPRILYNM* L*GNCSHRKVFCLNTKHKNT
2786	8966	A	2828	2	388	IRLPVIPATPEAEAGESELPQRWRLQ* FSCFSLPCC*DYRHLP RPVRFVVLV ETGFHHVGGAGLKLTLTSSDLLTLVSQ SAGITGVSHRSW/PEIGLS*RGEGSGG ERGEKMTKEEAENLTGVTNSATE
2787	8967	A	2829	3	135	EKESCCVAQAGVQWRNLGSLQPPPP GSSDSPASAS*VVGITAH
2788	8968	A	2830	36	450	TRFPMISYFLSLF*DRVHSCPGVSVV AQSWLTASASCIQAIIAHLPSWD YRRPSPHLANFCIFSRDR/SFTTLARLV SNS*PLVIRP/PWPPKMLGLQA
2789	8969	A	2831	1	307	LHCCWEGSVVPLLWERWQILT/NVH RQVPQAPAILPLSSHQKQPTAGSQRGI CTAVFTAALLTAVKT/WQAPTCPT/V *SEWVKKTWHSHAMEQYPTLRKKT LK
2790	8970	A	2832	160	464	KRDITTSLGQYQONPVSTKNTNFSRV LVVRACKSQPLRNVP/RPG*FCIFLV EMGFFHAGEAGLKLTLTSGDPPALPSQ SAGITSMHRARLIVSFLKEQTI
2791	8971	A	2833	2	281	APGFSPPPGGKPGPKLIW/AGSSSSP NFPSSSGKKWFF*KGPPSSSP/QQKTP PFFKGPKQRGDFGPPPE*NFVVKKNP GPNPPKNGDKNPGF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2792	8972	A	2834	3	477	RLYCSL/RLPGFKRFSCLSLPSSWDYR RVCHAG*FFVFLVEMGFHHVTQDGL NILSS/S/PPPTLA/FGKCWDYRRDDHT QPVLFSFEFRIDFSKGTGDELPDALL SSHRLNFSFGHQGVV/CSFPLLAHF DFTTHNRGQHL*LFNF*SALLSLGVC MEIKH
2793	8973	A	2835	2	313	FETESHVSAQAQGVQWRHLSLQPPPP RFRKRFCLLSLSSWDYRNGPPLANF/ *FLVQTGFHHVGGAGLELLTLGDPPT SASQSGITGVSHHTQPMWELKKKES
2794	8974	A	2836	195	1047	ASSRQWEQPVQALRWPRAGTWNNG QRDWCSRSGDGGKTGAWREREETV RSACWLGGMQILPKGDKVPHAIHRLF MLVLVF/LFFLTQSL/NSVAQAQGVQW PDLGSLQPPPPGFKRFSCLSLSSWDY RRAPQCPAIFLFLVEMGF/SMLARLV LNS*P*/CDPSTASQRPGITGVSQCTQ PCAGF*SSSPYISCFITYQSEAQGETQ SKVQDNFRYLHA/LKP*PTVLPRKSSL LWLHLFHDVNLGSPLAQEFFSGGS*D GLGGWAWRMSASPEFVVKMYSGAL LSARG
2795	8975	A	2837	1	276	VQWHDLGSL*PPPPGFKRLSCLLSL SWDYRRAPP*/PG*FLFSVETGLLRV GQAGLEVLTSGDPTTASQSGAGITGL* ATAPGPVIPNLPT
2796	8976	A	2838	2	280	FFFQTESRSCHPVQWRNHSSLPQ*AP/ GLK*TSCLSLPSS*D*RHMTACPANFL FFAEMGLAGLKLGGSDLLASASQSA GIIGVSHHTWPGI
2797	8977	A	2839	2	271	VWLC*PGWRALA*SWLTST*TPGLK GSSHHSPLNS*DYRNALPCLANF*TFF REVGEGRSP*VPRLSINSWAQAILPP WPPKVLGLQA
2798	8978	A	2840	32	267	RRCGESGLTSAILA VESS*KIDVQTILD IDAIDPQAEDEGTGA VILETELTEE KVVAEMEEHQHVHNVEIVLLED
2799	8979	A	2841	60	455	NSSKFPPEENSLYCI*DRVSLCCLG*SA VVQSQLSAASASRVREIL/CDHGLGQS RWNHRCITPLC/LANFCIFCSN/RGLTIL PRLVSNWSWTRVIMILPPWPPKVLGLW GRATAFGLKSTLIYTSOKLSDGKERH F
2800	8980	A	2842	15	278	QGGDSKPPKPKNPGGKKFSPTPPKK GG*KGNPPPPGDDSSSSSRKNSLFG PGGRPRGQFGAPQRPPPGVSALFWPN PPKKG GYK
2801	8981	A	2843	3	420	SHFFFWKIF/VLVLRLQSL/NSVAQA/G VQ/QRDLASLGPLSPRFKRLSC/SSLPS SWGRCRLPP/RSS*FFVFLVEMGFRCV GRAGLELPATGHPPASAS*GAGITGM SHQAWPVFFCLFCFCFCFFVLFETGP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion
						ALSCWSAVS
2802	8982	A	2844	2	230	YHLLIYLSVYFSIYHLSTIVVSTYHLAICH/PIYHLSSICLTYHLSMYLCHIITQL*TIYHV*CIYHLCIYLSV
2803	8983	A	2845	1	2404	FFFFETESHSLA/RLECSSTISAHCKLR/LPGSCHSPASASRVAGTGTGTHHALA/IFFCIFR*RQGFHRVSDGLNLNR/NLMIHPPRLPKVLGLQA
2804	8984	A	2846	1	460	QLSACSPOPOEGTTPNQATPKSR*R AHPGPLQEGLEDREGSQAGDSPGSPPTLGNALRPLQPSTCSLRGVGTGGGITQAPAQPYPCCALQPPFSAHALGGNGPLGPPPLAKLQAQSWYPPRG/PDSKQMSGSEGGGRQWAAAPSKTGSPE
2805	8985	A	2847	3	315	QVFTQTITVLQN*KIEEQIKLKANRRQEILKIIVEINDMENRKT/VRKVSETKSWFTSSPHKSNELVR*TKGRRPKLPISRLKQDITDSDADIKTYERKSRP
2806	8986	A	2848	1	309	SGSRAASPRGGGTVGPGDRGPAADG/POHRKVA/TEGVGTETPPASAAHHHLRKGCCAGARSSCRGDTSSSSPSPFGAF*LWAWPKAPGASPPPPRGVPVSKS
2807	8987	A	2849	79	341	VLLASTSYFFNLFNFYLFTHIIFETRSHSVITQAGVVEYHNSSSLHPTTPGLK*S SHLSLPSSWDHRRKPPHPANILFRKTI FTLPY
2808	8988	A	2850	1	349	DTASCSAAQAGVQWCNYS*LQ*PPGLKQSSHLNL/WRYGRITTLCLDNFFIFVEMRVHYVAHDDLELLGSSNPPSASQSTGITGMNPGYFSKSNWR/QIMKILFLKQNLFIQIYI
2809	8989	A	2851	1	360	LNIRLSYLGKFSPPPLYASS*PPLGKELGS/PVPPATPPAFPSLPISLPQGPPELPDWRASPAQPIRIHPPSPGAARFPGFIQPLLLFPIPISYCYCEAIGTRQPIHAGLGFLIFLTF
2810	8990	A	2852	3	116	VTVNLVHPGKA/TKMYKTTMDVFILIVGLRTHFGGG*TPERQONQVDHNGCHLHNSWTQNPFWWWLNN
2811	8991	A	2853	79	202	HLQFNCSLWKNREKGIRCPSTGFHVGSAIHDMGMNPNPSHPP/HGDPSSHP P*/HGDPPRSHP*HGDTPSSHPP*RGD \PPRSRPP*HGDAPSSHPP*CRDTPSSH PL*PCG*PSTGFHVGSAAHDMGMNPN SHPP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
2812	8992	A	2854	2	713	RWSFNLVAQAGVRFRLNNHHHHHH HHHHHDVRDKVLLCHPAYSAVAR* LTAAWNSWVKPSHLSLLSSWDYR* *TPPCLANFFCRDRVHYVAQLISNSW SQVILPPRPKALGLQVHVTTPHLPLR LSIHFFFLAEMNARGQTCRRRSPLIAP TLCSLPLVPKATLGPALPPQWDLSP GLSPITFSLPRWLAGRGMGGTAVSLLC LPVALSLAESTSHLTGLGLAMVLSLV AGAQC
2813	8993	A	2855	2	275	APSLHLKSQKKPSFFWETTF* LWQPP LGKFPKPPSSSSPPLKPLVFFPGPVV PP/VYSPTRLRGPS/VKDFLKLPSRPPW PKKPTPFFFILF
2814	8994	A	2856	277	268	ATVPGLWAIFFFF* DRILLCHPGWSAV VQSWLTFTAFTSQVRKSSHLSPSSWD YRYAPSHPAHILFSVEMGLAKLPKL VSNFWAQAILPPRPKLLGL* AGVQWC NHGSLQSPPLRLKRSSHLSPSSWDYR YAPSHPAHILFSVEMGLAKLPKLVSN FWAQAILPPRPKLLGL
2815	8995	A	2857	2	326	CGDRVCSVTQAGVQWRDLGLSHPPP PRFKQFSCLSLASSWSYRHVPHPAN F* FLVEVGFHYVQGAGALLTSRDP ALAFQSARITGVSYHTGLAMFIKAT LKKY
2816	8996	A	2858	3	233	GRGPCLP/PTSPAPLLPAHICRITKCCR P/CPPKCQSVSAPCPGRATVSSCLVSV VAFGPLPL* PPFALSYPGSLN
2817	8997	A	2859	74	363	NWGGANGSPFSPFPGS/PRKGD/YPS SGV* TPPGQNV* PPFLKQKINWGY WGGPLIPLFGGGRANKSL* PGRRGFQ LTKFPPWPSSPGARSNFF
2818	8998	A	2860	2	244	FLFCC* YRVLLCCP/GWSAVVQSWLT SFSTSVSWIADWDRHALPCANF* KQ GLSMLPRLVSNLSLA* AICLPKPPKVLG LQV
2819	8999	A	2861	3	274	FFETESRFAARLECSDAIHLACNLCLL GSSNSPASAS* VAGITGACHHTQLIFV FFLVETGFHHVGQDSLDDLNLVICPP QPPKVLGLQA
2820	9000	A	2862	2	325	FFFLRRSL/DSVTQAGV* WHDLSLQ ALPPGFTFPCSLSPSSWDHRCPPPCP ANFL* F** RRGFTGLAKMVSIS* PCDP PASASQSA GITGVSHRAPRTGVFLILC KY
2821	9001	A	2863	1	264	FEIESHSVA/RLE* SDVISACHNLHLP GSNNSPASAS* VAGITGACHHAHLIFV FLVETRFRCHVDQAGLEILT* VICPPWP PKVLGL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2822	9002	A	2864	2	333	QAAGLQRCDSLSSLQPLPPGFKQFSCLSL LNS*DYRCPSPHLANFFFLVLEIGF*HV GQAGLKLFTSSDPPASASQAGITGM SHCVQPCSNFSEEQFVITFSVKNIHFF GV
2823	9003	A	2865	3	325	ESQTRGQQRDLSSLQPPPPGFKQLSCL SLPSSRDHRHAPPHVAFNF*VLVETGS HHVVGQA GLELLISGDPPTSASQSGAM TGVS HQARLRHFKIALQLKKCTDSL KK
2824	9004	A	2866	76	474	FLVETGSPMCAACVKLSLTSNPLTLPP QSAGVLQGEPSLQAQSIDNFLVNLVLL FSFSTVLLCHTCWSAAVPSLRNPELEL K*SSYLTLPRS*DYKYMPPH/LS*LNF VFCKAKVC*MLNVMRVKEKYLQD AHLAL
2825	9005	A	2867	2	220	FETESRSVARLECSGMSIAHRNLRPL GSSDSPASAS*VAGITGTRHHAQLTIFV FLVEGFHHVVGQDGLDLLTS
2826	9006	A	2868	1	377	FFEIGSPSVAQAGVQWRNVG*LQPPP PGFKQLSCLSLSSWDYRCPPPHAAS F*FLVEMGFHHVVGQVLELLTSGDL PVSASQNAGITCVSHRARP/TLHLLQ L/PDRVERITSREIYCVFFSDV
2827	9007	A	2869	418	164	ASSSSPPPLPPFWGPRGGVPFSPGF* GPPGEKNFSSFFSSSSSP/SPGSSPPV VPGSFGGWG*MGEFRSRPGVSLN*P KDPGTG
2828	9008	A	2870	1	311	ETESHSLAQAGVQWGDLSSLQPLAAG FRQFSCLSLPSSWDYRCPPSCPTNFSF LVETRHHIGQAGLKLTTSSDPPASAS QIAGITGMSDRTWP*ADFSIIH
2829	9009	A	2871	2	558	FFFLRQGLNSVT*AGVQWPNHGSQ P*TPGLK*SSCLSLPSRWDIRAPPHP ARFFIFLL*RQSLAMLIRLILNSWV*EI LP/ASTSQSAGITGISHCARPDSVCL** LLDYSVWPSLHDTDRISTYPQKIPKPI FHFPPNSQTQSEIMPLVPLGSQILGRA GKRKEDINRVAGVITMPKEEMKG
2830	9010	A	2872	2	519	EKEFCSVAQAGVQHHGLSGLPPLPR PRRVCSLSLPSSWEYRCAPPLATFL VFLVEQGFI MLARLVSN*PQ/CDPP ASASQSAAGIIGVSYCAWL*FCIFSRER VSPCWGWS*TPDLK*STCFGLPKCW DYRCPPHALLYQSFYTEGV*EYFGI IITTKYHVMKSKRHT
2831	9011	A	2873	12	182	TRHVPPLHLANF*FLVETGF/HHVVGAS LELLTSGDLPTSAFSAETGVSHHTQ PWR
2832	9012	A	2874	3	351	LLDSSDPPPTSASQARITGVSHHTGL L FFLPA*IKSFCLFLFETESCSVAQAR VQWHHLGSLQHRTPRFRKFCSLSPS RWDRHVRPQHLANFCIFSRDGVSPC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WSGWS*TPDLR
2833	9013	A	2875	2	250	RSVTRLECSGMISAHCNLPVGGSSDP ASASGAAGTTGVRRAQLFVFLVEL GFHHIG*TLKLL/NLVIRPQPAKVL GLQV
2834	9014	A	2876	1217	12	TSSSPGGGRSGSKFTYAGCARK*/SF LLGPPKFNSRARV*QGRDGKNPGGS PIKTFLEGHPLLASGGKKEKGRV
2835	9015	A	2877	1	280	FFFFLETGSHSATRRECTAMITAHCN LNLLGSGDPPTSAVQVAGTTGTHHTI QLTFVILVEIGFVHWVAQAGLEILG*VI RPPWRPKVLGLQV
2836	9016	A	2878	2	548	FFFGDRILLCCPG*SAVARPQLTVTST LPDLKQFYCLSPSSWDYRHAPACLA NFLF**RWGFTMLPRLVSNS*QAQI/V LPWHPKVLGLQA
2837	9017	A	2879	493	210	RFGMQRQDLSSV*PLPSGFKQFSCVS LLSSWDYRGMPSCMANCFIVETQF HHVGQAGLELLA*SDPPALASQSVGI TGVSSHHTLA
2838	9018	A	2880	28	927	QNATYRVTAFLSWNFENKNCNLSLEA AV/CWDIRGKNHP*NPVLKTSMNIPF TNSSISTCHLSTGL*T*KPEE*EFIKDT HVCTFFIYCPFLFLRTGFSALS/QAVV QWRDLSSLQPPPPGLKRFSCLSLPSS WDHRHVPPHPANFCIL/M*RWGFTMF ARMT/CDLLTSASQTVRITG/VSHHTR/ LIY*YF*A*SDIFFFEKESCCVGQAGV QWHDGLSLQPPPSGLKQFSCNLPSS WDHKRTPP/HPGS/FCFSRDRVSPWG PGWF*TPDLKRSALLGLPKCCDYRRE PPRPAEVTIFYNKV
2839	9019	A	2881	25	312	VFHKIDATHICLKGYSRKGAKIIPTEK KDSLQ*Y*NN*AIKKEPSIAQWNE YPYSLINEWIKKIWIYIMYIYIYTHTM EYYSAFKKKEIWRGQ
2840	9020	A	2882	46	269	QTTADFLSETMEARRKQWONHFPVLN EKNYQCQL/SWRIKISIRN/EGEIKSVR QRSTSKFVTS*PTPKERLKAILWE
2841	9021	A	2883	2	259	LEVLL/RTIROEEKKGRIN/KEEKIKLS LFINDMINYVGN*KFTKRPLEKSKF NKVAGNKNFN*KSIIFLYTSNNKKLKL KILFT
2842	9022	A	2884	3	300	PGAMAVVPNSRGGKEKRSLSRKFG AEPALFGLGGPPLGQPPDGGPGKRGPP GALKRGVPPRSGIKPGQP/VP*GG PGREKPLVFRNGNPRREKGF
2843	9023	A	2885	9	191	LFCLSLPSSWDHRCRTPP/HPG*FLYF/C RDGVSPMLPRLALNS*PCQVHLPRPP

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						KVLGLHA
2844	9024	A	2886	245	565	LVTFFFLFVMEPSVAQAQVQWCNLSGLQPPSLRYKRFSCLSFLVTKDYRRTPPCPANF*FLVETGFYYVCQAGLELTSDDLPTSASQAGLIGVSHCTQPTGNP
2845	9025	A	2887	13	400	DRSRSVTQAAVQWWCHHCSTQLLSPLRLKRSSQLSC/LKLPSRWEH*HTPPRPKSGFCFLVLRVWCLFVETRFHHVPHAYLKLKSGNDPPASQNAVTT*VSHCTRPQQIFLKNEARLSIKRYGSICC
2846	9026	A	2888	1	397	RHQISVFSFQAHTSRLFHPTLFFFRDGVSLCCPGWLDLSSLQPLPPGFKQFSCCLCLPRLQAC*EYRHVTLCPANFCFSVMEMGFHHVQAGFKLLTSGDLPTSASRSAGIIGISHCAQPKFVCYTEFSDL
2847	9027	A	2889	50	479	CSSSFCLTNSHTIFIY/CIFETESCSVTQGGVQWCNLSLQPPPLPGKF*FSCLSLPSWDYRCVP*HPNF/CLFFIFYFIFRDEVSPCWPGWSRTPDLKWSTRLGLPKCWDRYRHEPAQAQPEKTLTPTESAFSELGCFCEQFV
2848	9028	A	2890	1	611	RKVDIMADAAYSIFQKAKSF/TGNFVIDENILKEEGIENFDVYAIKPGHLPQDFFLDEYPE/DS*QESGIQLVLPKFQRRKQLQMPQTQNRSGAVEETFRIVKDSLSDDVVKAITQAIYLFELSGEDGGTWFLDLKSKGNGVGYGEPDQADVVMSTMDDFVFMFSGKLKPTMAFMMSGKLKIKGNMALAIKLEKLMNQMNARL
2849	9029	A	2891	11	242	YSLDLAPFSFFLPILKNL*SKIFRGHPLFSSVNNVKKTALTWLHP/QDPQLFRAGLNGWRHCLQTCLELDGAYVEK
2850	9030	A	2892	3	274	SFVFCFLGFFFF*VESCSVAQAGVQW/SISAFCNLGLSQPPPGFKHFSCLSLPNWDYRCMPPHQSNFCIFSRDGVSPCWSDWSRTPDLR
2851	9031	A	2893	3	376	RQSFITLAAWAEVQWHDGLIGFSLQPPPRFKRFSCLLSL*DHRLPPRIANFVFLVEMGFLHARQGDLELLNSGYLHALTS*SVGIIGASHIRAWFLILKLIFLKSCKVSRRIKNDYYAKSLY
2852	9032	A	2894	54	473	LLSSILFAISLHFCFYFYF*DDFIEKTL*SCSVTRLECNMILAHNCLSGSSDSSALASQVTRITGARHYTWLIFLFLVETGFHHVGEAGLKLLT*VIHLPRPPKVLGMSHCTRSLLLFLIPSIFLGDFTFSASL

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2853	9033	A	2895	1	425	PSPRQGNFCIFSRREG/GFTMLASLVSN S*PRDPPASASQSAGITCVSHHARFQT GRFLFLFFFETESCS/VSPQAGVQW RDLGSLQAAPPFGFTPFSCSLSPSSWEL QAPATDARLIFFCIFIVEDGVSPFLAG\
2854	9034	A	2896	2	377	LCHPGWTAQAQS*LTAAPALGSKDS SISAS*NSWDYRGVPPHPANFSKIPFT DTGLTMLIRLGSNSWPQMTLPL/QPP* QLGYRWESHWPPPTGYLLFLFHIFMP KHAVLSTISYIFLYLFCGFIF
2855	9035	A	2897	41	314	QRGQPSHSSAPTGGHFAPHC*RPP/ LPQKSPORASFPFPPPMFASGVPHSKK TAQLAK*RLVPGTLAPHVCQESPCGH TAP*GSPEGPAAGDEGGQGGGLFP* MTAGNQSPEMAAS*GVASPP*ACVL AQPHCVDEETEAQRGSCPCPRPHSRM S*KIPEKLTAWSAFPQTVHPWPEDTSP PIVNVHRAPKIPTAFLPLSPHVCW SSPLEEDSTSVKVEAGPWDRTPCLS GKPLRSHGPMRKPGRGACWG
2856	9036	A	2898	24	411	AGQPRATOTTAACGPPYPLCPGLPVAL HPPLPGSPASTLSPLLPVVGLRGPAG\
2857	9037	A	2899	2	360	LHGPGF*GGA VSP/SLPPPTANTGLP PGLTTTLTRPQEA PNSTLSTPTQDPS KGTENPWSLETLPGRVGRCPKSG*SL VLRDTARTRGSMPIKIRI
2858	9038	A	2900	1	277	IDHVLFIHSSIDRHLGFFYLSALVN AMCICLSLCQFFGLMQRSFPFAPT*S SSSSSSSSSSSSSSSSSSCN/SLKGHA NSRTEGLRANPCLLTPHQLPPQWVPS NTPASRTPSPAQ
2859	9039	A	2901	2	861	VSLCHPGYSAVTQSCSLTA VSWTPVVIS NPTQVSLPSSWDYRC/MPPCPANFSIF FL*RQGFAMLLSWSENPSPNLHATP/ WP*KLLCLGVGGSL
						GLEHLPLLGGRTWRAARDADGCEAL GTVAVPFDDDDKIVGGYTCENSLPY QVSLNFG/SHFSGGSLISEQVWVSAG HCYKSRJQVRLGEHNKIVLEG*TV SSNAAKIIRHPKYNRDTLNDILLIK LSATARQSIPIVIRHLSCPPPLPSLLGT ECLISG/WGNTLSSGADYPDELKCL DAPVLTAQAECKA/SYPGKITNSMF/CV VGFLEGKDSQORDSGGP/VV/CNGQL QGVVSWGHGCATEDTGSQ/GSYTKV YNYVDWIKDTISCQLLKPLVPLQSLY PIK

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2860	9040	A	2902	2	531	KPHKCEKFGKFNKSSLTSAHNIHTG EKPHKYEECGNAFNQPSNLTKQN*Y* KCYKPEKC/GK*F*Q*PSNFSKHKGNH TGKKL*KCEERDIAFKWLSHLIVGKII HTGVETSQKCEEYGK/SFNSYTLHRK AFILQKMSY*YTECKAINMCLHLIQ H*RVST**KHYKCNVCQNSV
2861	9041	A	2903	3	64	GVLLCECSGTUSAHCILCLPG/SSDSPAS AS*GAGTTGARHHTLIFVFLVETGF HHVGQDGLDLL/NLVIHPPWPKVLG L*AVARLSAHCILCLPG
2862	9042	A	2904	3	242	RQFHSVAQARM*QP*SPELKRSSHLS LLGNWDYECVPL*LANFFK*FFCRNG LAMLPSLVSWAQAILLPWPKVLEL QA
2863	9043	A	2905	1	280	ENPFSCLSLSS*DYRCAPTRLAYFFV FLVEMEFHHVGQVGLKLLTSSDPPIS/ PPKC/WDCRHERLARLKSLSLEL*NFA TVVQNGVCPSYSFP
2864	9044	A	2906	3	262	DRVLLCHPGWSAIVVQSWLTAASTSW VKRFSHLSLKSNDYR/RQPPPLFFFF KLIVETGNLTM*PRLVFNSWAQAILSP QPPKVGLYA
2865	9045	A	2907	228	488	LNLEPFFFFELEFHSVTDQGVQWHD LSVQPLPPGFKQFSCSLSPSS*DYRHV PPHPTNFCFSKDGVSFQGS*SPD LMICPP
2866	9046	A	2908	1	311	VVVVVGWVLTQAHPGSPRLWCSGL NIAHSNLKLLGSSDPPASASWVARTI GACHHTWLIFYFL*ROGVGGGGGDS CFAQAQLQLQLQEILPPCSPKVLGLQ A
2867	9047	A	2909	3	475	FLRWSL/DSVAQAGVQWRNLGLSPA LSPRFTPFSCSLQSSWDYRPPRPRA/ NFFVFLVETGF/VLARIVSISLSDLP ASVSQSAGITGTVTRVPR*LFKFYNGE KRELFYQIQVAKIDRTIFPMENALQR YNTIAYCYVLLHKQCSLMKHGATSR K
2868	9048	A	2910	2	238	DDFFFLRRCL/NSVTQARVHLSHLGSL QPLLPTFKQFSCSLSPGS*DYRRLLLH PANFCFSRD/MGFTMLVRLVNS*PQ /CDP*ISASQSAGITGSPASRTIFIKVF LF/SFCFFEMDSLLSPRA/GVQWHD GSWQVLPFRFNT/RFSCLK/LSPSSWD YRRLPTMPS*FFVLYFLVKDGVSPC WSGWS*TPDLR
2869	9049	A	2911	28	393	AGVQSHNHSSLOPLQLLGHK*SSCLS FPGS*DYSHTPKLAMPG*FYFVEVTS CYVAQASLELLALQVDLPALALKVG RIIGLKPTAPKPKRIFYKYR*VRIFIG QDKMREKIPWEVIQD

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2878	9058	A	2920	1	1585	GTRALARQGAAAGRSARSLSRPAR SLSSLGWPATCGSCA/LLCRASGSRPA WAPAA/LTAPTSQEOPRRHYADKRIK VAKPVVEMDGDEMTRIIWQFIKEKLI LPHVDIQLKYFDLGLPNRD/QTDDQV TIDSALATQKYSVAVKCATITPDEAR VEEFKLKMMWKSPTNGTIRNLGGTV FREPI/CCKNIPRL/VPGWTKPITIGRHA HVDQYKATDFVADRAGITKMFVTP KINGSGVKWEVYNFPEGGVGMGM YNT/DESISGFAHS/CFQYAIQK/KW/P LHEAPRNTILKSLRM/VFDFPRRSF DKHY*DRLSSTKNKIWYEHRLIE*HC WPOVLKSSGGFVWACKNYDGDVQS DILAQQVGS/LGLMTSFLVCP/DGKTI EAEP/HAHGTVP/PPPIGEHQKGRATQH QPSSPSIFAWTRGLEAPGESLDGNQRP SSRFC/RLLEERFALETVEEWKP*PKD LAGLQFHGLK/SNVAATKHFLEHHR NFLDTHQATLEKSPWAGSGKRPPT HGLQWEGPRAEPGGSS
2879	9059	A	2921	60	233	VKDVTYNTYK/LTKEIKGDI/R*KDIL CS*SGKCNIVKMFILSKMIHRFSAIPV KIPVA
2880	9060	A	2922	3	696	GQTISARLQVLAYSTATTLLNFILAVL ELLTCDLPASASQSGAGIT/DVSHHTWP FFFFQTESRSVTQAGVQ*CNLSSLQPL PPGLKQFSRLSLPSSWDYRHMPRPRA SFVFLVETGF/TMLARLVWNS*/PSCD PPISASQNAGITG*SPSLAPHHPLRFFF ETKSGSVTQAGVQVWHNPTSQQLPP GFKQLSRLSLSSSWD*RYAPSCLAN/Y /CFSRDRASPCWSGWS*TPDLR
2881	9061	A	2923	108	64	CLEDLIDGLTSQKQGDQRWKQPKY RMNEWITYKMWHNTMGHYSIFLKEE IVTHAITWINIEDIMLSEISQSQDKKY ISLI*G
2882	9062	A	2924	2	560	FFFLRTGSCSAVQGVQVLDHSSLQ PPPGLKRFSHLSLLSSWDYR/*CMPPT LC*FFYFL*R*DFTKLPRLVSNLWAQR I/SGSSSPTSAS*SGGITGPRKDSLEKL LAKRLD*TKCVLFVN/L*LFYIFLKIY LFKIIF*K/CLIDMRSLSAQAAGLE/PPE LR*SSHLSPKC*DCRCEPPHPAKIS
2883	9063	A	2925	233	530	SLYFSVMFMF*DSVSLCCPGWNAVA QPQLTEVLT/LGLK*SSHLSLPSSWD YRCVPQRSAYLFFVGGGRSFLFWLR LVLSN*VQGHLPWPPT*VLGL
2884	9064	A	2926	3	278	LECAVGDLSSLPMPPRFKQLSHLSL* SN*DYRHVP/MPMG*FFVFLLERFHH DCQAAGLELLVSSDLPASASQSAIRTV VSHCIRPVVDF

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2885	9065	A	2927	1	355	LSFFLSLFFLSLFFPFLSFLPSYFSFFF FETDSCSVPRLECSGVSAHCSLHLP SCDLSASAGSVAGIIGARYHGWLFV LIETGFHHVQGAGLKLLT*VIRPPWP PKVL*LQA
2886	9066	A	2928	869	432	VLAPCNLPSSNSFALASRVAGITGV CHCTWPKLVFKLFLEMGS/SLTQA GM*WHNNGSLQ*TPGLK*SSCSLP SSWDYGYMPLHLAKFCIYLRN SRCPGWSQTPGLKQSSCLSLPKHCD YQV
2887	9067	A	2929	2	244	AAARDARTRRF/SCFSLPGSWDH/RV HPPPCPANF*FLIEMGFCVGDGLE LLTSGHPALAYQSAGITGVSHKSR NFM
2888	9068	A	2930	1	876	SQTRFCPGWSQTPGLKQSSCLSPK WDYRSEATAPGLPNHFYQSHHSFP AQWPMVPMV*HRNFQCLIRLIQPY F*HQSTTHPVFSLGREHQYV*ENPYK YNLLFLSYRNVMLFSFLSFLSDGVL LLSPOAGVQWRHLGSLQPPPGFKR FCSCLSPSSWDYRHAPPCPAIFVFLVE MGFHHIGQGWSTPDLK*SAPPLGLP KCVSHCAQPRVSIF*WYLLKEQLERA GSKLNHMKVYSPPPAPYKEPLMTRT QDQYPQPEREISDNPTIGSSEETLSNL LGIGQ
2889	9069	A	2931	2	264	CERVSLCHPDWRCR*HVHSFTAASTA SGSGDPPTSAFHRIAPP*LANFCIFCR D/R/SFTMLPRLLNSWAQVDPGQWP PAQSVFLMSSK
2890	9070	A	2932	1	380	IKYKYFPFYLRLCHSVGWFAACQA F*FDIVPLSMFFLFKF/RDRVFLCHPG WSAVV*QLTQLQPPGLRRFPHL SSWDHGR/VHPWLADFSNFL*R*SLLL LPRLLVNSWAQAILLPQSRVP
2891	9071	A	2933	402	143	VSFCHPGWCAVVGQSLTAALTS/VL M*SSHLCLQSSWDYRHALPHLANFST FCRDR/SFAM/LPRIISNSRAQL/LPR P*VLGLQDWSL
2892	9072	A	2934	112	572	YVSPFMYLCFVINLYMLIMLYIILCT CTCCNISLCSDRKWNTFKPSLVSNIT YTNTMYVHIIFLVFFPRDR/CHSGWI AVV*S*LPALNSWAQRIVLLSLS WDYRRVTPYLANFKFFL*RHLLIML PRLLINFWTQAILLPWPLEVL
2893	9073	A	2935	1	358	IQIPLFCF*TYLPVNM*VCRLLKSGRG KVTEDI*QIFTRNHDGNNIFSSFFETKS RSVAQAGVQQHDISSGQPPPGFKQ VCSLSLSSWDYGRPPRPANFCIFSR DGVSPYWSGWS
2894	9074	A	2936	2	272	FFFAMVSRSVARLEYSGAISAHNCLC LLGSSDSPALAC*VAGTTHCTCTQLI LVLLVETWFHHVVGQDGLNLLNLVIC

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2901	9081	A	2943	68	336	KNLCIKILTVALFLAKDHKQPKRPSI KDWNKL*YGVIVENYEAIREMREI FILLKY/VGTLYLC*SMISRIYAKKN EVQNRLLFSMLP
2902	9082	A	2944	3	339	NVFRVRIILCHPGWSGWHGDSSLSQ QTPGLKRSSCLSLSS*HRCSATMLD YYS/PILFYSLFYSILFFLEMGSRHVS QAGLKLLYSNGNPPALASQSTGIIGMS HPDSKNIF
2903	9083	A	2945	1	233	FFFWDSTFTVQ*AGVQWHDGLSLQ PHPGFKQFSCLSLPS*DYRCVPPCPA HFCLSRDGISPCWPGWSQTPGLN
2904	9084	A	2946	4	265	GRLSLRLEYNCAIKAHCTLNLRGSSD PPISAS*VSGITGMHNHAQLIFVFFFF VEMAFHHVAQLVSNWAKVIHPPWP PKVLGLQV
2905	9085	A	2947	3	232	KNFYPRIVHPVKISFKHEGEI/RFLDQ KLKRDFTGTPVLKGMKKEFFNLK*KG C**AVRNHLKVQNSLLIVSTGQAW
2906	9086	A	2948	681	1112	WVLGQASVWETFFFGGGRWSLPL AQAGVQWRNLGSPQPPPRFKRFSCL SLLSSWDYRHATP/*PG*FFFVFLVET GFHHVSQAGLELQTSADPPASAYQSA GITSMASHRAWAKWHFSRRKEALGFT EKLQCKIPKELKFDNS
2907	9087	A	2949	1	585	VSSLSPRHSVQCLHNNRGNTNLRVE EFSTLSERIGRYKGFSETVLFKLILFL LR*/PCSLAQDGVQWRDLSSQLPLT RFR*FFCLGLPSSWDYGHPPPHAI* FLVKTRFHVHGQASLKLL*GDPPTLA SQSAGIIGMSHARLI*ADSLRVSRNF FOVNTLSYYSKQRPVGAKTQGYRD VEVYQTLDD
2908	9088	A	2950	469	88	FFETELAPIAQAGIQWRDLGSLQPPPP GLKQF/SCLS*GYSRHPPLPANCFICR DGVSPSWSGWSLTPGPRVPPTFCLPK
2909	9089	A	2951	2	318	TESHSATQAGVQWPDLTSLQHLPPV* DLFSCLSFLSSWDYGHAPPRLTNFCSF IFLNRNGVSSCLQGWSLKILDPOQVIPP TLGLPKVLGIISCEATALAQRCIF
2910	9090	A	2952	1	284	FNFGSLQPPPP/GFK*LSCLSLASS*DY RDLTPCANFVFLVETGFHVGGAG LELLTSSDPPTSAQSA GITGMSHCAR SKSNF*MIHWKTKTAV
2911	9091	A	2953	2	11	FFFEMESRSVQAGAQGYNLGLQHL LRPRFKRFSCLSLRSRDRCAPPSLA SF*VLVETGFRHIGQAGLEPLTSSNLP ALTSQSTRITGVSHCSQPEVFKL*FFF

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2912	9092	A	2954	2	2159	PSGKMAA VQAAEVKVDGSEPKLSKK WW*SLVPGCSAMLTQAAVRLVRGSL RKTSWAEWGHRELRLGQLAPFTAPH KDKSFSDDQSELKRRLKAEKVAEK EAKQKELSEKQLSQATAAATNHTT DNGVGPEEESVDPNQYKIPQVKAIH QLAKVNGEDPYPHKPHV*DISLHLTFI QKFSHLQ/PLGDHLDLTSTLKVAGRI HAK\RAVSGGLLIFL*SFEGEGVEVCKS LANSRNYKSEEEFIHNNKLRRGDHGA VQGNPGKTKKGELSIIPYEVTLAVL PCLHMLPSFFHFGPSKDKVETRYQR YLDLILK*TL*RQKFIIRSKITIRSF DELGIPKRLKLPKMNIIPRGSRANPFI TLQTSWDMNLYMRIAPELYHKML VGWVGIDRVYIEIGTPFRNEGD*F*R HNPGVFTTC/ESFYMGLWQDYHDSS WEITGGRMVSGMVKHITGSYKVTY HPDGPGRPGPYGCLTFTPPFRINMV EELKALG\MKILPETNPLWKLKTR KILGWISGVAKSCLECP/PPSGPQGLP LNKLVGGSFLGS*LWHQFLHFNLVN HPQINEPLWLKWHRSKEGSDWSALK LFVMKKEICNAYTELNPSPIRQTAF LKETAQSQRPAS*LMRPMVP*MFNF CTAPWK*WAAPPTAGWGHGPLIRVA HVSSRDSNNIKGSTFLPAMKPEK\K ENVATVDTLESTTVGTSVLEN
2913	9093	A	2955	60	244	QYVNTETPTGWERGYKNTFCGPTAA AHAYNPNTLGG*G/GT*IQKLKTSLC NMMKPCLYKKK
2914	9094	A	2956	5	170	FSYLSLPSSWDYRHTPPCPDNF*FLV EMGFHRVQASLELLTSGDLPALASQ NV
2915	9095	A	2957	8	139	KDRVLSH/WPRLVSNL*LKLACLSLP KCWDYRCEPPCATSIFK

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2920	9100	A	2962	71	454	ATVPGLKRFS*LSLLSS*DYRNAPPRP ANS*FLVETGFHHVGGAGLKFLTPG DLPTLALKSAGIKGVSHHAQPPTLFF AQPDQDFMGQSLCQLSPRALGIFLR CNRFSLYVLEHRASNEGISFGRV
2921	9101	A	2963	2	372	LRQSL/DSVAQARVQW/RHLSSLQAPP PGFTPFSCLSLLSSWDYRRPPRLADF LHF**RRGFARMVLIS*SRYPAAASQ SAGITGVTYCTQP*ICMFLIDIFSLFS HMTLSSVTGQVERLAG
2922	9102	A	2964	3	357	FFLRWSFTLIAQAGVQWCDLSSLOPL PPRLKRFSCLSLPSSWDYRHAPRPA NFLCF/LVETRFHGAQAGLELLTSGD PPTLASQSAGITGASHRAQPAFSF*K VKYNRENCTKQKCSN
2923	9103	A	2965	1	280	FFFS*DRVFLCHPH*SAVAQSQLTVAS NSQA*AIIPLSLPGSWDYRHAPPHPT NFKFFCRDGVLTMLPRLVTNSWQAQ ILPP*PPKVLGLQV
2924	9104	A	2966	1	355	FFFVPESHDFDVQAGVQWHDLSLSQS PPPRFRKRFCSLSLSS*DYRCPPLRLAN F*FLVETGFRHVSQDGLDLA/S/GDP PASASQSAGITGVSHRAVPHFVLL FAYLYDVACVQSFD
2925	9105	A	2967	2545	0	RAPA/VGIDLGTITYS/CVGVFQHGKVR D*LPMYQGNRTTPSYVAFTGH*TG WIGDAAKNQ/VAMNPHQHSFLIAKRS DL DGRF*MNAVVPVIMKHWAlyW VGEMMLGRPQGP*K*DYKGEDQKAF YPPEGCLLWVPDKD*KEICRSPNLGE ELVTNAVGHSAQFTFNDSIQRQATKD AIGTIGWSSNVLK/IIKWSPTAACCYCL TALDKKGLEPERNGAHLTLWGGGT DVSILTIEDGIFEVVKSTAGDTHLGR KIL TTRMVNHFAEFKRKH/KDISEN KRAVRLRLTACEPC*AVPLSSRHPP VFEIDSLY/EKGIDFYILHLPVAF*R NLNGDLFRG/TLGPSRRKPFRAKLR TSHRFHDICPWLGRSTSYSPRIQKSC CODFFQWEKELELRISINPGWKA VAY GWQLVQAAHLCLGDKS*GMFQDLL LLADVTPLSPWVLKTAGGVMFTVL/LS KRNITPTKTQTFTTYFWTTQPGCG LFRFYEGERANDKRINLLGQVLNS QGQPPAPRLFPQ/VLEVHFWILDGH GYPSMSSGCGDKEYGEKRNKVITYSLI DKGPF*GKGRTLERMVPGLRKLQS WKVEEGRRT/RVSSNDFTWSPMPFN MKSTLLKDEKLSRAKINDEGQNRKILA DKCNEIINWLDKNSALLEKEEFHQ Q/KELEKVCNAHSSKLVPRVPGGM PGRSLGGFPGWWSLPPVGAS/SQG PPFEVD

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2926	9106	A	2968	174	342	MAQYCYVYFLFKQYIHFWLGAVAHTCNPSTLGVRRRIT*VQEFETSLGNIVR PCLY
2927	9107	A	2969	15	243	LPIYLPCQSIKQGPSVEPPAPCHPVER AAQPRVGIQPRPR*GVCCPRPCYDPT SMTAPARRAI*QQQGSFKAAPD
2928	9108	A	2970	1	267	ETVPHSVT/RG*LECSGVITAHCSLPSL GSGDLPTASRVAGTIGMCCQAWLSF VFLVEMGSCCVQAQGL*LLD*VILSP RPPKVLGLQV
2929	9109	A	2971	3	203	FSGEKRESQDSGRNPRGGDGSAG GRSGERCGRGSA/REGSSASSARSSS SPFCSKQF*WGTPRV
2930	9110	A	2972	26	398	RTRSIRKEEVKLFVFWV EALVYAEKP RKPKK*LELIYLARHKVSIQKS/SIFL YTYHK*NFKNFIKNSVKK/RIKYLEIN LTKNV*DQYLEDCKTLTGIEIENLNK R/NLPCSWTG*LSVVKISVL
2931	9111	A	2973	3	101	FFFSSSEYIVFLNIHGT/ SNIDLILGQQP SFNKF*RMETIWNVIFSDHKAIKLEKLL *LEKSHVWVGNLILSNPWVHPLT*TS S*LFKHTWHYINIDLILGQQPSFNKF
2932	9112	A	2974	3	429	STFTLLLLLLLFFSL/MSSSPSPSFFLF FQTQS/VFLCHPGWTA VA* S*LTATLN SQAQPIILLPQSSWD*RHVP PCAIFL DF**GQGLTMLPRQVFFVLKPEYSSGI YYFSKDSLLTLAHDHVFVSNYSSIFKP SFPLNF
2933	9113	A	2975	1	305	LRWLS/NSVT/HAGM*WCNL GSRQAL PPGFTPFSCLSLSPSSWDYRCPPHPA/N FFVFLVETGFTMLARMVWIS*PCDPP ASASQSGAGITGMSHCTWPRFILQS
2934	9114	A	2976	1	262	FFF*DGSHSAAQLKCSGISVHCNL*L PSSSNSPASRVGTTATCHHSRLTF VFLVETGFHHVVGQDSDLILRPWPWP KVLELQA
2935	9115	A	2977	90	482	HLKANILNKGKLDFTPLRSGRTRQRC LLSL*FNII/LEVSANAIMQEKTSIK VGKLSLLTDDLSDWEPSEVTEISES KQRKHGDMQSTCCLLCNVAFSLDG AGNRQKSNWLKHTQGTIVANTSSSW A
2936	9116	A	2978	13	416	MTIKKLATNVVF*NERLNAFPLKSGT RSGHLLPLCLFNTVLQILDKAIRQENE IQCI/QLGKEE/ELIPMYR
2937	9117	A	2979	2	364	PVGGGLSPPKNSLKGKSPGGPAVSP PPS/P/PETGGGKPPGPKP/EN*KPP PPKKSNNPKKGEKGAAPPGL* KPPFFK AKPRGGKSSSSSDKFSGGEKASP KVGTVKEVEGEAGGGKF
2938	9118	A	2980	2	191	NRDG/DLVMLPRI.VLNSWAQVIQ*SS HLSLPKCWNVYKEPPCLAIKENSMLF

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						NWRTEFINIQCY
2939	9119	A	2981	1	312	FFFFETEPSSVAQAGVQGHDLSSLQPLPPGLKQSSCLSLNSWVYRCMPPIPA NFV*FLIETGFHHVGOAGLELLTSSD LPTSALQAGITSVRHHNQPMMLF
2940	9120	A	2982	1	327	LRQSCSVAQARVQVHDGLSLQ/PLNL GFKRFFRLSLRLSSRNRYRPPSCFAN F/YIYIFFLVEMGVHHVGOAGLELLT SADPPASASQSVGITGVSHRARSLCSS FPPS
2941	9121	A	2983	225	217	QRQSSHLKKPTTKQLGKPNARRRK GTRSRSPAKCQGPVLNPRFNLGARP *CPSGVHGPSWVPGRLRWVLGQRAGF P**GSLPQGP*RTLALPGPQGPPE AVTPATCPNPAPVSPATPCSPHNS STTYTLTCTGPYG*AFQA
2942	9122	A	2984	288	748	NLIPLFSSRELMMHII GMLYRVAFPS SHINGQVF*DVRRKIMAC*SCFGASR VFSLYSDVFSEWPEHLWNN/CSNVFQ LASEY*TLNKKCF*CEQPYMTPLF*LE LIKTFMLAGRGTRPVIPALWEAEAGV SRGQEIKRILANTVKPRLLLKFQ
2943	9123	A	2985	2	246	LSPLRLECSGAISIAHCTLRLLGSSDSP ASAS*LAGITGARQHAHLIFVLVETG FHHVGOAGLGLL/NLMHHPRPKVL GL*AGVQWCNLLNLSLHPPPLGFKRF SCLSLTSDYDRCTPTQANFCIFSRD GVSPCWSGWSRTPDLMIHPPRPKVL GL
2944	9124	A	2986	8	294	MNLKEKIEKFNMKNLFFEKVTKIHK PVAGL/HREMIQMFNIRNETKST/TNS ADIKRIIREY/YDNYSHKFDN*DKTDQF L*KHKLSHFTQNKIDNL
2945	9125	A	2987	3	242	FSCLSLPNSWDYRCLPRQVNF*FSV EIGFHHVGOAGLELLTSGDLPLTASQ SAGITGVSHCAHPQWFLKVQNKQD KL
2946	9126	A	2988	415	292	FCFHHILNPLSLFLIF/NVCLCV*QSHSV TQAGEQWRNLGSLQPPPRFKPFSCL SLPSS*DYRHAPPQLADFICSSRDGVS PCWPGWSQTPDLR
2947	9127	A	2989	5	369	PKLLKKKCKIEKLPQRVFLHQD/NGNA PAQYSHQTKAIF*EFLWEAIRHPYP PNLTPSDVSFLLNL*KSSKGTHFSLV NNVRKIALM*LNSQDPQFFRDGLNGR YHSL*QYLECDGEYVEK
2948	9128	A	2990	2	139	FCFVVFVVFETGSHFVSRLRECCGTIM AHCSLNLGSSDPPASASHVARTTDT RTTMSG*FIFLEMGSHYVAQAGLK TLG*VILMPOPPKVLRL*A VAPSWLT AASTSWAQVILLPQPPM

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9,519,705	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2949	9129	A	2991	1	466	PSPRQGNFCIF/SREG/GFTMLASLVSN S*PRDPPASASQSAGITCVSHHARPQT GRFLLFLFFFETESCSVAQAGLRTQ WRNLGSLQALPSPGSH/RFSCLSLPISL AYSHLPPLHLANF/CIFLVEHRVSPC*P GWSRSPDLMIRPPWPVKVLGLQA
2950	9130	A	2992	215	1519	EETEVGPSASSSRIETTTYSACQIRASG S*SMSGGLLASSQFCSMTDFTWSFN RGRVPPSRASATNCCSSDSSSRASRKS RMAFARASTKTPAALKRLLRRGLSGS SMCSPSPERTSDTLCSRSCRISSLPRL AREFTSLFLSSVRSLRTLSSSNFSF MFLESSEPKDFP/TTG*STI/SSSSSPCW GRQAALLDSSGPDGLGWSLPFGPCV YS*DGPERSGSKIYIAGRFSGFPPSP EFLSPDTGFLSY*LIGMKRVVPSSASC FQG*PDTAGISGPSIS*FSDGGSPGNCL KL/SISLGNLTINSPVESLTSRI*NSAF* PWSPESSSNHLSPPSVSRMSIRVPV *CRHPKKVLFSPTRWKQRNLASTRL LTAIISPPASISLTITLVISSNTLNIAPGP TQKQKPSIVFGRRLVLVQVFKSSTFGS LR
2951	9131	A	2993	3	266	EFLKEKRTKKKECLQNPNES/LHRA NLKIVIGLKKETEREIGKKVFC*GLITE NVPNIEKDFNIQVQGYRTSPSRFNQNK TTILGYLIKL
2952	9132	A	2994	3	379	AYPSLVRGTAAPAGAAPPDPAAPVPPP PPPPLEPTTASPGRMNANN*LPSCTR AP/GWGLESPTGGTHCLPGEHSSA GLGPAPPEVAGCTLPEAPTRRGMQA GRPQSWWRASHSQVPLSVTP
2953	9133	A	2995	1	226	RPPGVKGLGPPGPPG*NPFFFKNPKLT PGYGPGLQFPPLWGVREN/CLLPRG PKMAGPWVPPPPFKPGGKSGPPF
2954	9134	A	2996	1	265	VQWRNLGSVEAPPFGCK*VSLCNLLS SWDYRHAPPRPANF*FLVETGFHHV GQAGLELLTS/DPPASASQSAGITGMS HCAEPLNWK
2955	9135	A	2997	424	310	TLWGPYEDLRNSQKSLDICKMLPNTH MLYTYGV*WRDFGSLQPPPPSFK*FS CLSISS*DYRHPLCLANF*FLVEMG FHHVGQAGFLELLTSGDPPASASQS AGITGLSHCAWPKPRTF
2956	9136	A	2998	1	289	SSKLECGGVSAHSSLHPGSSDSPAS APQVTDITGMHHHAWLIFVFLVETG LCHVQGAGLGTDL*VIQPAFGLPKV LGLPGVSRLSPATVQYF
2957	9137	A	2999	10	408	ELVGSKLTNKHITGVPEREEREKVV NLFE*VMAENFPNLMKGMNLYTLN*I YTLNKL*VA*TORNPQHRIHIIKLLKG KDKERILEAVGEEKGVSNKESRI*VMA DFSTETMEARGQ*NDLKIIVPESGKTH

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2958	9138	A	3000	2	160	PKLANFAFLVEMGFHHVVGQSG*LL TSGDLPALASQASARITGMYSYRAQSPFI
2959	9139	A	3001	1	301	FFFFLRRSLDSVAQAGVQWHDLSL QRPFPFGFK*FSCLLSSWDYRHPPC PANFFVFFFF**RWGFTVLARMISIS*P RDPPTSASQAGITCLVFSE
2960	9140	A	3002	1	370	CDGVLLCPTQAGVQWCDLGLSLQALP PRFKRFSCLSLSSWD*/PPGPA/NFV FVEMGFHHVVQAGLKLLT/S/GDPPA SASQAGITGVSHGAWPFI SYGFKFLF SILSFQHEGLPLAFLVGHVY
2961	9141	A	3003	2	437	FFFLRRSFVAVQAQGVQWHDLSNPQ PPPPGFKQYFCLSLSSWDYRHLPT SPANLFLYF**RWGFTMLGQAGLELL TSSDPPASASQAGITGVSHRAQPTNP TTLDFPKHIPQQQASDDLHSLCCL HSPRLSILRHQEWY
2962	9142	A	3004	2	416	ECVFCFKVTRTGELVLVFGSWFFFLR WSLALGRPGWKFKWRNLSLQPPPP RFKQFSCLSLPEISWDRHPPHPANF *LLVET/GFPHVQAGLELLTSGDPP ASAFQASAGITGVSHRAWPE*VFSFNLI SMKMDINV
2963	9143	A	3005	1	335	HRTCRIHFKLK/IKSKIKCFKKAKEKK ALYLGRGAKIRITCDVSSASRQARIE*R EVFKVL R*/KA/QPRILYPEKLFKSEG EMNFLKQTKIKFVASRPALEMLKH VLQRGGN
2964	9144	A	3006	63	272	DYIQRTQTQNVQVFVKALSTKNIPGC HGFPGEFHQ/Y*REELTPILLKLPFIT EEDGINPSKLLQOQQG
2965	9145	A	3007	3	403	YIFSRRDLVLCFPGWSQTPGLKQASAR LCLPKCWDRREPPQLAED/SYQFR ASLKMTL*GIVSMV/PLLQKLLWMCK AQGNQAEGBTGVALPEREASSWSC LQLFPFVDEPCSSFKRRESEKEPSPNG FPNLNI
2966	9146	A	3008	25	628	VFIVNKTI*ISDMKYHIFHMMMQYLY YGGTESMEIPTDILELLSAATLLHLD ALQRHCEILCSQTLMSESAVENTKYKA KIHNAPELALFCBGFLLKHKMALLEQ MPFGSSSTAAAAAKCRAWIHCRTCTP WQSACTLFPSPPGCETGGGSGRQQL WRCQGPCCRMVVGPLGARFTGLFP PPPPDVPPVTGQLTLISSALELFVQSL MGKGEM
2967	9147	A	3009	2	273	FHSGLGLGLWAPEYPYKSPLELIPKPP FQHLIWGFKTDLGFQKTGSGALQEA KEGGPFEGLNPFGIHQHVHTLPKGL *VPCRIYGGPG
2968	9148	A	3010	2	193	IGSPHPPEPNPARFPKPL/SPRCPLGFP SSSPKG*GSS/PSSPPKAFPVSKFETK PPCFSPFRLKPPPA*NPVFPRLG

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2969	9149	A	3011	2	314	CFCFSETGSRSVTQAGVQ*YNLGSLQ PPPSRFSQFLCISLPSSWHYRRAPPHPT DFCVF\QTGVSSRWPGWS*TPDLKCS ACLLPKCWIDYRHEPRPAQIISF
2970	9150	A	3012	598	196	FFFPQSPYSVVQAGVQWHDPSLSQPP LPGFK*FSCLSLPSSWDHRRAKKPPCP ASF*FLVETGFHHVGGGGLLEISSD LPASASQNAIGITGKSHYAHPCFYIFW MLQLLSYSE
2971	9151	A	3013	3	213	SFGKYGFFHFPLYFYHFLVLYFKTM/ CVWSIAKVC DY*IFMDNYSFNIKYP SL SFLNAAFYSICFCLRSIG
2972	9152	A	3014	75	208	CRCNRLGTVAHACNSSLTGGLGGWT A*VREFRTSLGNVVKPCLY
2973	9153	A	3015	4	317	PGSHSVTQARVQWHDHGSQP*PPRL R*FSLSLPSSYDYRRAPRLA\NFSIE TGFYHVAIQAGLELLCLRDPPASHSQ SAGITGVSHGAWPILSLSLSLITYK
2974	9154	A	3016	2	360	IDHVLFIHSSIDRHLGFFYLSALVNSA AMCICLSLCFQFFGLMQRSFPAPT*S SSSSSSSSSSSSSSSSSSSCN/SLKGHA NSRTEGLRANPCLLTPHQLPPQWVPS NTPASRTPSPAQ
2975	9155	A	3017	2	324	PNGGGVWVGATPRGG*SHLSSSKR RFGLLAPVKSSFFPSSSVSIKMYVW *QK/ROIDQGTDPHKKYSHLIFDKGTK TFQWRKNSLFNKWCQNN*ISTGKMK NLDD
2976	9156	A	3018	1	140	GAYHHT*IFVFLVEMGFHHVGGHGL DLL/NLVIHPWLPKVLGLQA
2977	9157	A	3019	1	684	SFFLSFLLSFFPFLSFSFLPSFLSLSL FLSFFLRWSFTLAAQAGVQWCDLGL LLFSMLVRLVLNSQPRVIRLRWPPKV LV*A/YCTRLRMHFSIF*CLNNGLS*E KNNLNHTSHQK*ILGGF*HFQKLL/CS LETGSHSVA*AGVQWYDGHSLQ*TP GLI*SSGLSLSKYWNKYHAPRPA*V GF*NPFKGGCSGSHLLIPILGKPRWG GFTLRPGSFEDQPGAT
2978	9158	A	3020	1	507	GRLWSKAIFAGYKRGRLNRQREHTAL LKIBGVYARDETEFYLGKRCAYVYK AKNWD*PLGVFSLSRPRTHTPWAPV PALSHPVDFHMGISPPFVLCFHGHLS ETFLGYLKWQ\NTVTPGGKPNKTRVI WGKVTRAHGNSGMVRAKFRSNLPA KAIGHRIIRVMLYPSRI
2979	9159	A	3021	1	327	ETESHCGSQGVQVQRDLGWSQPLPP RFKQFS*LLGLPSSGDYRYAPSRPANFF VVVVVFLVETGFCCHIGAGLKRLLASC DSPALASQARITGMSHCAQPGYILR EPQRK

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WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-6180, a mature protein coding portion of SEQ ID NO: 1-6180, an active domain of SEQ ID NO: 1-6180, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively
25 associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - 30 (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-6180.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- 5 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample under stringent hybridization conditions with
- 10 nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

- 20 a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

25 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- 30 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

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a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-6180, a mature protein coding portion of SEQ ID NO: 1-6180, an active domain of SEQ ID NO: 1-6180, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-6180, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 6181-12360, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-6180.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

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27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 5 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.